

AAACATTACT TTACGCTATC AATGGTGGTA AAGATGAAAA TCTGGTGCAC AAGTTGGTCC 120
 AAACCTTCGAA GGTATTAACA GCGAAGTATT AGAATATGCC GAnATTCAAG AATTTGATCA 180
 5 AATGATGGAT TGGCCTAGCA GGTGTTTACA TTAACTCATT AAATGTATnA CTACATGCAC 240
 GATAATACAG CTATGACGAT TGAATGGATT ACATGTACAG AATTGTCCGn CCATGGCACA 300
 GGA 303

10 (2) INFORMATION FOR SEQ ID NO: 3090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3090:

CTTTCGTTAA AGGGGCATAT TCATATAATG GATGGTCATT AATAATAATT CCTGCCGCAT 60
 GTGTAGATGT ATGTCTTGGT AAACCTTCTA ACTTTTTTACA AATACTGAAC CAGCGTTCAT 120
 25 GTCGATGGTT TCGATGTACA AACTCTTTAA AATCGTCAAT TTGATATGCT TCATCAAGTG 180
 TAATTCCTAA TktATGTGGG ATTAACTTG GAAATTCAT TtAATGTAAC TTCATCAAAC 240
 CCCATAATTC TTCCAACATC TCTAGCAACT GCTCTTGCAA GCAGATGACC GAAAGTCACA 300
 30 ATTCCAGATA CATGTAGCTC GCCATATTTT TCTTGACGT ACTGAATGGA CCCTTTCTCG 360
 GnGTGTATCT GCAAGGTCAA TTTTCATtnt CAGGCATGGT 400

35 (2) INFORMATION FOR SEQ ID NO: 3091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3091:

45 TTGTTTTTTC ACGTTCAATn ATTATCTTCA ACTTGTGACT ACAGATTTTA AAATGGAATT 60
 TACAAGTATC TTCTTCAATA TTTTGCATCA TGATATCAAA TAATTCATGA CCTTCATTTT 120
 GATAGTCACG TAATGGATTT TGTTGTGCAT AAGAACGTAA GTGAATACCT TGACGTAATT 180
 50 GGATCCATGT GTCGATATGG ATCAGTCCAA TGGCTATCAA TAGAACGAGG TAAAATCATA 240
 CGCTCAAACC CCATCCATTG GnTCCTCTAA GATACCTTTT GACCTTGGAT AGCnGCTCAA 300

(2) INFORMATION FOR SEQ ID NO: 3092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3092:

CGACACCTCA ATAATCATAT CGTAATGTTT AACTTTTCCT GATTAAATG TAATTTTCATT	60
TCCATTGATA GCATTAAATTT CCTCATTTAA ACGGTATGGA ATCTCCCGCT TATCTAATTC	120
ATCAAGTATA GGTGATTCA GTCGGCATCC ATAATTTATT TATCTTATCA GATCGATGAA	180
TAAAGTAGGG TGTAACCAC GTTCCATAAA GATTTCAAGG AACTCCAATG GAACATAACC	240
TGCACCTACC ACCAATACTT TATCCACTTG GATTGGCTTG GAGGAATGGT CGGATAGGCA	300
TCCAGGGCCT CAAAATTCC nAGGGGAAAn GGTAATATCC ACCTTCCAAG GCCAAGGGCC	360
AATTGGCACC TGGCCACCCA GGGnCTTAA AAGGGGTAA	400

(2) INFORMATION FOR SEQ ID NO: 3093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3093:

TTATACCCGn CAAATTCATA AATATAGTnC CTTTTCAATA GATTGATATG TATGTCTAAA	60
TGTATCGATT AACTTTGCTA ATGCTGCTC ATCTAATGGT CGGTCTGCTA ATTTTAAAAA	120
TGTATTCTTC AATAGGTATT CCCATATAAT GCGTTATTTT TTTAGATGAT GGTTCCGTTA	180
AGCCACATGC TTAAATGCA CTTTGTGTG CTACTTCACC ACATTTTTTC GTGTCTGCCA	240
ACGTACCATC AA	252

(2) INFORMATION FOR SEQ ID NO: 3094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATCTATTAA TAATGAAGAA AAAATTGTAC TAGCACGTAG ACGGTTAATA AAGTTCGATA 60
 AAGATATCAG TATTCCATAT ATTCTAAAGC AAGCATATTC TAAAGAAAAA AACAGTTATA 120
 5 TATTCTTGTT AGAATCACAA GATTCTATAT TCTTTTCACA AACACCTGnn CAATTAATAA 180
 AGGTCAATAA TAAATCTAT CGACTAAAGC TGTGCAGGTC AATTAAACGG TCACAAGTGA 240
 GGCCGAGGTA CAAAAAATGT TGAGCATTTC AAAGTATAAA CTTATCGACA CnTTGTGTG 300
 10 CAGTTTTTCAT GTTT 314

(2) INFORMATION FOR SEQ ID NO: 3095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3095:

GGTGAGGCGG CATTGAGAAA AAATGCTGAA GTAATCGAAG CTGTATCGCA GTCTTGTTTG 60
 25 ACAACAGGAT TTTGTTTATG GTGCCAATTA GCTTTTTCAA CGTATTTAGA AAATGCCACG 120
 CAGCCACATT TAAATAATGA CTTACAACAG CAATTGTTAT CTGGAGAAAT ATTAGGTGCT 180
 ACCGGATTGT CTAATCCCGA TGAAGTCATT TAATGGATTT AGAAnAAGTT GGACCCTTTG 240
 30 AAACACCACC TTAATGTTGG ATGGGACCAA TTGGGTGGTC CAGTGGGAnC GTAATGCCCA 300
 GCTGTAAAGT nATAATCCAA GGAAAGACCC AT 332

(2) INFORMATION FOR SEQ ID NO: 3096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3096:

TTTATGCATA CGCGCACTCA TCACACTACC GACAACAACA TCATCTTTTC GAGCATATCT 60
 ACTTAACAAC GTCATGACCA CACTCATAAA GAACATAAAA TCAGTAATTT GATGCTTTTC 120
 TACATACTTT TGAAGTAGCT GTCTCATTG TTGATTCATG TAAATGACAT CATGCTCCAT 180
 50 TTGTCGGTTT AATAATTGGT CTAACATAnT CTGTCGGGTA AGCCTAAAAT AGGGTACTTC 240
 ATCCTTGAAT TGAGGATACC CATATTGGTC CTAAGGTTTC GTCCATATCC ACGGATGGCG 300

ATTTAAGGTT GGATAAAGGT GCCGTTAAGG ATCCAATTCC

400

(2) INFORMATION FOR SEQ ID NO: 3097:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3097:

15	ACTCTGGTCC TTCTGCATAA CTGCCGTAAA TAATTCACCT TCATCACACG CTGTACCTAC	60
	CAATAATCCC nCACGATATA CGTGAATTC GAGGTGTACG GTAGAAATAC TTCACCAATG	120
	ATGCACTTAC AATTTTAAAT AGATTTTAA GACCTTGTG GTTTTGTACA ATTAATGTGA	180
20	CATGACTAGG TCTTGCACGT TTATATGCAT CTTCACTACT GAGTTTTTTG GTTGATTnC	240
	GTTATGATTT AATACGGCTA ATTCT	265

(2) INFORMATION FOR SEQ ID NO: 3098:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3098:

35	CTAATGTATC AGTTTGGCAT GAATTCTTTT GCATCTTTCA ATAATTGTTG TGATCTTTTT	60
	TAGTCACATC ATCAATTTTC TTATCTTCGT ATAATGCTTT TTCAATCTTA TGATATCCTG	120
	ACCATTCTTT TTCCTTTTTC TCTTCTTTCA TATCTGCAAG CGGGCATCCA ATTTTAGGAT	180
40	CCTAAATCTC CCAAATGCTT CTGAACTGGT CAGAGCGTCA TAATACATAC GACTTTTGGG	240
	TATACGCTTT TnCTTGGGCA TACATTATTT CAATCGTTTA CAAATTTTTC TGACCTTTTA	300
	AAATCATTTnA CTGTCAnCAG A	321

(2) INFORMATION FOR SEQ ID NO: 3099:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

ATCCGCAATC TGAGAAACAT CATCTTCGAG TTGTTGGAGG GTTCCAATTT TCAAGTCATA 60
 AATCAGATGA TGAATGGCGA GAGTTTGGAC TAAATCATT TGTATTACCT GAAGTTTTAA 120
 5 TTTCAACTGA TAATAATGGG ACATTTTTAA CTTATACAGT TAAAAGGGAA AGTTTTACTG 180
 TTGAGGCATT GAACGATTTA ATGGATTGTT CAACAATATA TCGGACATAG AGTGGACGAC 240
 CAATGGGGGA ATACCAGAAT GAGATATTAT AAAACA 276

10 (2) INFORMATION FOR SEQ ID NO: 3100:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3100:

GTCATTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAC nTAAAACGTT 60
 GTTAATAACT TGCCGGGCTT CACACTAATC AATGGTGGCA AAGTAGGGGT GTTTAGTCAT 120
 25 GCAAnGTTAA GAACGAGCAT GTTTGATTCA GGAGATAATA AGAACTATCA AGCACAAGGA 180
 AATGTAATTG CATTAGGTCG TATACATGGA ACTGATACGA ATGACCATGG CGATTTT 237

30 (2) INFORMATION FOR SEQ ID NO: 3101:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3101:

40 nCGATATAAC AAGGTTGTTA GACTTAAAGG TGGCGATCCA GCGATATTTG GTCGTGTGCA 60
 AGAAGAAGTC GACATACTAA ATGAACATCA TATTGCGTTT GAAATTGTAC CAGGGGTGAC 120
 ATCAGCGAGC GcNAGTTTGG CTACTATGCA GACAGGTTTG ACAATGCGTA CAGTTGCTAA 180
 45 AAGTGTGGAC ATTTTCTACA GGTCACTTT AAAGATTCAG AAGAAAATGA AGTGGGATGG 240
 TCCATTCTT AAGT 254

50 (2) INFORMATION FOR SEQ ID NO: 3102:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3102:

CAATCACTCA TGTAGTAATT GATACCTAAG AAGTCGTTTA AATCTTTGGC TGCATCTAAA 60
 5 ATGGCATAAT CTTCATnTGT AATGTTTAAT TTACCGCCAn TAACAGATAA GATATGTTGC 120
 ACACCTTCCA TCGTTTCACG AGTAATACTT ACCTAAATAT GTTGCACTA AGATGAATTT 180
 10 ATTATGGATG GATATCTTCT AAATTCTGCT GCACGGGACA TCTTCAGGAT TTGGATGGTT 240

(2) INFORMATION FOR SEQ ID NO: 3103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3103:

GTTGTAACT TCAATTGTTT AAATAAATAA CACATATCAT TGGAGGTGAA TTGATATGCC 60
 AGATTCAATC ACAATTATAG ATGAAAACAA AGTGGTTGAT GTTGTATTAA TTGCAGGTAG 120
 25 AATTTTACTT GAATCAGGTG CTGAnACATA TCGAGTTGAA GATACAATGA ACCGTATCGC 180
 ACATAGTTAT GGTCTTCATA ATACATATAG TTTTGTCACT TCAACTGCAA TTATTTTTTC 240
 ATTAAACGAT CGAACAAGTA CAAGATTAAT TCGTTACAAG AGCGTACAAC AGATTTAGGG 300
 30 AAnGTGCGAA TAAGCGGGGn AATTCTTC 328

(2) INFORMATION FOR SEQ ID NO: 3104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3104:

TTTTGCTTTG TCGCCTAATA ATCTAATGTT CGTGGAACCG nAACCAGAGA TATTACAAAT 60
 45 ACATCATCGA CTAATCGCAG GTGTCGTTGA TTCTCCAACA ACATGTGCCT GTTTGCCGAG 120
 CTGATTTAAG GCGGCATTGC AAACTATTTC GCCACGAATC CTGAACGTCC TTTGCCAGCT 180
 ACAAATATAT GTTCAGCATG TAGTATTTTG GATGCAAAGT TGAAAACCTCA TCCGCTTCAA 240
 50 CATGTGACAA AGTCACTTTA ATCnA 265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3105:

ACTAGTAGAG TATCTAATGG TGATTTAATC ATTATTACTG CTGGTGTACC AACTGGTGAA 60
 ACTGGAAC TAATATGAT GAAAATCCAC CTAnTTGGTG ACGAAATTGC TAATGGTCAA 120
 nGTATTGGAC GTGGATCAGT TGTTGGTACT ACATTATTGC TGAAACTGTT AAAGATTTAG 180
 AAGGTAAAGA TTTATCTGAC AAATTGATCG TTACTAACTC AATCGATGAA ACGTTTGTGA 240
 CCT 243

(2) INFORMATION FOR SEQ ID NO: 3106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3106:

CTATTGCGTT TGGGTAAATC TAAAGCAGGC GTAnATTATC AAAGTTTGGG ATATGCAACC 60
 AGCACACTTA TTCTTTATGA TTGCAGCGCC AGAAGTGGnG CCCAAACACA TCTAGATGCT 120
 TTACTAAGTT GTCTGGTATT TTAATGGATG AAAATGTACG TGAGAAATTA TTACATGCTT 180
 CATCACCTGG AAGAAGTACT AGCGATCATA GATGAGGCTG GATGATGAAG TGGA 234

(2) INFORMATION FOR SEQ ID NO: 3107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3107:

TTTTGAAGCG GCATAATCAT GAAGAATAGG ACTAGGATTA TAACCTTGTA CAGATGATGT 60
 CGTTGTAATT GACGCACCCG GTTTTAAATA TTCCAATGAC TTTTGAAC GTCCAAAATA 120
 GCGGnTAGAn ATTCTTTTCA AATGTTTCTG TAAATGCCTC AGTTGTAAAT CCATGAATAT 180

(2) INFORMATION FOR SEQ ID NO: 3108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3108:

CTTTAAGTTA CGTTCGGCTT TGATTAAAGT AAAACGTGGT ACTGTTTCCT ATGACAAGAG 60
 TCTAATTGGA TACAATGTAA ACAAATGGT GnATTTGTAT TATAGATAAT AAACATTcGn 120
 TATACATTCA ACATATCGAT GACCACTTGG ATTAAGCAAC GTAATATCAT TCGTACTGCT 180
 CAAGAAATGA CAAACGAAAT ACGAGAAAAT TTTGAGTCAT ACACGTCATT TAGAATGAAT 240
 AGTATTATGC AAGTACT 257

(2) INFORMATION FOR SEQ ID NO: 3109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3109:

CTTAAAGCCA AGTCGATCTG CTAATTTTGC AAGTGTCACT GAATCTTGCA ATGCCTTTTG 60
 TGCATCCTTA CCTTCATCTA TTAAGGCATA GTCTAATACG CTTAATTTAA CCAATCCGTC 120
 ATCTCCAAAC TTATCCTGTC ATGTCAAACC GACATAACAT TTGTAGCGTT CTTAATACCA 180
 TTCCCTCTGC ATATACCCAC GTATATGATA ACGTnTTTCA nTTAACT 227

(2) INFORMATION FOR SEQ ID NO: 3110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3110:

TTTCTTCATC GTTTGTGAGA AAGAGGTATT TTTAATTGGG AAAncAGGTA AAAAGGATGG 60
 AAGTACATAA AAAGAGCAAT GCTTGGGCAT TATTCcNCTT GTTATTATTT GTGGCGTTGT 120

GATAACGTAA TTGTGCGTTA TTAATGAATC GAAAAGAATC ATTGCTAAAA AGTGAGTCTC 240
 CGAAAGGCGG CCTTCAACTG TTAAGAGTGA TTTATTGCAG GCTTCAATCG CGAAATGGTG 300
 5 CnAAGCGCGT ATTAGCACTA GCCGAA 326

(2) INFORMATION FOR SEQ ID NO: 3111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3111:

CTACGGCGCC TTGCATCTTT CCCAACAATT AACCCCAACT CTATTAGCAC AGATTTATCA 60
 20 ATTGATTCAT AAGCTTCATC AAAGGGTGAA CTAACATGCA TTAACGCTTC TTTAATATCA 120
 ATTAAGTCGG CATGTTCAAC ACCAATTTTC CCTTTTTTAT TTTTAGCTTT TTCTCTATCA 180
 ATATACGCAT GTTTAACACC TTTGACATGT TCAGTAAATT GTGACTTCCT nAATTTTTTA 240
 25 TCCTCCCTTG GTGnnGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG 300

(2) INFORMATION FOR SEQ ID NO: 3112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3112:

TTATTGTTAA CACAAGGnTT CGAACAAGGT TGGTTTAGTA CATTTTCAAT CATTTGTCTG 60
 40 AGCATTTTTA TCATCACTAC GTTGATATTC ATCATCATCG AACGTCGACA TGAAGTACCT 120
 TTTATTGATT TCTCAGTATT ACGCAACCGT CCGTTCATTG GTGCATTTTT AAATAACTTT 180
 GTTTTAAATA GCGGTCTAGC GTAACAGGGT CTTTCATATA TGCTCAACAC ACCTGGTTTA 240
 45 TCGCGCGCAA TCGGACTGTT ACATGCCAAT GCCATGGGCG TTCGAGATCG TTAGTGAAAG 300
 CACATAGTTC GGGCAATGAG CCACATGGTC GTGTCCGTCA CGCACACATA TAGCAGCT 358

(2) INFORMATION FOR SEQ ID NO: 3113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3113:

TCGGTCTTGA AAACCGACAG GGGACTTAAC GGCTCGCGGG GGTTCGAATC CCTCTTCCTC 60
 5 CGCCATCAAT ATTTATATTA AATTCTATAT ATAATGAAGG TAAGTGCTCA AATTTTGAGT 120
 ATTTACCTTT TTTATTTGTC TTTGAATGGC TCGTAATTTT TGATAATAGA AATGATAAGG 180
 CATTGAGATT GGAAGGGCAT TTGGCTTGTG CAAATACAT AGCAAAATGT CGTTGTTGTT 240
 10 TTGTGATAGA T 251

(2) INFORMATION FOR SEQ ID NO: 3114:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 6591 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3114:

TTTAAGTGAA TTnCTTTGGG TTACAGAAwT TTCAACAACT TTAAAGCACG TATAATGATG 60
 25 ATTTTCAGCT TGTACAAAGG AGAAAAAAG AAGACAACCA AGCCCAATAA TGGACTGGCC 120
 GCCTAATAAT AAAAActCTA AAAGTTGTAT TTtAAAAATA GTTCTTTAA TATATACCC 180
 ACCACATTG GTGGAGaACC GTTAAACAAT GCATAGTTGC TTAACCTCCA ATATTGAACT 240
 30 CATCATTACA ATTTGACATA GAGTCTATTA AAGCGTGTGC CATTGAGTC CACTTTTATT 300
 TGTATTGTAT AGAGAGAAAT AAAAAGAAAC CTtGTTTTAC AAGGTTTCTA ATACGTTATG 360
 TTATGTAAAT AACAGTTAAT TATACCGGTG GTCGGGGTCG AACCGACACT CCACAAGTGG 420
 35 AACGgGATTT TGAGTCCCGC GCGTCTGCCA ATTCCGCCAC ACCGGCTTAA TGGTAAACAA 480
 AAAACTTCCC TTTGGAAGCA ATTATGGAGC GGAAGATAGG ATTTACACCT ATACCTCGTT 540
 CCGGAAGGA ACGTGTtCTA AAAGTTGAAC TACTCCCGCA AATATTAAAT TATGGAGCGG 600
 40 AAGATAGGAT TTACACCTAT ACCTCATTCC AGGAAGGAAT GTATTCTAAG AGTTGAAATA 660
 CTCCCGCATT ATTATTAAAT TATGGAGCGG AAGATAGGAT TTGCACCTAT ACCTCGTTCC 720
 45 GGGAAGGAAC GTGTTCTAAA AGTTGAACTA CTCCCGCATA AACCTGGAGG CGGCAACCGG 780
 ATTTGAACCG GTGATAAAGG TTTTGCAGAC CTCTGCCTTA CCACTTGGCT ATGCCGCCAA 840
 TAACTGGGCT AGCTGGATTc GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG 900
 50 CTTGGCTATA GCCCATTAAAT AATAAGGGCG GCTGAAGGGG ATCGAACCTT CGAATGTCGG 960

55

	CGAACCCACA CCAAAGGTTT TGGAGACCTC TATTCTACCG TTGAACTATG CCCCTATTAA	1080
	AAATAATAAA TGGAGGGGGG CAGATTTCGAA CTGCCGAACC CGAAGGAGCG GATTTACAGT	1140
5	CCGCCGCGTT TAGCCACTTC GCTACCCCTC CATAAATGGT GCCGGCCAGA GGAAGTTGAAC	1200
	CCCCAACCTA CTGATTACAA GTCAGTTGCT CTACCAATTG AGCTAGGCCG GCTAAGAAAT	1260
	GGTTCAGGAC AGAGTCGAAC TGCCGACACA TGGAGCTTCA ATCCATTGCT CTACCAACTG	1320
10	AGCTACTGAA CCATAATAAA AATGTAATGA TGGCGGTCTC GACGGAATC GAACCCGCGA	1380
	TCTCCTGCGT GACAGGCAGG CGTGTTAACC GCTACACTAC GAGACCTATA AAATATTGCG	1440
	GGAGGCGGAT TTGAACCACC GACCTTCGGG TTATGAGCCC GACGAGCTAC CGAAGTCTC	1500
15	CATCCCGCGA TAATAAAAAA TAATGGCGGA GGAAGAGGGA TTCGAACCCC CGCGCCCCGT	1560
	TAAGGCCCTG TCGGTTTTCA AGACCGATCC CTTAGCCGG ACTTGGGTAT TCCTCCATTA	1620
20	TTATAGGTAA ATCGCTATTA ATTATAAAAT TAAATGGCGG TCTCGACGGG AATCGAACCC	1680
	GCGATCTCCT GCGTGACAGG CAGGCGTGTT AACCGCTACA CTACGAGACC ATTAGTAAAA	1740
	CGGAGGAAGA GGGATTTCGAA CCCCCGCGAG CCGTTAAGCC CCTGTGGTT TTCAAGACCG	1800
25	ATCCCTTCAG CCGGACTTGG GTATTCTCCT AAAATTATAT GGaCtTGCAG GACTCGAACC	1860
	TGCGACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA	1920
	ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG	1980
30	AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAG TAATATGGTG	2040
	GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAAA GCAGGCGCTC TCCCAGCTGA	2100
	GCTAAGCCCC CATAATAATT ACAGTATATC GGAAGACAG GATTGGAACC TGCGACCCCT	2160
35	TGGTCCCAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA	2220
	TAGGAGTCGA ACCCATAACC TCTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG	2280
40	GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAcGgTGATC	2340
	ACTCACCGCA GGATTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA	2400
	AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TGTATTCTAC	2460
45	CGCTGAAC TAATTCTGATA TGCGGGTGAA GGGAGTCGAA CCCCCACgCC GTAAGGCGCT	2520
	aGATCCTAAG TCTAGTGCGT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG	2580
	GATTGGAACC TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGA GCTAATGGCT	2640
50	CTTCCATGGT GCCGGCCAGA GGAAGTTGAAC CCCCCAACCTA CTGATTACAA GTCAGTTGCT	2700
	CTACCAATTG AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA	2760
55		

	AAACTGCCTG	GCAACGTTCT	ACTCTAGCGG	AACGTAAGTT	CGACTACCAT	CGACGCTAAG	2880
	GAGCTTAACT	TCTGTGTTTCG	GCATGGGAAC	AGGTGTGACC	TCCTTGCTAT	AGTCACCAGA	2940
5	CATATGAATG	TAATTTATAC	ATTCAAAAC	AGATAGTAAG	TAAAAGtGnA	TTTTgctCGC	3000
	AAAACATTTA	TTTTGATTAA	GTCTTCGATC	GATTAGTATT	CGTCAGCTCC	aCATGTCACC	3060
	ATGCTTCCAC	CTCGAACCTA	TTAACCTCAT	CATCTTTGAG	GGATCTTATA	ACCGAAGTTG	3120
10	GGAAATCTCA	TCTTGAGGGG	GGCTTCATGC	TThAgGATtT	TCAGCACTTA	TCCCGTCCAC	3180
	ACATAGCTAC	CCAGCTTATG	CnTTGGCACG	ACAActGGTA	CACCAGAGGT	ATGTCCATCC	3240
15	CGGTCTCTC	GTAATAAGGA	CAGCTCCTCT	CAAAATTTCCT	ACGCCCCACGA	CGGATAGGGA	3300
	cCGAACTTcT	aCGACGTTCT	GAACCCAGnC	sTGTACCGCT	TTaATGGGCG	AACAGCCCCAA	3360
	CCCTTGGGAC	CGACTACAGC	CCCAGGATGC	GATGAGCCGA	CATCGAGGTG	CCAAACCTCC	3420
20	CCGTCGATGT	GAACCTTTGG	GGGAGATAAG	CCTGTTATCC	CCGGGGTAGC	TTTTATCCGT	3480
	TGAGCGATGG	CCCTTCCATG	CGGAACCACC	GGATCACTAA	GTCCGTCTTT	CGACCTTGCT	3540
	CGACTTGTA	GTCTCGCAGT	CAAGCTCCCT	TATGCCTTTA	CACTCTATGA	ATGATTTCCA	3600
25	ACCATTCTGA	GGGAACCTTT	GAGCGCCTCC	GTTACCTTTT	AGGAGGCGAC	CGCCCCAGTC	3660
	AAACTGCCCC	CCTGACACTG	TCTCCCACCA	CGATAAGTGG	TGCGGGTTAG	AAAGCCAACA	3720
	CAGCTAGGGT	AGTATCCCAC	CAGCGCCTCC	ACGTAAGcTA	GCGCTCACGT	TTCAAAGGCT	3780
30	CCTACCTATC	CTGTACAAGC	TGTGCCGAAT	TTCAATATCA	GGCTACAGTA	AAGCTCCACG	3840
	GGGTCTTTCC	GTCTGTGCGC	GGGTAACCTG	CATCTTCACA	GGTACTATGA	TTTCACCGAG	3900
35	TCTCTCGTTG	AGACAGTGCC	CAAATCGTTA	CGCCTTTCGT	GCGGGTCGGA	ACTTACCCGA	3960
	CAAGGAATTT	CGCTACCTTA	GGACCGTTAT	AGTTACGGCC	GCCGTTTACT	GGGGCTTCGA	4020
	TTCGTAGCTT	CGCAGAAncT	ArCcACTCCT	CTTAACCTTC	CAGCACCGGG	CAGGCGTCag	4080
40	cCctATACAT	CACCTTACGG	TTTAGCAGAG	ACCTGTGTTT	TTGATAAACA	GTGCTTGGG	4140
	CCTATTCACT	GCGGCTCTTC	TGGGCGTTAA	CCCTAAAGAG	CACCCCTTCT	CCCGAAGTTA	4200
	CGGGGTCATT	TTGCCGAGTT	CCTTAACGAG	AGTTCGCTCG	CTCACCTTAG	AATTCTCATC	4260
45	TTGACTACCT	GTGTGCGTTT	GCGGTACGGG	CACCTATTTT	CTATCTAGAG	GCTTTTCTCG	4320
	GCAGTGTGAA	ATCAACGACT	CGAAGACACA	ATGTCTTCTC	CCCATCACAG	CTCAGCCTTA	4380
	ACGAGTACCG	GATTTGCCTA	ATACTCAGCC	TTACTGCTTA	GACGTGCAAT	CCAATCGCAC	4440
50	GCTTCGCCTA	TCCTACTGCG	TCCCCCATC	GATTAAACG	ATTATAGGTG	GTACAGGAAT	4500
	ATCAACCTGT	TATCCATCGC	CTACGCCTGT	CGGCCTCAGC	TTAGGACCCG	ACTAACCAG	4560
55							

	TTCGCTACTC	ACACCGGCAT	TCTCACTTCT	AAGCGCTCCA	CATGTCCTTA	CGATCATGCT	4680
	TCAACGCCCT	TAGAACGCTC	TCCTACCATT	GTCCAAAGGA	CAATCCACAG	CTTCGGTAAT	4740
5	ATGTTTAGCC	CCGGTACATT	TTCGGCGCAG	TGCTACTCGA	CTAGTGAGCT	ATTACGCACT	4800
	CTTTAAATGA	TGGCTGCTTC	TAAGCCAACA	TCCTAGTTGT	CTGGGCAACG	CCACATCCTT	4860
	TTCCACTTAA	CATATATTTT	GGGACCTTAG	CTGGTGGTCT	GGGCTGTTTC	CCTTTCGAAC	4920
10	ACGGACCTTA	TCACCCATGT	TCTGACTCCC	AAGTTAAATT	AATTGGCATT	CGGAGTTTGT	4980
	CTGAATTCCG	TAACCCGAGA	GGGGCCCCCTC	GTCCAAACAG	TGCTCTACCT	CCAATAATCA	5040
15	TCACTTGAGG	CTAGCCCTAA	AGCTATTTTCG	GAGAGAACCA	GCTATYTCCA	GGTTCGATTG	5100
	GAATTTCTCC	GCTACCCTCA	GTTTCATCCGC	TCACTTTTCA	ACGTAAGTCG	GTTTCGGTCTT	5160
	CCATTCAAGT	TTACCTGAAC	TTCAACCTGA	CCAAGGGTAG	ATCACCTGGT	TTCGGGTCTA	5220
20	CGACCAAATA	CTAAACGCCC	TATTCAGACT	CGCTTTCGCT	ACGGCTCCAC	ATTTACTGCT	5280
	TAACCTTGCA	TCAAATCGTA	ACTCGCCGGT	TCATTCTACA	AAAGGCACGC	CATCACCCAT	5340
	TAACGGGCTC	TGACTACTTG	TAAGCACACG	GTTTCAGGTT	CTATTTCACT	CCCCTTCCGG	5400
25	GGTGCTTTTC	ACCTTTCCCT	CACGGTACTG	GTTCACTATC	GGTCACTAGA	GAGTATTTAG	5460
	CCTTAGGAGA	TGGTCCTCCC	AGATTCCGAC	GGAATTTTAC	GTGCTCCGTC	GTACTIONGGA	5520
	TCCACTCAAG	AGAGACAACA	TTTTCGACTA	CAGGATTATT	ACCTTCTTTG	ATTCATCTTT	5580
30	CCAGATGATT	CGTCTAATGT	CGTCCTTTGT	AACTCCGTAT	AGAGTGTCCT	ACAACCCCAA	5640
	CAAGCAAGCT	TGTTGGTTTG	GGCTCTTCCC	GTTTCGCTCG	CCGCTACTAA	GGGAATCGAA	5700
35	TTTTCTTTCT	CTTCCTCCGG	GTACTAAGAT	GTTTCAGTTC	TCCGGGTGTG	CCTTCTGATA	5760
	TGCTATGTAT	TCACATATCG	ATAACATGAC	ATAACTCATG	CTGGGTTTCC	CCATTCCGAA	5820
	ATCTCTGGAT	CAAAGCTTAC	TTACAGCTCC	CCAAAGCATA	TCGTCGTTAG	TAACGTCCTT	5880
40	CATCGGCTTC	TAGTGCCAAG	GCATCCACCG	TGCGCCCTTA	ATAACTTAAT	CTATGTTTCC	5940
	ATCCTACAGG	AAACGCGTTA	TTAATCTTGT	gaGTGTTCTT	TCGAACACTA	GCGATTATTT	6000
	CTTATGAATT	CAAGCTTATT	TAAAACTCTT	TATTCACCTG	GTTTTGCTTG	GTAAATCTA	6060
45	TATTTTACTT	ACTTATCTAG	TTTTCAATGT	ACAATTTCTT	TTTAGTCAAG	CGCTCGCATA	6120
	AGCAATATCA	CTTTAACCAA	AAAATATTTG	AATGTTAAAT	AAACATTCAA	AACTGAATAC	6180
50	AATATGTCAC	ATTATTCCGC	ATCTTCTGAA	GAAGATGTTT	CGAATATATC	CTTAGAAAGG	6240
	AGGTGATCCA	GCCGCACCTT	CCGATACGGC	TACCTTGTTA	CGACTTCACC	CCAATCATTT	6300
	GTCCACCTT	CGACGGCTAG	CTCCTAAAAG	GTTACTCCAC	CGGCTTCGGG	TGTTACAAAC	6360
55							

ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC AATCCGAACT 6480
 GAGAACAACT TTATGGGATT TGCTTGaCCT CGCgGGTTTCG cTkGCCTTTG TAATGTCCAA 6540
 5 TGTAGCACGT GTGTAGCCAA ATCCATAAGG GGCATTATGA TTTGACGCAT C 6591

(2) INFORMATION FOR SEQ ID NO: 3115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3115:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC 60
 20 GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTGGAATAA AGGTAGCATA 120
 TGTAATTGTT TGTGTTTACG TATTTCTGGT GTAAGTTCCG TGAAACCAAT GTCTATATTC 180
 CCATTAATAC GCTATTATAA TGTGTCAGGT CCAATAAGCC CCGGATGACA TGTGTATCCA 240
 25 TTTGGAAATG GAACCGTTGG GAAAGTGGGA ATAACATGGG GGAACGTCAa TCCCCnCCAA 300
 GCCCATnGAG GTACCTTTAA TTTTA 325

(2) INFORMATION FOR SEQ ID NO: 3116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3116:

CCGnTTGAGT TCGGTGGCGA CATGATTGAT TTTGTAAGTA AGTATGATGC AACATGGGCT 60
 GnTTTACCTA CTAAATTTGA GGCGGGTACT CCATTAATTG CTCAAGCATT GGGCTTGTCa 120
 GAAGCTATTC GCTATTTAGA ACGCATAGGT TTTGATGCAA TTCATAAATA TGAACAAGAA 180
 45 TTAACGATAT ATGCTTATGA GCAAATGTCT G 211

(2) INFORMATION FOR SEQ ID NO: 3117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3117:

AACGThTTTT GAAATGATTG CGGCGATGTT GCGACAGTT AAAGTAGGTG GCATCTTATA 60
 5 TACCTATCGA TATTGATTTT CCGAATAAAC GACAAGGTGC AATTTTGGAG GATGCTAAAG 120
 TAACTGCAGT CATGTCTTAC GGC GTT G n A A TTGAAACGAC ATTACCAGTC ATTCAATTGG 180
 AAAATGCTAA AGGCTTTTGT GAATCAAAGG 210

(2) INFORMATION FOR SEQ ID NO: 3118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3118:

TTAATTGATC CTAGCTTGGT TTGCCTCTGT CACTTTATCA TTGATATTTT GGACAGTTGG 60
 GTTGCCATTC AACACTTGAT TAATTTAGT TAACTTTTGA CGCGCTGCTT GTAATTTTTG 120
 25 GGTGTACGCA TTTAACGAAC G n C GTCATA CCTGTTGTAT CCGTTGGTTG ATTAATGCTT 180
 GTTCTAAATT GCGTTTCCAA GTTT n AAGCG GCGCTTATCT GGTGT 225

(2) INFORMATION FOR SEQ ID NO: 3119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3119:

CCAACATGAT GCTAGTTTGA TTAAGTTTCT TCTAAACAGA CTTCAAACGG CATGGTTTAG 60
 CATATCCTAT TAAGGTTGAA TCGCGTTAAC AGCACATAGG AAATGCTGTT AGGCGATGCA 120
 GAGTGCATGATT AGGCAGCTAC TGGAAAATTA TTGTTTGATT TGCCAGTTAT TATAAACTGT 180
 45 GTGTGTTGAT G n C G A n C A C A C C C C T C C G A A C A C G C T T A A T G 222

(2) INFORMATION FOR SEQ ID NO: 3120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3120:

CGGCGATTAT ATTAAAAAGC CAATTACAGA ATGTAGTGGT AATGAAATAT GCCAAGAATG 60
 5 GCTGTATCAC TTAGGTGTAT CAACTGACAA AATTGAAGAC TTAGCAAAAC ATGCATCTAA 120
 TACGATTCCT GTTTATATGC CATATATCAC ATCTTATTTT ATGGACGCGT GCTATCGGCG 180
 nACAGACCTT TTAGTCGTGC CCGGCATGCA ATCTnCAGGA ACTTAGGCAT TTATTGGTGA 240
 10 ACTTTG 246

(2) INFORMATION FOR SEQ ID NO: 3121:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3121:

CAAATACCTT CTCAACnTTG TACTTTTTTGC CTAATTGAGC TGCACGAATT GCTGCAACGT 60
 25 ATCCACCAGG ACCTGCTCCG ATTACTATAG aTCTGTTTCA ATTGGGAAAT CTCCAACCTAC 120
 CATGTTTTAC CCCTCCATTA ATAATAATTC TGGATTATTT AATAAACGTT TAATGTGATT 180
 CATTGCATTT TGGCCAGTTG CACCATCAAT TTGTCTGTGG TCAAAGCTTA ATGakrtGCT 240
 30 AATACTGGTG CTGCAACAAT TTCTCCATCT TTAACGATAG GTTTTTGAGC AATACGGCCA 300
 ATTCCTAAGA TTGCTACTTC TGGGGTGATT GATAACTGGA GTGAACCATT GTCCACCAGC 360
 35 TGAACCGATA TTAGTGATTG TGCATnnGCA CCTTnCATT 399

(2) INFORMATION FOR SEQ ID NO: 3122:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3122:

CAGACAAACC TTGAATTATT CTACCTATAA TTAAAAATGC TGGCAAAGGT GTAATGATGA 60
 TGAGTAATGA ACCTACAACA TTTAATATCA ATCCTACATA AGTAATTTTG ACGCGACCAA 120
 50 ATTTATCAGC AACATCACCA GCACCTACGT AAACCAACCA GCCAATAAGG CAGATAAGCT 180
 AACAGCGTAT TATCGTTCCC ACGTCACTAC TATATGTGGA TGTATGGGAC ACAGTTTACC 240

G

301

(2) INFORMATION FOR SEQ ID NO: 3123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3123:

GGAGCAAATT TATCATCTGC AACTAGACAC AACATCACTG TTATTAGTAC CGGGTTATAT	60
AGTAGCAGTC ATTGTTGGTG CACTAAGTGG TAAATCGGC GAATATCTGA ATTCAAACC	120
AGCGATTATC ACAGCAATTA TTTAATAGCA CTGAGCTTGA TTTACCTGCA TTGCAGTAGG	180
TAATCACATT CAATCTCGTC ATTCTATGAT ATCTTGCACT AGCTTGCTTA ATGATGCACT	240
TACTACGAGC ATAAACATGT CTATATGCAG GTGCATGTTA TATTATATAT GGCGACGAGA	300
TCGTnGGCCn ACGTTAACTA ATTnGCATG TCTAGCCTCG AATTATATAG TAGGAGCGTA	360
GTACGCCAAC TGCCACGA	378

(2) INFORMATION FOR SEQ ID NO: 3124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3124:

TATTGCAAGA AATGAACTGC TGATTTTTAT AGTTTTAGTG GTCATAAAAT GCTTGGACCA	60
ACAGGTATTG GCGTATTATT TGGTAAACGT GAGTTACTAC AAAAAATGGA ACCGATTGAG	120
TTCCGTGGCG ACATGATTGA TTTTGTAAGT AAGTATGATG CAACATGGGn CTGATTTACC	180
TACTAAATTT GCAGGTCGGG TTACTIONCAT TGAATTGGCT CCAAGCCAAT TGGGGCTTGG	240
CnAGGAAGCC T	251

(2) INFORMATION FOR SEQ ID NO: 3125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3125:

CGGTTAAGTA ATACAGGATG TTCTCTAATT ACTTCTTCCA ATACGTCCCA AACTTCATCA 60
 5 TCCATACGTT CGATTTTACT CTTCGCATTT TTAATGTTAG TTGCAATTTT CAGTTGAACT 120
 AATTCTTTCA TTACGAATGG TTAAATAGT TCAAGTGCCA TTTCTTTTGG TAAACCACAT 180
 TGGTACCATT TCCAnGCTTG GACCCnACGG CAATTACCTG AACGGTCCCG GAA 233

(2) INFORMATION FOR SEQ ID NO: 3126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3126:

AATAGATTCC CGGGATTCAA AAGCATGGAT GTTGTACCTT GTTGTnCTCC ATTGGCAATG 60
 TACTACCTGA TGTCAAGATG AATTATCCAT CACTTTGTTG ACGTGCTTTA TTTTACAGCA 120
 25 TCAATTTGAT CCAATCGAAA TACCAGATAA CTTAGACTGT GTCCCAGTAA AATAACGATC 180
 AATCACATCA TGAGACAAGC CAATCGCTTC AAATATTTGT GCCCCTTGAT AACTTTGCAC 240
 TGTCGAAATT CCCATCTTAG CCATTACTTT AATGACACCT TCTGACAATA CATCCGTATA 300
 30 TGTCTTAACA TTATCGACAA CGGTGCCTTG TAACCCTTCT GTCAATGTCA GTTGTTC AAC 360
 TGTACGTTGC GCTAGGTATG GCACAATTGa TTCGCGCCAT ATGCGAGTAA ACA 413

(2) INFORMATION FOR SEQ ID NO: 3127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3127:

GTCGTAAATA CTGAACAAAA ATCACGGCAT ACTGTGCAAA TTTnTGAAGA AGCTCAAAAA 60
 CTATTACAAG CACATCATGC GATTGTAGAA GGATATATCG AATCAGCTTT AGAGCGTGCG 120
 50 TAnATCATCT TCTACATACA TAGGTAATTT TATGGCGATT CCTCATGGAG CATCCTGTAA 180
 AAAGTTTTAC AATCACATGT GCTTATTTT 209

(2) INFORMATION FOR SEQ ID NO: 3128:

(A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3128:

10	TAAATTAATG GAGTTTGGTA CACGTCGTCG CAAGAAATTG ATGCAGTGGG GCGCTAGAGC	60
	TGCTTACATC GGGGGCTTTG ATTCTACAAG TAATGTTAGG GCGGGGAAAT TATTGGGTAT	120
	ACCTGTGTCT GGTACACATG CACATGCATT TGTCCAAACT TATGGAGACC AATATGTTTG	180
15	CCTTCAAAAA ATATGCTGAA AGnC	204

(2) INFORMATION FOR SEQ ID NO: 3129:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 239 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3129:

	GAAATACCAT TAATATAATA GTCGGTAAAT TAAGAAACGT GGTGCGCGAT TCACAACAGA	60
30	AATCTTAATC TATCGAAGTA TCCTGTTTTC TCTGCAACAC CAATACCAAT CATCACTGCT	120
	AGTACTAAGC CTAATGCGGG AACTCTGAGA AATTTTAAAT CGTATTCTTC TTATCATCGT	180
	AAATCCATCT GGCTATTATA TTTTAATATA AnGGTTTGAG CTACCGGATG CTAACGnAC	239

35

(2) INFORMATION FOR SEQ ID NO: 3130:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 259 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3130:

45	ATCACAATAA ACATTTTAAA ATTCTTGTTA TCATAATCAT TAAAAGGTAT TAACCTTAAT	60
	AATATATTCT CTnGTCTCAA CCTTAATCGT ATACTTCAGA CGTCTGTTTG TAGACAATAA	120
50	AGTCATTACG GTCTTCATAT GTCATCAnAT GTTTATCATG ATATGATGAT ATATAATCGG	180
	TATATACTGT AGATATTACA CATAAGAGAG GATATAATAT GAAAAGGTCA TTAAGATGTG	240
	CTGAGAGCTG TGTATCAGT	259

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3131:

TGTGCCTGCC ATTTTGCAAT ATCTTCATCT TCACGTGGTA ATGCACAAAA ATGTTTACCA 60
 TGTGCATTCA CAACTTCAAA AATATGTTGA CATGTGATGT TACTTGATCA TCACGCGTTG 120
 CCATGGTATG CAAGTGCTGC GATAAATCTG CGGCACCTTC GACTATCATG CTAACCTTCG 180
 CTTGThnATA TCGCAATGGC ATACCCCTTC AACATCTTCT ATCATGG 227

(2) INFORMATION FOR SEQ ID NO: 3132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3132:

ATCGCAGTGA TGThnATCATC TGCTGCTGTA GChnTAGCAGG TTCAATTTCA TTTATCGGAT 60
 TAATGGGTCC GCATATTGCC AAACGTATCG TTGGACCACG TCACCAGTTG TATTAACCAA 120
 TTGCCATTTT AGTAGGGGCA TGTATACTTG TAATAGCTGA TACAATTGGC CAAAATTGTA 180
 TTACAACCAG GTGGGGTTCC AGC 203

(2) INFORMATION FOR SEQ ID NO: 3133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3133:

AGCATTTAGT TTAGCGGCAG TAGCTGCAGA TGCACCGGTA GCTGGCACAG ATATTACGAA 60
 TCAnTTGACG AATGTCACAG TTGGTATTGA CTCTGGTACG ACTGTGTATC CGGACCAAGC 120
 AGGTTATGTC AAACTGAATT ATGGTTTTChn AGTGCTAATT CTGCTGTAA GGTGACACAT 180
 TCAAAATACT GTACCTAAGG A 201

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3134:

CATTTGTAAC TGTTATTGTT TATAACTTCT GTGTGAAGCG CAATATTACA ATTAAAATGC 60
 CGAAAGAGGT ACCGnCGAAT ATTTCAACAAG TATTTAGGAC TTAATTCCAT TTTCAGCGGT 120
 AATCATCATT CTTTATGCAT TAGGATTTnG TCAATCGCAA CCAGCTTTAA ATCAAAATGT 180
 AGCGGAGGTA TTTTAAAATT ATTCGGT 207

(2) INFORMATION FOR SEQ ID NO: 3135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3135:

AACACCTTTA GGTCGTGCAG GTCAACCTGT TGAGTTATGT GGTACTTATG TGCTATTAGC 60
 GTCAGAAGGA ATCAAGTTAT ACAACCGGAC AAGTnTTCGG TGTTAGCGGT GGAGTGCAAn 120
 TAGGTTAGGT TTGTATGAGC TTTTAATTGA GCACCATAAT GTTAATTTAG TTACTTCAAT 180
 CCATTAAATT AAATGAATTG GTG 203

(2) INFORMATION FOR SEQ ID NO: 3136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3136:

CACATCCAAT GCAnTCTACT AAATCAGACA CACCACAATC TCCAACCATA AnACAAGCAC 60
 AAACAGATAT GACTCCTAAA TATGAGGTTT AAGAGCGTAT TATACAAAAC CGAGTTTTGA 120
 ATTTGAAAGC AGTTTGGATT TATGCTCAAA CCATGGACGA CGGTTAGGTT TATGATGTTA 180
 TTCCAATAGG TTCACTATAA ATAGCTTAGT T 211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3137:

ATTGGGAAAT GTTCCCCCAC CACCTACAAT TTGTGAATAC AAACAATACG TATTGCAATG 60
 GACTTTACCT GGGCTTACCA AGTGAATGTA TACGTCACGT ATGATACGAT TGTAGTTGnA 120
 AAATAATGCG AACAGAAAAT CGTTATAAGT ACAAATAATA CAGGTGACTC AACTCCTGCT 180
 TTTAGATTAA CAAATCTCCA ACCGATACAA TGAGTGCTTG CAACATACCA AGCATTATAA 240
 AGAATCCTGC CTTACCTAAG 260

(2) INFORMATION FOR SEQ ID NO: 3138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3138:

CATAAGCAAT TAATGACTTC GTTAATTGCG AAAGTGTATC TTTTGTGATTA TCATTGCGCTT 60
 TTGCATCTTC AAGCTTTCTC ACATCTGATT TGACAGCAAT ACTTTCACCTA TTATCTTCAA 120
 GCGATAATTT CTTAACTGCA CTTACCACTT GCTCAATTGC TTCTGCTAT TGTCATTCTGA 180
 TATCGGAGTA GTAGGAAGTG CnGAATTCGG CA 212

(2) INFORMATION FOR SEQ ID NO: 3139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3139:

TATTGGTTTT TATGCGAATA TGGATAATAA AAGGTCTCAC GACATCATTG ATAAATCGCT 60
 TGAATGTTG CGACGCTTAG ATCACAGGGG CGGGGTCGGC GCAGATGGCA TCACTGGTGA 120
 TGGCGCAGGT ATTATGACTG AAATACCTTT TGCATTTTTC AAACAACATG TAACGGAGGA 180

GCACCTGTTA GAAAAGAAGG GAAATTACCT CGTGAAGTCA TTCGTTATGA GTATGACCTA 300
 GAATATGGTA CAAATGTTTT AACAAATGGCA CAAAGATGCA ATTGAAACCA GGTnCAACGT 360
 5 GTGTTAnTAC AGG 373

(2) INFORMATION FOR SEQ ID NO: 3140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3140:

AGCCTTATAA TAAAGTGCCT TTCATAGCAA TAAGTTGTGT CCATTGACCT ATTACATTTT 60
 20 TCGTTTTGTA CATTAAATAT AAGAAATACG GTGCACCAAT AATTGCTACG ACAATACCTG 120
 CTGGAACCCC CACCTGGTTG TAATACCATT TTGGCCATTT GTATCAGCTA TAACCAAGTA 180
 ACCnTGCCCC AACTAAAATG GCATTGGGTA AAACCACnTG 220

(2) INFORMATION FOR SEQ ID NO: 3141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3141:

GAGGAGCAGC ACAACCAAAT ACACAACCAG CTGGACAAGG TGATCAAGCT GATCCGAATA 60
 ACGCTGCACA ACACAACCTG GAAATCAAGC AACACCGGCA AACCAAGCAG GTCAAGGnAA 120
 40 TAACCAAGCA ACACCTAATA ATAATGCAAC ACCGGCAAAT CAAACACAGC CAGCGAT 177

(2) INFORMATION FOR SEQ ID NO: 3142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3142:

CTTTTTTAGC ATTTGGTTTA ACAACnGGT GTTGCAAGTAT CCCCACTTAA GGTCTGTATA 60

ATTTTCATTTT TATGTTTCCTC GATAACTTGT ATTGCTGCTT GTTTTCCTCC ATCTGTCAAT 180
 CCATCATTTG ATTGAGAGAA nCAG 204

(2) INFORMATION FOR SEQ ID NO: 3143:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3143:

GTGATGCCAT ATAAATTGGC AATAATGGCA CAAGTACTGT CAGTCCAGCA ATCGCTATAA 60
 ACTGACTGAG CCATAAAATG CGAAAGTTAC TGCGCCATAT AGACTGATTA ATCATATGTC 120
 ACCATTGGAT TTGGTACGGT AGTTAAACCT GAAGGCATAC TACCCTCCAC CCACTTATTC 180
 AACGTTGGAT nATAGGCAAT GGGTAATTAA AAATTTTGTT TTTGAAATGG GCCCACGGGC 240
 TTGTTTTAAT CAAAATTAAA AAATTGTGGT nCTTGGACC 279

(2) INFORMATION FOR SEQ ID NO: 3144:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 514 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3144:

TGACTTAATC AAAGCATTG ATCAAAACAC CAGAATACCA TTATTCTTTA ATATGTTGTA 60
 CAGTAAACTC TnTATTATTT GTTGCTGTTG GATCCATTGT TCGTCTTTCA ACAAAAACnT 120
 GACCCAGAAT GAAGTCCGAT AGAGTCAACA AAGCtATAGT ATTTGTAACC ATCTTTTAGT 180
 TGATaAATGC CACGCGCATC TGTTATTGCG TCATTTTTAG GTACAAATTG AATTTkGAGA 240
 TTTCTCaCaT TATCAGGTAC TTAAATAAAA CGCAAAGTTG GACCGnCTTC AACAGTCTTT 300
 TCAGCAATCG TATCATTAGT ATCAGCATTT TTGATAATAA CATTTGTTGC GCCTTGACCG 360
 TTTTITAGTAG TCATTGTATT AAATCAAGGT TAATTCAGAA TTCGGATTTA CTGTTAATGC 420
 TTTCTCGATA CCATTAAAAT CGCCATGGTC ATTCTGATCA GTTCCAGTAT ACGGCCTAAT 480
 GCAATACATT TGCCTGTGCr TGATAGTnCT TATT 514

(2) INFORMATION FOR SEQ ID NO: 3145:

- (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3145:

10 ATTCAGACTT TGCATGTGGA ATGGCCACGT TCATGCCAAT AGCTGTCGTA CTCCCATTTC 60
 ACGTTCTAGT ATTGCATTTT TTAAATGCGA TGTGTGCTCT ACATAACGGC AAATTTTAAG 120
 TTTTATGAAT CAACATATCC AATGGCTTCG GTTTCGAGAC ATGTCCGTGG ATTCAGTAAT 180
 15 TAACCATAGT TTGGTTGGAT CAAAACCAT GAGnAGGGTT TAATGGAGGA TGTnGAATGG 240
 TTCnCCGGTG GTTAATCCTA CATGGTCCAC CCTCCTGGTA ACCATGGTGG TGGTAATAAC 300
 CC 302

20

(2) INFORMATION FOR SEQ ID NO: 3146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3146:

30 CAGGAATAGG ATCATTTGCA TCCATAGCTT CACTTATTTT TTCAGAAGCT AGCGTACAAT 60
 CATTTAAATC TACGCCACCT TCTTTATCAA TAGAGATTCT AAGAAAATGA TCTCTACCCT 120
 35 CTTTGACCAT ATTCAACGTC TACAAGTTCC AAAATTCAAG GTCTTCCCAT AATTGGGTTT 180
 AACCAATCCA CTTTCTACCT GGTTCCGGT AAATTTTAC CTCCATACCA GGGnCCCTCC 240
 CCTTTTTTGG GCCAAATAG GAAAAAnGAG GCGGGGAAA TCCTCCCCC AATTCnTTC 300
 40 CTGGCCCTGG AGGTTTCCAC CTAAATTTTT TT 332

40

(2) INFORMATION FOR SEQ ID NO: 3147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3147:

50 GAGAGTGTT AACAAAGCAA TAGAAATAAT TAAAAATGCA GATGCAGATG CATCGGCGAA 60

55

ChCCAACAAA TGCAGAAGTT GCTGAATTCC AAATGTAACG ATACCTGCCC ATGAGCGATG 180

TGCTCAGAAT GATCAGAGCT AATG 204

(2) INFORMATION FOR SEQ ID NO: 3148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3148:

CAACCGGGAC AGGTGGGGTT ATTGGACGTT ATTTTGGCC TTTGGATTTT AAGATATTGG 60

TCGAAAAGAG ATTACATAAA ATTGTGGCCA AATGCGGATT GCATATTATT GTAACGCCGn 120

CTATTGCATT GTTGATTGTT AGGnCTATTA ACTATCTGGA TCTGTATGCC ATTAGCCAGG 180

TTTTGTTTCA GACAGTTTAG TTTCAGTAGT TAACGGA 217

(2) INFORMATION FOR SEQ ID NO: 3149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3149:

CTATTATTAT ATTCCGCGGT GTACGTATAT GTGCTACGTT ATCTTCGTTA ATTGTACCGA 60

TTATGGCTAT CATTTACATT GGTATGGTTT TAGTAATATT GCTATTTAAT TTAGATCAAA 120

TTGTTCTTAT GATAGGTCAC GATTATTAAn AGTGCATTTG GTCATCGAAC AAGT 174

(2) INFORMATION FOR SEQ ID NO: 3150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3150:

GGGACCGAAT TGACTTCAGC ATTACCAGCA AATTGATTAA TnTTGTGGGC TGGTATTGGC 60

TCTGGCGGTA CCATTTACAG GTACCGCAGC TTATTAAAGC AACATCACGG GCAATGTTAT 120

A

181

(2) INFORMATION FOR SEQ ID NO: 3151:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3151:

GTTTTAATTG AGCGACATAC TCTTCTGTGA GCTCTGCTAC TTTTAAAAT AGAGCGATTG 60
 ACATCAAACA TAACTGCTAA ACGCTCAACG TCTGCCTTCG TAATGGCTTT TGTAGAAATT 120
 CTAATAAAT AATTCGAAT GCTATCATTG GTTGThTCAA CAGCTTGATG CT 172

(2) INFORMATION FOR SEQ ID NO: 3152:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3152:

ATGGACGTTG AGACATTTAT AAGCGATATA GATTTCGCAT GTTGCAATTA TTAAACCTAA 60
 TAATGGTAAA CGACAAGTGT GACTGTACTT GGACTTTAAT GAAGGTAGTA ATCAGAATGG 120
 AAATCAACCA AAAGTAGGTA TTTGAAThTT GGGAATAATG AGACATAGCG AGAGTGATA 180
 TGCAATACGA CAGTACThTA AATTAAGAG 209

(2) INFORMATION FOR SEQ ID NO: 3153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3153:

TTCTCACAAA GCGCTCAGTT GAAGTAAATC CACCTGGACA ATCCAAATGT ACCTGCTTCA 60
 TTGCCTAAAG GTTCAATCGT TAnACCTTCC AATAAATTG CTGTTGCTGG ATAAGGAGAA 120
 ATTATTGGTA TATTGTCTTA AATTACTATG ATGCCAATTT AAGGTCTGGA TGAT 174

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3154:

```

10  GGATCACATC GTTCATTTAC ACAATCTATT AATATTCAAT GGCACAATAT AGTGTTTATG      60
    GCATTACGGA TATGATTTAG TAGCnCACCA TTATTAACCG ATCTCTATCT GTTAAAAGGA      120
    15  ACTTAAGAGC AATGTTTTCG CATCATCATT TTATGTTGCG TCTTTGCACG AGTTTTGCGA      180
    AACTTTACAA TATTTGTTGC GGATGATTAT TTAACTTTTC GAGAATGTTG ATGGCACAGT      240
    CCACTATAnC AATCAGTATC GCAATGG      267
  
```

(2) INFORMATION FOR SEQ ID NO: 3155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 490 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3155:

```

30  AATTAAAAAT CAAGCAACTG CTGCAAAAAT GCAAGATCAA ACTGTTCTCTC AAGAAGCAAA      60
    TTCTCAAGTA GATAATAAAA CAACGAATGA TGCTAATAGC ATAGCAACAA ACAGTGAGCT      120
    35  TAAAAATTCT CAAACATTAG ATTTACCACA ATCATCACCA CAAACGATTT CCAATGCGCA      180
    AGGAACTAGT AAACCAAGTG TTAGAACGAG AGCTGTACGT GTTtAGCTGT TGCTGAACCG      240
    GTAGTAAATG CTGCTGATGC TAAAGGTACA AATGTAAATG ATAAAGTTAC GGCAAGTAAT      300
    40  TTCAAGTTAG AAAAGACTAC ATTTGACCCT AATCAAAGTG GTAACACATT TATGGCGGCA      360
    AATTTTACAG TGACAGATAA gTGAAAyCAG GGgATTATTT TmCacGAgTT ACCAGATatT      420
    TACTGGTAAT GGAGACGTGG GATTATTCTA ATTCAAnATAA TACGATGCCA ATTGCAGACA      480
    45  TTAAAAGTAC      490
  
```

(2) INFORMATION FOR SEQ ID NO: 3156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3156:

CCTTCAGTAC CTTGTAATAG TTANTTAAAT GTTCCGATCA TCGTGTAGTG TGATTCATCA 60
 5 TACCGGCCTT TTCAATTGAA TACGATCTAA ACCGTTTCGT CAGGTGCTAG TAAGTTACCT 120
 TCGCCACCTA AATAAGAAGT TCACTCGTTA CGATTTTTTC AGATAGCATC ATTGGTGGAT 180
 TCGTAACTTG TGCAACAGCT GTTTAAGTAT TAATAGTGAT TCGGTCGTCT TCACATGCAT 240
 10 TGGCGCACAA TCCnTGCACC GT 262

(2) INFORMATION FOR SEQ ID NO: 3157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3157:

ATGGTAAAAA TTGCACTATC TGCTCGGGAA ACGATTTTGC ATAACCTATT GTTAATTTTT 60
 25 TACCTGTTGA TTTAGCTGTA TCTGnCCATT TTTGAGCTT CTGCTGTCGT TTTAGCCATT 120
 GGGTTTTTCAC ACATCACATG TTTACCAGCA TGCAACCCTG GCTACAGTAA 170

(2) INFORMATION FOR SEQ ID NO: 3158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3158:

CCAGGCAGAG GAGCAGCACA CCAATACACA ACCAGCTGGA CAAGTGATCA GCTGATCCGA 60
 40 ATAACGTGCA CAAGACAACC TGGAATCAAG CAACACCGGC AACCAAGCAG GTCAAGGAAT 120
 ACCAAGCAAC ACTAATATAA TGCACACCGG CAAATCAACA CAGCAGCGAA TGTCCAGCAG 180
 45 CAGCGAACCA GCAGCACTGT AGCAGCAACG ACAACTCAGn CCAATGTAGC ATATGGTGAG 240
 GCAGTTTATA GACATACATT GTGnCCCTGCA TTCACAGTGG ATAGCAGGTC CACTGTACTG 300
 TACAGTAAGT An 312

(2) INFORMATION FOR SEQ ID NO: 3159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3159:

AATCACATCA AAAACTTCAA TTGTTTACGT TGGCAACTAA CTTTATGTTA GAACGCACAC 60
AATATCTAAT GTTTAAAATC TATCGTCGCA AGATGCTTCC TGrTAATTAT CAGTGCCATT 120
TTCGATTGGG TTATACAATC TAGTAATCGC ATGATAATTT AATGCTACAA G 171

(2) INFORMATION FOR SEQ ID NO: 3160:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3160:

CTTGTTTCATT TAATCCATAT AGTATACGAC GATGTACTGG TTTTAAACCG TCACGAACAT 60
CTGGCAATGC ACGAGCAACG ATAACACTCA TCGCATAATC TAAAAATGAT TCACGCATTT 120
CACTGGTAAT ATTTCTGTTCA TTAATCnTGA TTGAGGGAAT TCCGCCCATC CAGAnGTCCC 180
CCCTCCAAAG TTCAGTTCCA CAGGGGCTAG A 211

30

(2) INFORMATION FOR SEQ ID NO: 3161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3161:

GCACAGGTAG CGGTAGTGGC GGTCTATGA TGACTTTGGT AATCTAAAGC AAAATGTACC 60
ATAATAATAA ACGTCGTTTC GTTCTCTGA TGTAGCAGGG GCAGTGAAGA AACAAGATTA 120
TTGAATTGTT GATTCTTGA AGATATAAAA ATTCAAGAAT GGGTCTAGGA TTCCTAAGGT 180
GTCTTCTTTT GGGCTCAGTA CGTAAACATA TTGTAGAGCG TGCAGTGAGT GGCGCACCAT 240
CTCTTTTGGG TCAGnTTTGG AGTTTTGTTT GTCGGCTGTC GGATTnTCGT ATGTAGGAAC 300
GGCTGTTTAC TTrCGTGGAT G 321

50

(2) INFORMATION FOR SEQ ID NO: 3162:

55

(A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3162:

10 AACATTTGAG CAATATCAAG AAACATTAGA GTATATTTTA TCCCATCATG TAACTCGTAA 60
 TACAGCAATT ATTGCTTTGG GTGGTGGTGC ACTGGTGATT TTGCTGGGTT TATTGCGGCG 120
 ACACTTTTAC GAGGCGTGCA CTTTATACAA GTGCCAnCG 159

15 (2) INFORMATION FOR SEQ ID NO: 3163:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3163:

25 GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGAC AAGTCTTACG GCATCTTCTA 60
 TTTTAAAGCT TGAAATTTAA CAAATCATAA GCCGTATGAA TATTTAAATA TGCCACCATG 120
 ATTGAATGGC CCCTTTCTAT TAGTTAnGTT TTGTGCG 157

30

(2) INFORMATION FOR SEQ ID NO: 3164:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3164:

40

TATAAAAATA TAACGCGGAC AAAAAAGTGA GTTATTACTG ACAAAGTATn TGAGATTGTA 60
 ACAGGATATA TGAAGCAATA TCAGTTGATC CAACTGTCAT AGGTATTTCA TCAGCAGGnG 120
 45 TTGTTGATGA ACAAAAAGCG AAATTGTATA GCAGGCCAAC ATTCCGATTA TAAAGGTATA 180
 ATTTTAAGGA TTATTAAAAT CATGTCTCTT ATGTCA 216

(2) INFORMATION FOR SEQ ID NO: 3165:

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3165:

5 AGAAACACTT CTATTGAATC GTCTTACTGC TGTTCCTCTAT TTATAACACT TCGTATTGAA 60
 TGAATTCATT ATGCCTATTT GACACATTAT TGAAGTTTTC CTAATGCCTG GATCCTTTAT 120
 ACGTTACGGC TTCGTGCTAT GTTTTGGTAC ATAAAGCTTT GACATATCGA nATTC 175

10 (2) INFORMATION FOR SEQ ID NO: 3166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3166:

ACTGTTACAA CAAATTAAAA ATACAACAAG CGAGATATAG TTATTGTTGC TGGAnTGTAC 60
 CAAGTAGTAT TCCAAGCGAT GCTATGGCAA ATTGCACAAA TTACAGCACA GACAGGTGCT 120
 25 AAATTAGTAG TCGACGCTGA AAAAGAATTG GGCTGAAAGT 160

(2) INFORMATION FOR SEQ ID NO: 3167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3167:

TGTGGGGGAA ACCTGCACAG CAAAACTAA AGCTTATCGA TACATCTAAA CATTGTATTA 60
 40 TAAATCAGT GCATCCTAGT CCACTGTCTG CATATAGAGG ATTCTTTGGA TCAAAACCGT 120
 ATTCCAAAGC GAATGCCTAT TTAGCGTCAG TAGGnA 156

(2) INFORMATION FOR SEQ ID NO: 3168:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3168:

55

GTGGCGAGAA ATACCGCAAG CATAAAGATA TCTTTGATCC AACTTACCAA CAGATCAACG 120

GAAAAGTACC AGGTAACCAG GAATCAAGAT CCAGACACAG GAAAAGTGAT CGAG 174

5 (2) INFORMATION FOR SEQ ID NO: 3169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3169:

TCAAACGGGG TCAATTTCAA ATGGAAAAAT TATACCGCAT CTTCTCCTGA TAACTACGTG 60

ACCTTATCTT CTTTATATTT GCAGACCACG AACATTCAAA CTGCATGCTT GCTCGATTGG 120

20 CAATGTCATA TAACTAGTAA CATGATCATC nCATCAAATT TAGTATGTCA AATGTCCCAA 180

TCATTAATTT GATCGGTGTT GCTCAATTGA TTA 213

(2) INFORMATION FOR SEQ ID NO: 3170:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3170:

35 AAAGCACCTT TTCCTAATGA AAGTTGTGCT ACTGGTATCT GTGTTTGATT TACAAAATCT 60

TCTAATTCTT GATGGAGGTG AAAACTGTTA ATTTTCATGTC CAGTAATGAT GATAGGCTGC 120

TTCGCTTGAT GCAGTTTAGT TGCTAATAAC TCTATATATG TTGATGCATC CGTATATTTA 180

40 GTTGCCGTCA CTTCAAATGG TGTCGGTATC TCAATTTTCAAG AGATTGCGAC ATCGATTGGT 240

AAATGTAAAt GAACTGGGCG TCTTTCGGCG ATTGCTGTAT TAATTAAACG TGGTATTTTCG 300

GTTGTTGCAT TTTCAGGTGT GATATAACCT GTGCACGnTT ATATGTGCAA ACATTTTTTCG 360

45 ATAGTCGTCA AATGTACCnn 380

(2) INFORMATION FOR SEQ ID NO: 3171:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 401 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3171:

5 TAGAAGGTAA GAAGGATCCT ATCGGTGCAA TGGGATATGA TGCGCCAATT GCAGTGTTGA 60
 ACGAGCGACC AGAATCACTA TTTAATTACT TTAAACAGCT GTTTGCACAA GTTACGAATC 120
 CACCAATTGA TCGGTATCGT GAAAAAATCG TAACGwGTGA ACTTTCTTAT TTAGGTGGCG 180
 10 AAGGTAACCTT ACTAGCACCT GACGAAACGG TTTTAGATCG TATTCAATTG AAAAGGCCGG 240
 TATTGAATGA ATCACACTTA GCAGCGATTG ATCAGGAACA TTTTAAAT AACTTATTTA 300
 TCAACGGTAT ATGAAGGGGG ATTTGGGAAG ATGCGTTAGA AGCATTAGGC CGAGAAGCAG 360
 15 TGGAAATGCTG TTAAGCAAGG GCGCTCCAAA TTCCTAGTGG T 401

(2) INFORMATION FOR SEQ ID NO: 3172:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3172:

25 ACATAATTTA AAATAATATT ACATTTGTAA TGGnCACCAA GTAACGTTTC GGTTGCTTGG 60
 30 TGTTTTTTGG TATGAATTAC TTTCTGTAC AAAACAATCT AAAGCGTTCT GTTATGTTTT 120
 ATTAAGATTT AATTACAAAC GGAAACTAAA TGTAATAGAA TAACT 166

(2) INFORMATION FOR SEQ ID NO: 3173:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3173:

40 ATAATGAGAn TGTTGTACGT TATGGTGGTG GAAGTGCTGA TGGTGATTCA GCAGTAAATC 60
 45 CGAAAGACCC AACTCCAGGG ACCGCCGTT GACCCAGAAC CAAGTCCAGA CCCAGAACCA 120
 GAACCAACGA CCAGATACCA GAACCAAGTA CCAGACCCAG 160

(2) INFORMATION FOR SEQ ID NO: 3174:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3174:

CTTTATATAA AGAAGGAATT ACTAAACATA CAGTTAGATT ACTTCATGCA ATCGAATTAG 60
 AACGTTTGAA TTAAAGCCGT AGATTAGGTT TTGAATTATC AACAGCnAAA GAATCACGTA 120
 TTGAACGGGG GTTATTTAGA ACGTGATAAA GAAGGATG 158

(2) INFORMATION FOR SEQ ID NO: 3175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3175:

TATTTGAAGA TGGCTGTGTA CAAAAATCGG TGTTACGTGA TCATGATACT GTCAGAATTT 60
 ATAAACCATG GCTAACAGCA CATCAGCTTT CATTGCCnA GTATGTCGTC AGAGAAGATA 120
 CACCTAATCG CTAATTAATG AGGTTTGGAA ACAT 154

(2) INFORMATION FOR SEQ ID NO: 3176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3176:

AGAAGGTATT TTAGCTCAAT CTCCAGGTCT AAAGGTTGTT ATTCCTTCAG CCCATACGnT 60
 GCGAAAGGTT TATTAATTTT TTCTATTAGA AGTAATGACC CAGTCGTATA CTTAGAGCAT 120
 ATGAAATTGT ATCGTTCATT CCGTGAAGAA GTACCTGAAG AAGAATATAC AATTGACATT 180
 GGTAAGGCTA ATGTGAAAAA AGAAGGTAAT GACATTTCAA TCATCACATA CCGTGCAATG 240
 GTTCAAGAAT CAATGAAAGC TGCAGAAGAA CTTGAAAAAG ATGGTTATTC TGTTGAAGTA 300
 ATTGACTTAC GTACTGTTCA ACCAATCGAT GTTGACACAA TTGTAGCTTC AGTTGAAAAA 360
 CTGGTCGTGC AGTTGTAGTC AAGAAGCACA CGTCAAGCTG GTGTTGGTGC ACAGTTGTAG 420
 CTGAATTAGT GACGTGCATC CCTTCATTAG AAnnCCTATG GAAGAGTGCA CA 472

(2) INFORMATION FOR SEQ ID NO: 3177:

- (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3177:

10 TGAAAGCTGG CGAATACAGT GATTGTCATG ATGCGGATCT AntTGTGTCATC TGTGCTGGTG 60
 CTGCACAAAA ACCTGAGAGA AACACGTTTA GATTTAGTAT CTAAAAACTT GAAAATATTC 120
 AAATCAATTG TTGGTGAAGT AATGGCATCA 150

15 (2) INFORMATION FOR SEQ ID NO: 3178:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3178:

25 TTACTCTATC TTGATTGAC GAAATACTAT TAnGCTAATA TCGATATTTT AAAAACGAGA 60
 TGATGTTCCA AAGCAAGCCA TTTGATGGA CTGCTAATAT TCTTCAGCCA AACGTATCAT 120
 30 TTTACTCGCA TTTGGTGAAA AGAAACGGCT GCTATTACAC ATTTAT 166

(2) INFORMATION FOR SEQ ID NO: 3179:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3179:

40 CTTGACTCT AGAGGATCCC CGCGCTCAAA TTCTAGTGTT AGATGATAGT GGATTAGTTG 60
 45 ATAGCAATGG CTTTGCAATG CCGATGTTAC TCGCAATAAG TCATGTGCAT CAATTACTTA 120
 TTAAAGCAGA TTTACGTATG TCTACAAGTT TAnTTCGCTA AATCTGGTGA 170

(2) INFORMATION FOR SEQ ID NO: 3180:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3180:

AGCTAAGGTT GCChTGGGCG TTGCCCCAnT TGGTTAGTCC AGGTGGTCGC GGTGGCCATC 60
 5 GGTGTATTTCG CCAGGTCCTT CAGCCAGGGT TTTTACTATT ATATCCAGTT GTAGCATTCA 120
 TGATTGGGGC GATTTCGAGAT AGATTCATCA ATGAAATTAA TTTCTGGATT TTATTCGTTG 180
 GTATTATTTT GGTATACAT AAGTATGGTA CATGATAGGC AGATATACAA CATTACAACA 240
 10 TTCATTCTAC TATGCTGGAA ATAACATGAC AGTGATGACA CTACTATCCC CGTCGCA 297

(2) INFORMATION FOR SEQ ID NO: 3181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3181:

CACTAGGTAC CCCAAAACGC CAGAGGAACT TGGTTAAATC GCACTTACTT GGTGGCTCCA 60
 25 ATCAACTGGT ACTTCATAAC GTTTGGCATC TTCGCCACTT CACCACTATT ACTCTTTCCA 120
 CCTAATTGGT TCATGGCTTG TGCTAACGTT TCATGTGCTT CCGCTGAAAT CGATCCATAA 180
 CTCATCGCCC CTGTATTAAA GCGTTTGACA ATGTCACTTA CCGGTTCAAC TTGGTCGATG 240
 30 TCAATCGgTG TACATGCTTT AAATTCAAGT AAATGTCTAA TGTGaTCTGT TCTATTTTTG 300
 TTnCACCGnT TnCAGAGTAT GCTTTAAATT GCGCCATAGT CCATTTTCT 349

(2) INFORMATION FOR SEQ ID NO: 3182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3182:

TACCAACACG TACACCTTCT AAAATAACTG CATTTGCACC GThTTAATAC ATCATCCTCG 60
 TTTATAACCG GTGTAAGCAC TAGGGGGTTC AATCACACCT GCTAATACTG CGCCAGCCCT 120
 ACATGTACAT TTTTACCAGT TGTAGCACG 149

(2) INFORMATION FOR SEQ ID NO: 3183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3183:

GCGGTGCCGG TGTTGCAATT GCGCAGTGG TGTTGGTAGC ATGTGGTCTT TCAATCAATG 60
TTCAATACAC CAGGAGATCC GGAAAAGATG CGTATGAATT TTATGGTAAG TGCACCAGGC 120
ATTACCACAC CACGCAAnAA CATGCAT 147

(2) INFORMATION FOR SEQ ID NO: 3184:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3184:

CAGCGATATG TTGGCGTTGA AAATCTGCAA TTTGTTTATA ATTCTCTGTT AAAGAACGAC 60
TTAAATTGAT AAAAATGGAT ACGATCTCTT GGTAACAGT GACATTTTCT CAATCGGCGT 120
ATGATGTTTG TGGCACCGAC CATCGAGAAC ATGAAAATCT CATGTCCCAC GCTAGTCGnC 180

(2) INFORMATION FOR SEQ ID NO: 3185:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3185:

GGTAAATACG TATTAATCAG ATTAAGATCT GGTGAAGTTC GTATGATCTT ATCTACTTGG 60
CCGTGCTACA ATCGGGnCAA GTTGGTAACC TACAACACGG GTTAGTTAAC GTTGGTAAAG 120
CCGGCACGTT CAAGATGGGA AAGGTATCCG 150

45

(2) INFORMATION FOR SEQ ID NO: 3186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

GAATTTnAGG TGAATCAGAA GATTAACGCT GTTGCCTCCT AAGCTAACAG ATACTGGTTC 60
 GTCAGTTGTC GTTGAAAAAG CGAATGAACA ATTTAATAAA ACCGTAACTC GAGCATTATT 120
 5 AGAGGAAGCT AACCAAAGCA GGTTTA 146

(2) INFORMATION FOR SEQ ID NO: 3187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3187:

AAATTGGCGA GTATGTTGTT ATTGGGTCAG TACTCTGAAA TTAACAATAG nTACGATTGA 60
 20 AAATGGTGTC ATGTATTCAA CAGTCTGTG TTAATGTATG CTAGTCGTGG TGCGAATACT 120
 AAGGTCGGAC CGTTTGGCGA ATTGAGACCA GCGCGCAAT TAGGG 165

(2) INFORMATION FOR SEQ ID NO: 3188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3188:

CAGTTTAGTG GAGACGAATC TAAACGAAAC AAAGCGATTG GACGTGCATC AGTTGTACCA 60
 35 ACATTCTTTG GTGTAAACGn AACCAATTTT ATTTGGTGCC ACCACTAGTT ATTGGAATCC 120
 TGTGTTCTTT ATTCCATTG TATTAGCACC AATTGTTAAC GTATGG 166

(2) INFORMATION FOR SEQ ID NO: 3189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3189:

AACCCTTTAT CTAATCCATT TTCAGTTAAG CGATGACCGC CTGCTAAAAT TTGTGCATCT 60
 GATTCTTTTG CTGCATCAAT ATATGATTGA ATTTTATCTA ATTGATCCTT ACCAGTTTGA 120

(2) INFORMATION FOR SEQ ID NO: 3190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3190:

TCCCCCAAAG GGTTTAAGGG GTTAACCCGG GTTTGGGAAA AATTTTTTAA CCCCCCTTAA 60
 AnTTCCCGGG AAAAAGGAAA CCCGGGTTTT TAAAAAAAC CCGGGGTTCC CAAAATTTT 120
 TTGGGAAAGG GAAAGGAAAA AAGGGTTAAA AAATTTTGG GAAAAACCG GGGCCAnAAA 180
 AAAGGGTTTT TTTCCCCTTA AAAAAAATTT AA 212

(2) INFORMATION FOR SEQ ID NO: 3191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3191:

CTTCACTGAC TTTAGCAATT TCATCACCTT TGCCCCCTAC AACGATAGCT AATGATTTAT 60
 ATTGTAAACT CAnATGACCT TGTGAATAC CTCTGACAC AAGCGCGCGA CATGCTGCAA 120
 AGTTTTGCGC TAAACCAACG GCAGCAAC 148

(2) INFORMATION FOR SEQ ID NO: 3192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3192:

CTGCTAATCC GAAATCTTTT TGGAGTTTTA TTAACCAGC TGCTTCTAAT AGTTTAAGTG 60
 CACGTGCTTG GTTGACACA TCATTGGAA TGACAACTTT AGCnCCATCT TTAACCTTTT 120
 TGACATCTTT AATTTTATCT GCAGAAATAA ATCCATCAGC GATGGCTCTT AAATATATGT 180
 TACGTGATAA TTTCTCGAnA AATGGCTTCC CT 212

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3193:

TCGTGCAGTG GTCTTCTGTT AATTGGTGAA TTTGGATACT GGTATATTC AGCTGCACCG 60
 CAAGCAACTT CTATTGATGG CCAAACTGCC TTTTACCTC AAGCAATGGG TATGGTAGTT 120
 GTTGCAGTCA TTTATGGCTT T 141

(2) INFORMATION FOR SEQ ID NO: 3194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1290 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3194:

AATAACGTTT TGAAAAACGA AGATGTTTTA AATGCCTATA TCCGCGGTCG TGGCGGAATG 60
 GCAGACGCGC TAGGTTGAGG GCCTAGTGGG AGAAATCCCG TGGAGGTTCA AGTCCTCTCG 120
 GCCGCATCAA AATTCTTAAT TTAAATAAGC GGGTGTAGTT TAATGGCAAA ACCTCAGCCT 180
 TCCAAGCTGA TGTGTGGGT TCGATTCCCA TCACCCGCTC CATAGATAAT TTTAATGAAC 240
 ATTGAAAACG GAATGACAAT ATGTCAACGT TAATTCCTAA AACGTAACCTA TAAGTTACAA 300
 ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTATGGAGA GTTTGATCCT 360
 GGCTCAGGAT GAACGCTGGC GGCCTGCCTA ATACATGCAA GTCGAGCGAA CGGACGAGAA 420
 GCTTGCTTCT CTGATGTTAG CGGCGGACGG GTGAGTAACA CGTGGATAAC CTACCTATAA 480
 GACTGGGATA ACTTCGGGAA ACCGGAGCTA ATACCGGATA ATATTTTGAA CCGCATGGTT 540
 CAAAAGTGAA AGACGGTCTT GCTGTCACTT ATAGATGGAT CCGCGCTGCA TTAGCTAGTT 600
 GGTAAGGTAA CGGCTTACCA AGGCAACGAT GCATAGCCGA CCTGAGAGGG TGATCGGCCA 660
 CACTGGAACT GAGACACGGT CCAGACTCCT ACGGGAGGCA GCAGTAGGGA ATCTTCCGCA 720
 ATGGGCGAAA GCCTGACGGA GCAACGCCGC GTGAGTGATG AAGGTCTTCG GATCGTAAAA 780
 CTCTGTTATT AGGGAAGAAC ATATGTGTAA GTAAGTGTGC ACATCTTGAC GGTACCTAAT 840
 CAGAAAGCCA CGGCTAATAC GTGCCAGCAG CCGCGGTAAT ACGTAGGTGG CAAGCGTTAT 900

CGGCTCAACC GTGGAGGGTC ATTGGAACT GGAAGCTTG AGTGCAGAAG AGGAAAGTGG 1020
 AATTCCATGT GTAGCGGTGA AATGCCGAGA GATATGGAGG AACACCACTG GCGAAGGCGA 1080
 5 CTTTCTGGTC TGTAAGTGAC GCTGATGTGC GAAAGCGTGG GGATCAAACA GGATTAGATA 1140
 CCCTGGTAGT CCACGCCGTA AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCCTTAG 1200
 TGCTGGCATA ACGCATTAAG CACTCCGCCT GGGGAGTACG ACCGCAAGGT TGAAACTCAA 1260
 10 AGGAATTGAC GGGGACCCGC ACAAGCGGTG 1290

(2) INFORMATION FOR SEQ ID NO: 3195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3195:

TGGTACAGAG TTATCGCTGG TGGTCCTGTT CGTGCCGTAC TTGAATTATC AGGTATCACT 60
 25 GATATCTTAA GTAAATCATT AGGATCAAAC ACACCAATCA ACATGGTTCG TGCTAACAAT 120
 CGATGGTTTA CnAAACCTTA 140

(2) INFORMATION FOR SEQ ID NO: 3196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3196:

CTATTGGATC AGGAGGCAAC TACGCTTAAG CGCAGACTGC CCATTGAAAC GCCATGCATC 60
 40 GCATTTGTCTG CCTGAAGAAA TGGCATATGA GAGCTTGAAA GTAGCGGCTG ATATTTGTGT 120
 CTTTACCAAC GnTAATATTG TTGTC 145
 45

(2) INFORMATION FOR SEQ ID NO: 3197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TGTCGAGTTG GAATTGGACG ATTGAATATC CCATCTCCAT CACTATCAAA GTATGGGAAT 60
 TGAATTGTTT CTAATTCGTA TCCACCTTCT GTCATTGATA ATGTAGGGTT AATTTTAGAA 120
 5 CCATCTkCTG TTTCTAGTTT TAAGTTCAC TTCTTACCTT CTTCCCAACG TTGACCCATT 180
 GTGCCATTAG GTACTACTAA ACTATCGCTG ATTGCATCAT GAATAACTGG CTTCCATTCh 240
 CCTTGCTCTG TTGTTTGACC TAAGTCACTC GCGCThAAAA ATCGACCCGC TTTATATCCA 300
 10 ThTTCAGCTG 310

(2) INFORMATION FOR SEQ ID NO: 3198:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3198:

20
 25 TGCTTTATTA ATGCATTGGC TAATAATCCA CTTGTACCAC CACCGGCACA AAGTACTAAG 60
 AGGTTTGTTT TGTGATATTT GAAGCTTTAG TGCATCGTCT GATACACCAC TTGCCGCTAA 120
 AATTGAATCA GCTTTThTCG 140

(2) INFORMATION FOR SEQ ID NO: 3199:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3199:

40 TGGTGATTTC AAATCATGAG ACTGGGACAA AATGATGTTT TCATAAAAAT TATTTCGTTG 60
 TTCCACTCTC ATGATTTTTT TGATGAACAT AATTACATGA TTGATTGCAT CATTTGTAA 120
 45 AACCAGTGAT TGCAACCTGC CATTCAChG GAAAATTACC TAATAAGTGG CGTATTTACC 180
 AGTC 184

(2) INFORMATION FOR SEQ ID NO: 3200:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3200:

TTGAGAAGCG TTTAGGAAGT AACGTTTAAC GACGACAGTC GTTCAATGCG ATCAAAATGT 60
 5 TTTAACACAT GAATCGCTCT CGTACTATTC GTGTGTGACA CATGTTCTTC CAGCATTTC 120
 TTAATGAATG CTTTTTCTTC TTGGTnTTTA ATCTTTGTAA ACG 163

(2) INFORMATION FOR SEQ ID NO: 3201:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3201:

20 GTTATGTTTG AGACTATAAT GAATAAATAT TTAGAAATAT GACTCCGATT GTTCGATGCT 60
 TAATTCAGTT AGAAGCATCA TAAGAATGCA TGATTACTGG TGTAAAGATA CGTAATGTnT 120
 TGTATTGACT GGATGTCTTT GGATAGAGT 149

(2) INFORMATION FOR SEQ ID NO: 3202:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3202:

35 CAAGTGACTG AGATTACTGA AGTAAACCCG TTACCGCCAC ACTATATTTG TCCGAAGTGT 60
 AAAACGAGTG AATTTTTCAA TGATGGTTCA GTAGGATCAG ATTGATTTAC CTGATAAACG 120
 40 TGTGAAnTTG TGGAGGCCAC TATTAAAGAA GACAGAATCC GTTGAACATT TAGATAAGGG 180
 AAAGTCCGAT TC 192

(2) INFORMATION FOR SEQ ID NO: 3203:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3203:

CGCCATCTAA CGTTTTTTGT ATTCGTTGTT GCTGAGCTAG TTGTAAGTGC CnCATTAAAGC 120
 ATCTTATAGC GTGATAGCCA TGCGCCAACG TACAAATCTG CTCCGTATTG TACGCACCAC 180
 5 TAAGCAGTAC ACACCAGTAA CATTGTAGAT CGTTATAGCG CAATATACAG TACA 234

(2) INFORMATION FOR SEQ ID NO: 3204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3204:

AACGCCATAA GCTACATGTA TGCTTCTTGC ATGGTTATCA TCCTCTCTTA ATGACTATCT 60
 20 TTTAATTACG NAATGGCTTA CCAGTTTTTA ACATATGTGC AATTCTTTCA TATGATTTTT 120
 AGATTTAGTA GCATAAGCAA TTTCTCCACG TTGATGTACG TGATGTAATG ATTCTGGG 178

(2) INFORMATION FOR SEQ ID NO: 3205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3205:

TATTAATCAC GTTGTTGTGC GTTCGTGTTT TCGCAGTATT GATTTGTTGT TGCGCATTAT 60
 35 GCATTGCATT ATTGTACTGC GTAATTGTAC CTGGCTTTTT ACCTTCAGTG CTTACTGGnT 120
 CATCTAAATG ATTTTTAGCT GTGATTA 147

(2) INFORMATION FOR SEQ ID NO: 3206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3206:

CAGCTGTACT AGTTGAGCGT ATTATCCAAA ACATTTTACG TGATGGCATT GATGTCGATC 60
 50 GACTTTCAGT CGTAACGTTT ACAAACCTTAA GCGCACGTCA nATGAAGCAT CGTGTAGACC 120

(2) INFORMATION FOR SEQ ID NO: 3207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3207:

TAGGGACTTT GAAGCGGAGA GTCTAATGCA TATGGGCAGC ATTATGATCA GCAACTGCTG 60
 AGAAAAATCC AGTTCTAGCT TGGGATTAA ATGTGGAGTG GntTAATGAA TGCATTAAGA 120
 AGCTGCAAGA ACTTATAAGT GTGCA 145

(2) INFORMATION FOR SEQ ID NO: 3208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3208:

AAACGGTTTT AGATCGTATT CAATTGAAAA GGACCGGTAT TGAATGnAAT CACACTTAGC 60
 AGCGATTGAT CAGaACATTT TAAATTAAC TATTATCAA CGGTATATGA AGGGGATTTG 120
 GAAGATGCGT T 131

(2) INFORMATION FOR SEQ ID NO: 3209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3209:

ATAAATTTAT CTATAATCTG TTGCTTGTTT TnCTGTTCTA CAAGTATTTT CACATTAGGT 60
 CCCGCATCCA TTGTAAAATA ACACGGATAC CCCGCTTCTC GGCATTCTGT AACAGCGCCA 120
 TGACATCATA ACTTTCTGCA CACTAGGAAC GGGGGTG 157

(2) INFORMATION FOR SEQ ID NO: 3210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3210:

AACGTAATAG ATATGGTACT TACTACATGG GAGAGAGTGC TAGATTCACA AACGGCAATC 60
10 AACCAATCAC AGTAAGAGAA GTGGGGCCAT TCTTATCTnG TCCAGTGGGT TATCAGTTCC 120
AACCTGGTGG GTATTGTGAT TAT 143

(2) INFORMATION FOR SEQ ID NO: 3211:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3211:

ATGCATACTG TATGTGTTCC AGCATATACA ATTTTGnCCA TCTTTAATGA CAACTGTACC 60
25 ATTTTTCACA ACATTTAATT CATCTAATTC CTTACCCTTC AAAGTTTATC TGTGATCTC 120
GGTAAAATTA ATTCTGC 137

(2) INFORMATION FOR SEQ ID NO: 3212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3212:

40

ATTCACGCTT TAAAGGACGT AAATACACGA CTAGGCTGTT TACCTTTAGA TCTAAATCAG 60
AACAATTTTT TTACCATGGT GTTCCCCTTG AATTAGGAAT TTTATATAAA AATAAGCGGG 120
45 AAGCGTTGTG CCCCCTTAC TCATAAGCTT TAATTAATGC TAAATAGTCT GACACTAGCG 180
ATTTGATAAA ACTATACTAA AATTATTTAG AAGTCACTAA GATGCTAATG ACGACnAnt 239

(2) INFORMATION FOR SEQ ID NO: 3213:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3213:

CATCCTCAGA GTAGGAATAG CCATACCATC GAATAATTCA CGTACTGTTT CGAATTGAGG 60
 5 TTCAAATTCT TGAGTTGTAT AGAGCTCGAA AATnTTTGCC CATTAGCATA ATCAGACTTT 120
 TCAAAAGTCT TGATATTGA TACCCACGCT 150

(2) INFORMATION FOR SEQ ID NO: 3214:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3214:

CTAAGCATTG GTTTAAACTA ATGTTTCAGAG CTTTnTGTGG TTTGTAAAnA CAAGTATATT 60
 nCGAGAACAC GTTTTTGTAT AGAGTCTCAA TTATAAAAGT TAGAATAGTT GACAACAGTG 120
 TTACGATATT ATTAAACAAC TGTcTATCAT TAACGAAAGC AATTAACAAG AGTACTTGTT 180
 25 GTGAAATCAT CGTTTAAATAG TCAAAGATGA TCATCGTAGG gTAGACAACA TATCaTTGAC 240
 TtAAGGAAGG GGAATGACCG ATGGGATTAA AAGATCAAGC TGTTACCTGG AGAAGGTATT 300
 TTCATCAATT TCCAGAACTA TCCGATAAAG AATTTAAGAC TACACAAAAA ATTAAAGATA 360
 30 TTTTAACAGA ACATCATATT AGAATATTAG ACTTACCAC 399

(2) INFORMATION FOR SEQ ID NO: 3215:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3215:

CAGGTGAAAG CACAAGAGGA TTTGCTGTTT ATTTCTCTCC TGAAATTAAG AAATTCATTG 60
 45 CAGATAATTT AGATAAATAA TTAAACTTA GACATTCACC CAATCCTGAC AAAATATACT 120
 ATAACTAACA TTTATTAATA TATATTGCAT TATTTAATAT GCATCAAAGC CAATCAACGr 180
 TTGATTTTCA CCAACTCAAT TGTTGATTGG TTTTATTTAT GTATGAATGA ACAACTTTTT 240
 50 GACATCATTa AGAATATAAA TGCGTTTGAA AGCATTTGAA AGCnACAACA TTTCTATAAA 300
 ATTTTTCAAT AACAAATTGCG CCACTAAAAC TCAAAATTTc CACCACCAAC ATCCAAATTA 360

(2) INFORMATION FOR SEQ ID NO: 3216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3216:

AGTTGCATCA ACTGAATCCA ACGCTACGCA ATACGAATTA TTCCAATCTG GCATGCGTGT 60
 TGGTAGAGAA ATTTTAGCGA CATCTCGAGC ACGGTTTACC TTGCCTTTnT TGGTGGCCAA 120
 CTTGCTTTAT GCTATGGGTT TTTCAAACIT AAA 153

(2) INFORMATION FOR SEQ ID NO: 3217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3217:

CTTTGCATAT TCTGGTTTGT AGTATTCATG GTCCGTCAAT TG TAGACCCA TCAATTGCAG 60
 CCATTACATA TCGGAATAT CGAAGCGAAC TTCAAGTTGC TTCAAGCTGG TAGAACACGC 120
 AnATAAAATT ATTACATC 138

(2) INFORMATION FOR SEQ ID NO: 3218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3218:

CACTCCAAAC CAAGGATTTA CGTGCTTTAT ATnGAGGTAA AGCACATCAT GTkGTTaATT 60
 TTATGcmTTT TaTTGcmCmA GraTTAaGAG AAATTTTAGC nTCTTTAGGT TTGAAACGTG 120
 TAGAAGACTT AGTTGGAAGA ACTGATTTAT TACAACGATC aTCAACATTA AAAGCGAATA 180
 GCAAAGCGGC TAGTATTGAT GTTGAAAAAC TGTTATGTCC TTTCGATGGG CCAAACACAA 240
 AAGAAATTCA ACAAATCAT AATCTTGAGC ATGGATTGA TTTAACAAAT TTATATGAAG 300

AACAACGTGA TGTAGGGGTT ATTACAGGTA GTGAGATTTT GAAACAATAT GGAGAAGCAG 420
 GACTTCCTGA AAATACAATT AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTTGACAG 480
 5 ATATGCA 487

(2) INFORMATION FOR SEQ ID NO: 3219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3219:

ACCAACTCGG AATCATGCAA TGAACACCAT GGTGAAATA AGTGAATTGC ATAAGTATCC 60
 20 TGGCCTGGCA ATGCTGGTAT AACCTAAAC CTTGTTGCAC GAAATGTATT CGCTACAATT 120
 AATGTACCTG CAAAACCGTT TAATAAGAAG TTCGAAATCG TTGCACCTGT ATATGG 176

(2) INFORMATION FOR SEQ ID NO: 3220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3220:

CTGATTTAGG TAATCTTTGC GCAATTGTTT TTTTACAGTT TCGGCAAATG GGTGCCCGGG 60
 35 CAAATAAATA TTGGCTATGC TCAAACCTGA ATTAATGGTG GGTGTGTCCG CCATCGTAAT 120
 TGGGnCCGCC TGAAGGGCCG CATATAAATG ATAGTGCTCT TCCGAATAAA AGGTAGGCCA 180
 40 TATGTAATTG TTTTGTGGTT ACG 203

(2) INFORMATION FOR SEQ ID NO: 3221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3221:

AGCTAAATCT TGCCAATATG GTATCAACTT TTCATTCCAC TGATAATCAT AAATTTTCAGA 60

GCAATGCCAG AAATGTATTA ACAACTGGCA CGTCTAATAG ATTGCTAACG GATTGTTTAC 180
 GTACGTTTCAT CGGCTTCTTT CGCTTCTATC GGATCTGGAG AATTGGGATG TTATGACCAC 240
 5 TGAACCACTT ATTTGTAAGC TCTGTCGTGA TTGACTTCAT AATGCTTGCG CTTGn CCTCA 300
 TTTCTAACAA CTCATCCTAC TTACnAAATT ACCCnGGGG TACACCTGGT CCACTTCATC 360
 A 361

10 (2) INFORMATION FOR SEQ ID NO: 3222:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3222:

GGGGCTCCGn GGAGGCAAGG GTAGAAAATG ATGTAAACGC TGCATTACTA GGCGAATTGA 60
 AATTACATCA ATATCAAGCA GAACGGATCT TTTGTATGAC GCTTGGTACA GGCATTGGGG 120
 25 GTGCGTACAA GAATTAATCA AGGTTTCATGT TG 152

(2) INFORMATION FOR SEQ ID NO: 3223:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3223:

TTTGTTAAAT ATAGGCCCTG CAATGAGTGT ACTGGAATGG CAATAATCAT ACCATACAGT 60
 40 AATACATCTC CAACATTTGC CTTnAATTCT TTTCCCATGA CTACCGGTCC TGGGATGTGG 120
 TGG 123

(2) INFORMATION FOR SEQ ID NO: 3224:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3224:

TGGTTGGTAA CCGTAAATTA ATGCCTGACA ATGATATTAG CTnCCTAAGC ATATTTCTGA 120

TGATTTAACA CATTATGAAA CGAGA 145

(2) INFORMATION FOR SEQ ID NO: 3225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3225:

GGTATTGTCT AGTCAATTAC TAACACCATT TAATTGTGGn AAGCAAAAGC TAAAGGTTAT 60

CGTGCGCTAT TGCAGGCATT GATGCTTCCA ACAAAGTCGA GTATTCAGTT GCATCAAAAG 120

TTTGCTTTT 129

(2) INFORMATION FOR SEQ ID NO: 3226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3226:

GACACTACCG TTCCCACGTA GCATCAATCG TCTCAGTCGC ATCGTAGTCA TCTGTATGTG 60

TTCCAGCATA TACAATTTTG CCATCTTTAA TGACAAACGTA CCATTTTCAC AACATTTATT 120

CATCTAnTCC TACCCTCAAA GTTATCGTTG ATCTCGTAAA TAGTCGGCAA 170

(2) INFORMATION FOR SEQ ID NO: 3227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3227:

TTACTGCTTT ACGTTTATCA TTTTCTAATT CAnAAATTCG TCATTCAGTT TCAACTTTAT 60

CGACAGCTGG ACTTTGCGCA GATAAATGTG CTGCTGTAAT ATCTAACACA TCGATTGCTC 120

TTATCTGGCA ATAATCGTTG 140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3228:

GCGCCTATAA TTGCGCTACT TGATTTAATT GAGTAGATAA ATCTAATCCG AATAAATCCG 60
 TGACTTGCTT GATAAATAGC AACAAATGCTn CAACTAAACC AGTTAGTACT GCTTTGTTTT 120

(2) INFORMATION FOR SEQ ID NO: 3229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3229:

GGCTATACAC CGACTACAGT AACATCTGGT AGCGACATTG AAAAAGACTC TAATGGTTTA 60
 ACAACAACAG GTGTTATTAA TGGTGCTGAT AACATGTACA TTAGATAGTG GnTTCTACA 119

(2) INFORMATION FOR SEQ ID NO: 3230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3230:

TGGGAATAGC AACCAACAAT GCGACAACAA AGCCCGCTAC AAATCTCCAT nAACTAATTG 60
 CTAAATGTTG GAAAAATTTT TCCAGTCAAC AATGAAAGGC CATATGACTT TTTCCTACAA 120
 GAGCAGGG 128

(2) INFORMATION FOR SEQ ID NO: 3231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATGCAGCTA TTACTTTTCA CAGATTCCAT ATCGTTCAAC ATTTAAATAG AGAACTTAAT 60
 AAGTATCGTG TACAAGTTAT GAATGANTAC CGTAATAAAA AAGGACCTGA TTATACAATT 120
 5 TTC 123

(2) INFORMATION FOR SEQ ID NO: 3232:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1656 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3232:

GCCTCAAAGA ACATGCTGAA CAGTCATCGC aTTCATATAG TTTGAAGTCT CGTTTAAAC 60
 20 CATATCTATC ATTACGGTAT GCATATCTTT TAAACCTAT TCTTTTGTTA TTAGGACATA 120
 TAAATTCATC ATTAAGTTTCG TCATATTTCC AATTTTGAGT GTCGAAAATG TCACTTTTAA 180
 ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGCGGTT TTATTAAAT 240
 25 CATCTATAAT GGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT ACAAATAACC 300
 GAAGtATTTT GAATCATTGT TAAAAATGGA ATTAAAGTTC TAGTATCTGT CGGGTTTTGA 360
 AATAGGTCAT AGGATAAAAC AAATTGAGAA TTTGTCGCTA TTTGTAAATT GTATCCTGGC 420
 TTAAGTTGGC CATTTTTTCAT ATGGTCTTCC TTCATTCTCA TAAAGTTGC ATCATGATCA 480
 GTTTTAGAAA ArCTATTTCT ATCTTTAAGA ATCGATTTT GTTCTTCATA TTTATTTTTT 540
 35 CTTTCGGAAT AATCATCAA TTTmTTTTTG AACTTCTTAA TCTTAGTTCT TTTTtaCGGG 600
 TCTGTTTTCT AATTTGAGTA CTATCTTCGT TCTCAATAGA ATGATTTAAA yCTTCGATTT 660
 CTTTATCTAA ATGACTACCA ATTAAATCTA TTTCTTCTAT TGTTAAATCG CTATCTCCAT 720
 40 CTTCTTTTAT CTCTGGTATT ATTTTTTCTT CAACTAAGTC ACGATATAAT GTTTTTGAAT 780
 TTTCGTTCAA TTTCGATTTC TGATTTTGAA TACTTTTCTT CCACACAAAT GTATACCTAT 840
 TGGCATTAGC TTCTACTTTT GTACCATCAA TAAGATTTTG CTTTAAACAT TGACTATGAA 900
 45 ACTGGATAAA TAAAGATTCA ATTAACGCAT CAGTATTAGG ATTCACTCTA ATACGATTAA 960
 TAGTTTTATA AGAAGGTGTT TGATTTTGAG CTAACCACAT CATTCGAATA CTGTCATGAA 1020
 GTAATTTCTC TATTCTACGA CCAGAAAATA CAGATTGAGT ATATGCATAT AAGGTGATTT 1080
 TTAACATCAT TTTTGATGA TAGGATGTTG CGCCACGATG ATGTCTGAAT TTATCGAATT 1140
 CGCTATCAGG TATCGTTTCA ACAATTTTCAT TAACATATCG CGAAATATCA ATTTGAGGAA 1200

GGCACTTCAT TAATTTAGTT TAGTGGTATT TATTAAATTA TACGAAGGGA CCCAACACAG 1320
 AAAATTCAAA TTATTGAATT AAACATTTAT GTGCAAGTTT GGCAAAGTGT CTTATTTTTT 1380
 5 AAAAGTATGT AAAAGTAAAA TTACATGTTA ATACGTAGTA TTAATGGCGA GACTCCTGAG 1440
 GGAGCAGTGC CAGTCGAAGc CGAGGCTGAG ACGGCACCCT AGGAAAGCGA rCCATTCAAT 1500
 ACGAaGTATT GTATAATAG AGAACAGCAG TAAGATATTT tCTAATTGAA AATTATCTTA 1560
 10 CTGCTGTTTT TTAGGGATT TATGTCCAG CCTGTTTTTT GTGATTTTAA ATAATTTGAA 1620
 TATGGrAAAT GTATTaWTct CTCATTTGTA TAGATT 1656

(2) INFORMATION FOR SEQ ID NO: 3233:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3233:

25 TTGCTCATAA ATCTTTTCTT GGCGCTCTGA ACACTATCTT CTATTCTGTC GGAATTTTTTC 60
 AAACATAGTC TTATCATTTn CTTCTAATCG CGTTAAACGC CAATCTTGTT CATGTCGTTT 120
 GGTAATCCA 130

(2) INFORMATION FOR SEQ ID NO: 3234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3234:

40 GCCACGATAA AGAAGTAAGA ACAACACATG GTGTTACTGG TACAGGCTCA TGTTCTTGGG 60
 AAAGTTATTT GTGnAAAATG GTGTGAATTA CCTGGGGAAA AATCAACAAA CTGACTATCC 120
 45 AA 122

(2) INFORMATION FOR SEQ ID NO: 3235:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3235:

5 AACCAGGATA TGAAATCTGT GACTTATTGC GTTAGATCGT TTTGTAAGT CTACTATTGA 60
 AGAAGCAGAC CAATATAAAG GTACCATTCA TTGCAAAGC ATTACATGCA TGAACCCAGT 120
 TGACATTTAG TTAGAGATGG AAGATAGTAT TGTGCATTTG CAGnTTCCAC ATG 173

(2) INFORMATION FOR SEQ ID NO: 3236:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3236:

20 GCGGTGTGCA TTTGAAAATG TTATCAAGAA TATTGAGTTA ATTCGCAACG ACATTATACC 60
 AGCGATTAnA AAGCATTTAT CAAAATACGA GGGGCGTCAT CATGAATATT GTATTATTGT 120
 CA 122

(2) INFORMATION FOR SEQ ID NO: 3237:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3237:

35 TTTTTTGCCC AAAATTTTTG GGTTTTTTTT GGGTTAAAGG AAAAAAAATT TTAAAGGGG 60
 GGGGGGGGTC CCCCAAAAT TTTTTCCCT TCCCTTGGT TTGGTTTTTT GGGGGGGGGG 120
 40 CCCCCCCCCT TTGAAAACC CCTTAAAAAA ATTTAAngGT TAAATTGGAA AAAAAATTT 180
 AA 182

(2) INFORMATION FOR SEQ ID NO: 3238:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3238:

GATGAnGTTG GACAACGTAT TGTGGCAGAT GTTGCAGTTG ACTTTGAAGA A

111

(2) INFORMATION FOR SEQ ID NO: 3239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3239:

AGTTGATCGT ATTTTCCAGA AGAGACAGAA TTAATTGATT ATCGTGTTAG TTCTGTCACT 60

GAAGGTACTG ATGCCCAAGC AGnAGTACAT GTAAGTTTAT TGATTGAGGT AAGACTGTCA 120

(2) INFORMATION FOR SEQ ID NO: 3240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3240:

TACACATCTn TCTACGATTG TAGTTTATCG ATAGGTTTCG CATCATGAAA CGTGATAAAC 60

AACCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCAGTGTTT 120

AGCATAT 127

(2) INFORMATION FOR SEQ ID NO: 3241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3241:

GACTAAAATA CATGTTGGAA TACTTGGTCC CATGGGAAAA TATTGGACTG GGTAACCCAA 60

TCACGGCTTC TGAAGTAGTT CTTTnTCTTC TATTAAAATA GCGACGGAAT CACACCTTCT 120

GCGG 124

(2) INFORMATION FOR SEQ ID NO: 3242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3242:

TACGTGTATA CACCGTTATC TTTATGGCTT TGAATTTC TAATAAATAC ATACGGnTTT 60
10 TGTGCAGAGC TCAGCACATA ATCATCTTTA ACTATAGTTT CTGGAATCA CTTCATAGTT 120
TT 122

(2) INFORMATION FOR SEQ ID NO: 3243:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3243:

AACCTTTTCT GCAACCATAC GCCATAGgTA TGtTTTCTTT TTACAATTAA AGaGCCAACC 60
25 GTTGTTATAG TCTAACAATG GTTGGCTCCT CTTÀTTTTAT GTGCTAAAAA TTTATAGGCA 120
ATTTTATTAC AACAAATGTAC ATTTAAGGTG ACCTTCATGC CAAAATCGCA TCACTCATTT 180
30 AATGGAAGCA GCACGTCTTC ATACAAAGTC ACGATCCTAA T 221

(2) INFORMATION FOR SEQ ID NO: 3244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3244:

TTGCATTTTG ATTGTCTGGT GACCTTGGCA ATGACAATTC CCGCTTGCAA TCGGTATCTT 60
45 CAATATTATA ATCAGGTCTT GCCTTAGATT TTCGCTAAGT ACCGGTGATT CTCTACCATC 120
ATACTCACCT CATGnGCTAT TTTTCTAGAG TGCTTCTTTT CACACTTTAT CTTATAAAAG 180
GCTAGCTACT ATTACCGATT TATCATTATT AGTGGTTTTT ACCh 224

50 (2) INFORMATION FOR SEQ ID NO: 3245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
55 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3245:

5 GAAAGAGATT AGTGACAAGT TGGTTGTA CT ATTACGTTAA AATTTGGAGA TTATGTGTGG 60
TGTTC AAGTA TGC GTTCa nT AATTGATATT GGCGCACCGT ATAACCATGT CAAAGTA 117

(2) INFORMATION FOR SEQ ID NO: 3246:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3246:

CTACAGGCTT TCGTACCACA GGATCAAAAC TACGCACTGT GCCTTGTACA TACGCATGAT 60
20 CAGCAATGAC ATTCCAAGTA TTACCACATG ATATTTGnCC AATTGTTACT ACCGTTT 117

(2) INFORMATION FOR SEQ ID NO: 3247:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3247:

TACACa nCTT TCTACGTGTG TAGTTTATCG ATAGGTTTCG CATCATGAAA AGTGATAAAC 60
35 AGCCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCATGT 117

(2) INFORMATION FOR SEQ ID NO: 3248:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3248:

CCCGTCCTTT GGTGGAACCG TTTTGTAGAA TTAAATAATA TTACAGAGCC GCTAGCAGTA 60
50 ACGATCCAAA CGAATTTACC ACCATCACGT GGATTAGGAT CGAGTGCACT GTCGCGGTTG 120
CnTTTGGTCC TGCCA 135

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3249:

10

AAAAGCCAAC CCATGnAATG TTGGATTGGC TTTTACATG CCATCTGAAT CTCTAATTTT 60

AAAAAATAT GGAATATAAA TAAGACAGTA AAAATTAAAT TTCAGT 106

(2) INFORMATION FOR SEQ ID NO: 3250:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3250:

25

AACGCTGAAG CAGATAAAAA ACGTCGTGAT AGAAGTAGAC TTAAGAAACG AGTCTGACAn 60

TCTAGTATTC CAAGTTGAAA AAACCTTTTAA CTGTATTTAG GCGAAAATAT CCGTGAAGAA 120

GA 122

30

(2) INFORMATION FOR SEQ ID NO: 3251:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3251:

40

GAACGTTGAG ATGTCACAAA CTGGTGAAAG TGCACGTTCA ATGCCAATGA CTGATAAAAC 60

CAAATTCATC AATCACAATT ACTCCGAAAG CnGGTACAGG TCACTCAGTA AGTAGTAATC 120

45

CCAGTACATT AA 132

(2) INFORMATION FOR SEQ ID NO: 3252:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3252:

GGAAAATCTT CAAATTCTGC AAATTGCCAA TTTACCTAAT AACCAAACAT CTAAGGCATG 60
 5 TGTAATGCTG CTACnTCCGC TTCGTCATCA GCTACAATGA CAAATACAGG TGCCA 115

(2) INFORMATION FOR SEQ ID NO: 3253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3253:

TTTCGTCAAA TTATGGGAAT AAAATAATCA TATTTAAGAT AGTAAATATT GAATAAGTTG 60
 20 CTTTGAAATT TATAAAATGA AAGTATAGTG TCATGGGnAG TATAATAGTC AGATATATAT 120
 GTAACGGCAC TATATTGAAA 140

(2) INFORMATION FOR SEQ ID NO: 3254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3254:

AAATCTCCTA CTTTTTCTAC CCATAAATAA TTGGCTAACT TTTTCATCTT ATCTTCATCC 60
 35 TTTCTCTTCT ATTTAAATG CTACAAATAA ATTTCCGCGA GTAATTTTAA TGTTTTACAA 120
 CGCTGTTCAA TACCTGGAAT AAGCGGTGCT ACTAACACCT CATCAACTTC ArACGTAGCA 180
 40 ATGAAATCAT CTAATTGTGC TTAAACCTwT TCTTGTGTAC CTGcAATGAT GCGTGCTTg 240
 ATGTGCTTGA ATCATCTCTT TGTCTCGATC ATTAAGCTTA TACTTTTGTG CTGTGTCTAC 300
 TGAAGGAAAA TCTTCAAATT CTGCAAATGT AATTACCAa ATAACCAAAC ATCTAAGGCA 360
 45 GTTGTAAGCG GcACTTCCG CTTCGTTATC AGCnACAAG 399

(2) INFORMATION FOR SEQ ID NO: 3255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3255:

ACCATTTCGTC AAAATATTCC AACACGCATT TAGGTGTGCA AGGTATCGGT ACCTAACAAAC 60
 5 GAAGCTATCG TCTCACTAnC CTTAAAGAT TTTAGAACAA CAGCTGCACT CATCAT 116

(2) INFORMATION FOR SEQ ID NO: 3256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3256:

AAAGACCTAA GGTTATGTAA TTGGCCTAAA TTTATTAATC GTTTAAAnTTC AGTTAGTAAA 60
 20 AAGTCTGTGA GTAAGGGTGT ATGGAAACTG GTTAAATATT ATAGAG 106

(2) INFORMATION FOR SEQ ID NO: 3257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3257:

AACGTCCATC GTAATACCTT TTGTGTCTAA TGTAACCTGT ACATCGTCTA ATAATAAGTT 60
 35 GACGATATCT TGACAATGCA TCTTTATCTA GATGTAAGAn TTCAACGGAT GCCG 114

(2) INFORMATION FOR SEQ ID NO: 3258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3258:

TTAAAGCAGT TAATCCACAG GGAAAGTGGT TAATACAGTT GGGCTCTGGT GGATAGTACA 60
 GTTGCAGGCA TGGTGGGCTG GGAATGCTT CAGGGTTTAA CGAnTGGGAA AAGCCTT 117

(2) INFORMATION FOR SEQ ID NO: 3259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3259:

GGACCGCCAT ATCGTTGGCA ATCATCGCAC CTATAATCAT CGCAAGTATA ATAATATTAG 60
CACCTTGCAT ACTTTTAAAC CAGGTTGTTA ATGCCTCAAA AATATTAGAA ATTGGTGCCC 120
GnTT 124

(2) INFORMATION FOR SEQ ID NO: 3260:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3260:

TACCAATGTA TATCCATATA CTTTATCAT AATCATTTCA GCGGACTTTA GTTTGATGTT 60
TTTGCTTGAT TAAATCTTT CGGCGATCTT CAGCTTGATG TTTTCGTTTG ATTAAATTGG 120
TACAATAnAT 130

30

(2) INFORMATION FOR SEQ ID NO: 3261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3261:

GGCCTTTTGG GGCCGGGGTT GGAAATTGGG GTTGCCTTAA TTTTAAATT AAATTTTGA 60
ATTAAAAAAG GAAAAAnTCC AAAGGTTAAT TTAAAAAAA GCCCAAGGTT TAAAAATTC 120
CCCCAACCAA AAAGGGGGGG AAAAAAGGTT GGGGGTTTTA AAAATTAnCC AAGGTTTTTG 180
GGGCCCTCCC TTGGGGGTTG GGAATTAAAG GTTAACCAAG GTTTTGGGCC AAGGGGCCCA 240
ATTGGGGGTT GGGGCCCTGG GGGAAAATTT TGCCCTTTC CCAAGGGGTT TTTTAAACC 300
CGGATTTTGG GAAAAAAGAA AGCCATTTT CCCCCAACCC CnAAAGCCCA GTTCCCGCCC 360
ATTTTCCCGG GGTAAACCCTG CCCCCACCGG GGCCATTTT 400

50

(2) INFORMATION FOR SEQ ID NO: 3262:

55

(A) LENGTH: 134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3262:

10 TGGTTCAATG GAAACGTGTA CCGCAAATnC CGTTAAATGT TGTGGATGT TGAGAGACGT 60
 GGCTGAACTG GCACATTTGG GCAATGACCA ATGGAACAAG CTAATGGGCA AGCGATTATT 120
 GCGACGGCTG ATGG 134

15

(2) INFORMATION FOR SEQ ID NO: 3263:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3263:

25

TTTTTTTCTG TTGGTACTTG TTTTGTGGTT GCGGATTGTG GTGTGTCTGA nTTAGTAGAT 60
 TGCAATGGTT GTGGCGTGTG TGCTTGATGG AGGTGTTGTC ACTTT 105

30

(2) INFORMATION FOR SEQ ID NO: 3264:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3264:

40

GTTCCATCAT TCCCACnAT ATCCAACATG TGGGCTACTG CAATGCTTTA GCGTCAATG 60
 CCTCATCATC ATCACAGCGC CAGTAAATGC GTATAATTAA ATTAATT 107

45

(2) INFORMATION FOR SEQ ID NO: 3265:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3265:

55

GTCGTAACAA TGGTTCGTTA CCAAAGCATA nTTGCCTTC TTGGCATCG

109

(2) INFORMATION FOR SEQ ID NO: 3266:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3266:

TTACCTTTAA AATAAnGTTT TCCACTAGTT GGGCTAAACA AATTACATAT TTTGCTTTTG 60
GAAATGTACT TTTTACCACT ACCTGATGGA CCTATAATGG GCAA 104

(2) INFORMATION FOR SEQ ID NO: 3267:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3267:

TAAGCCATCA GAAACAAATG CATATAACGn AACAAACACAT GCAAATGGTT CAAGTATCAT 60
ACGGTGCTCG TCCGACATAC AAGAAGCCAA GCGAGAACGA ATGCATACAA TGTAACA 117

(2) INFORMATION FOR SEQ ID NO: 3268:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3268:

GCTGCACAAG CACAACCTGG AATCAGCAAC ACCGGCAAAC CAnCAGGTCA AGGAATAACC 60
AAGCAGCACC TCATAATAAT GCAACACCGG CAATCAAACA C 101

(2) INFORMATION FOR SEQ ID NO: 3269:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3269:

CATACCCTAT TTTAGATATT ACCTTATTAC AAAATATTTT TACATTAATG TCAGCTGCAG 60
 5 GTTAGTATTG TTTTCCAAAA TTTACCGGTC ATCTTTGCCA ATTGGGTGTC GCCAATCGGG 120
 ATTTATCCTA GGAAGCCGAT TAAAAGGGTA CTGCCAGGGT TTTAGCCTGC nGCTGCCTCG 180
 GGGTTTTCTT TAAATTAATG nAACCGC 207

(2) INFORMATION FOR SEQ ID NO: 3270:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3270:

ATATTCGCAC CACCATAAAC ATAGATGGTG TTTTGTCTT CTGCATTCAC AGTGATAAAA 60
 GGGCTTGGn CCGTTTTTGC TTCAGCTGTT TTGAATAATA TATGATG 107

(2) INFORMATION FOR SEQ ID NO: 3271:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3271:

TTGGTTACAC TTCTGCTAGT TTTAGTAACG ATGGTCCAAG ATTGTATGAG CCTATTCATG 60
 GATCAGCACC AGATATTGCA GGTAAAAACG TTGCCAATCC ATTTGGGATG GTTCTnATGC 120
 TT 122

(2) INFORMATION FOR SEQ ID NO: 3272:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3272:

GAAGGATGAT GATTCCGGAGC AnCTTCTTGC AGAAGAnGCG GnAATAACGT GACATATTGT 60

TGCGAGCGCT TGACAATCTA TTCTTTTTAA AGAAAGCGGT TGTAGACAA TGCATTAAGA 180
 GAAATTAAAG CGGmGTTTAC TTTTGTAAT GAGCATTGA TTTTcTGAAA ATAAAGCAGT 240
 5 ATGCAGGCGC TTGACTAAAA AGAAATTGTA CATTGACAAC TAGATAAGTA AAGTGAAAAT 300
 ATAGATTTTA CCCAAGCAAA ACCGAGTGAA TAAAGAGTTT TAAATAAGCT TGGATTCATA 360

(2) INFORMATION FOR SEQ ID NO: 3273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3273:

20 TCAATTTTAA CTGCAATAA TAAAGCTGCA TGATTACTT TGTACATTAT TGTAATTTCA 60
 GTAATACGAG GCAATGTCAG TnGCAGTGTT TAATAAATTT TGTTCGCTAT TT 112

(2) INFORMATION FOR SEQ ID NO: 3274:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3274:

35 TACATTTATG CAATCAACGT TACATTCAAT CGTTGGAGAA AATTGGCTTT ATTGACTTAC 60
 TAAAATCTAA AAAATCATAT GAAAGAATTG CACATATGTT AAAAActGGT AAGCCATTAC 120
 GTAATTAAAA GATAGTCATT AAGAGAGGAT GATAACCATG CAAGAAAGCA TACATTGTAG 180
 40 CTTATGGGCG TTCAGCGCAG CGAAAGCAAA GCAAGGCGCA TTATTCCACG AAAAGACCTG 240
 nTGATGTCGC AGCCAAAGTA ATTACAAGGC GTATTTGAAA ACGTATTGAC GGGAnAAAATT 300
 CCAATAAGGA TTATGGATTG nAAGATGGTC CATTTG 336

45 (2) INFORMATION FOR SEQ ID NO: 3275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC TGTTTTCGAA ACTAATTTTA 60
 CCGGCGATAT CTGGCATCTT TTATTTCCGC ATTTTTCCTAA ATCATGGTTA TTCCAGTTTG 120
 5 GCGGCTTAAA AATTCnTT 138

(2) INFORMATION FOR SEQ ID NO: 3276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3276:

CATTATACGA GnATAAGTAA AATTGATGAT GTGACTAAAA AAGATGCACA ACAATTATTG 60
 20 AAGATGCAAA AGAATTGCAT GCCAAGCTGA TACATTAGAT A 101

(2) INFORMATION FOR SEQ ID NO: 3277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3277:

TGGTTATTTCG TTCCTGATCG TTGTTGGTAT CTCACTATTC AAnATTATTC GTGTGGCATT 60
 35 ACTTTAGTTA CACCAGGTAC ATTTGAACCT GGCACCTGTT GCGAGTATTT CCGGTCTCGT 120
 CATT 124

(2) INFORMATION FOR SEQ ID NO: 3278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3278:

GACTTTTTGA CCAGTTGTAG CACGACCACC GAGAGTAGCA TTGCATATGC AATCATTGTA 60
 50 CCTTCGCCAA CGACTGnGCC AATATTAATT GTTGCGCCCA TCATAACGAC 110

(2) INFORMATION FOR SEQ ID NO: 3279:

- (A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3279:

10 TTGGTATATA GAGGGCAACC GCACCTGATA AAATGTGnCA CAGTTTTTAC AAGAGGTTAA 60
GGAATGAGTT TGGAGGCATA CGAGCATCAA GATACCATTC GATGTTAGTA ATT 113

(2) INFORMATION FOR SEQ ID NO: 3280:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3280:

25 TTACCGTCAC CGTAATCAGT CCATACTTTA TCAGCTATAC CGGCTTTAAC AGCATAAATG 60
TTCGTTCTG TAGGCATACC AAAGnCGATA CCATAGTGAC G 101

(2) INFORMATION FOR SEQ ID NO: 3281:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3281:

ACTATGTTTT AnAAATTCGA CAGAATCAGA AGCACAGTCT GAGAACGCAA GAAAAAATTT 60
40 ATGACAAGTT AGATAGAAAT TTCGACGAAC TAAGGGCGTG ACCAAGAAGA AGATGA 116

(2) INFORMATION FOR SEQ ID NO: 3282:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3282:

ACTTGGTAG ATAATATAGC GTCGATTGTA TCACGAGTGT CTGTTCCAGT CATTATAAAA 60

55

CGTCGTTCTG ATGCTTTTCC TGAATCAT

148

(2) INFORMATION FOR SEQ ID NO: 3283:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3283:

AAATGACGAT AGAGTCAGGT ATTAATCAT TTTCAATAG TATCAGGAAG ACTACCAAGC 60
 TTATGTTGAA GGGCATCTTT TGGCGTTACC GGGTTGGGCA 100

(2) INFORMATION FOR SEQ ID NO: 3284:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3284:

TTAAGAAACC GAGCAGCGCA TAACCTGCA GTACCTTATC GCTTCTAGAT AATCCGATTG 60
 CGACACCATT GCAAGATGAC CGGTAATTTT GGAACATATA C 101

(2) INFORMATION FOR SEQ ID NO: 3285:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3285:

TAAATATTT CGCATCCCTA CACGCTAAAA TAATACATTA CACTTAAAC GGCTGTTTTA 60
 AAGCATCCTC CCATAAACAT CATCTAGTTG ATAATAGGGG GGGGGn 106

(2) INFORMATION FOR SEQ ID NO: 3286:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3286:

TTTAAACAATA CCTCAGAACA TACTATGGAA ATTGCTGCAA AGTTAATTGG GCATGCATAT 60
 5 TGATCATAAT GCGCTTTTAA ATAAAATGGT GGAGA 95

(2) INFORMATION FOR SEQ ID NO: 3287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3287:

TCGAAATAAT ATCTACGCAC ACTGATAACA TAAAAATGCC TGGTAGAATA CTAATGAAAT 60
 20 AAGTGCATAC ATGACCACAT GAATGCTAAT AACATGCTAG AACCCATTTT TTGAATATTT 120
 CACCACTCGA ATCATCAATA C 141

(2) INFORMATION FOR SEQ ID NO: 3288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3288:

TAGCTGGACC AGAACACGGT TCGACGTTGC AGGAAGTCTT GAACAGTCGC TGAACGCCAA 60
 35 GGCGATACTT GGGTTATCCA TGGTGAAAGn AATGGATTGG TGGTGCA 107

(2) INFORMATION FOR SEQ ID NO: 3289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3289:

GCTTTGCAAT GCCGATGTTA CTCGCAATAA TCATGTCGCA TCAATTACTT ATGGAAAGCA 60
 50 GATTTACGTA TGTCTACAAG TTTAGGCGC 89

(2) INFORMATION FOR SEQ ID NO: 3290:

- (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3290:

10 TGTTACGCCA ACAACAAATC CTACGTCGAC AACTATTTTT AAGCGATGAT TGCAATTAGA 60
 CAGAAATCCA ATCATTTTTG CATTCCATCC AGTGCACAGA ATnTCGAG 108

(2) INFORMATION FOR SEQ ID NO: 3291:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3291:

25 GATCAAGnCC TGAGAATTTA ATTTAATTTA TTTTATATT GGAGATGGTT AAAATGCTAA 60
 AACTCAACAT GAGTAACCAA AATATTGCCC TTAAAAATGC TGATCATTG 109

(2) INFORMATION FOR SEQ ID NO: 3292:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3292:

TTGATAATTT TGATATAGAA AGTTATTTAA AATTGGAATA AAAATAATAA CTCATCGACG 60
 40 TTTAATGGCT AGGTTCCAAT CAACTATGnG ACATAAATTC AAATTGATC ACGTAACGAA 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 3293:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3293:

55

GCGCGTAATA CCTGCAGTAC CTCTATCGCT TCTAGATAAT GCGGTTG

107

(2) INFORMATION FOR SEQ ID NO: 3294:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3294:

AAAATGTTAA ACCAAAAAGT TTGGTGAGTT ATAATATGGA ATATTAAATC TGTAGAAGAT 60
 AAAGCGAATA TAAAGTGATT AACTTTGGTA ATAAAGAATT AACAGCGAAA n 111

(2) INFORMATION FOR SEQ ID NO: 3295:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3295:

CCCCGACTAA ATCGAACGCT TTAATGTAAT GATTTGTCCG AATCCCCATC CTGCACCTGA 60
 TAATAAGGCG AATAGCAAGT TGTTCCCGT nGGAAGCCA CTGA 105

(2) INFORMATION FOR SEQ ID NO: 3296:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3296:

ATTTATTCAA AACCCGCCAC ATGGGGCAAC GGTGCCATG GCATGATAGT CCAGATACAT 60
 GGAAAGGAAT ACAGTCCGGT TAACACTCCA TTAAAAACCT GCGGGTTGGT TAAACCATT 120
 AACCTAAATG GGTCCAAGG GTTAACGCGG TTAAATGTT TGGAAAGGTT TnCCCAGTTT 180
 CCAAAAAGTT TTTnATTCCC C 201

(2) INFORMATION FOR SEQ ID NO: 3297:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3297:

	TTTAGACTTT CATCAGTGTT GAATATTTCT CCTTTAACGG TTATAGGTAA TATTTCTCTGA	60
10	GAAATATTTT CATCTTTTAC ATTTTCCGCT GTCAATTGAT GACTTCGATA AGCAAATTCA	120
	TCTTGTAATT CTCTTGAAAC ATCATACATC TkGGCCACAT TTTCAGCACC TkGAATCATT	180
	GATGGGTGCG TCATTTTCAGG TGCAAATGAT GCACGCTCAT AAAACTCAGG TAATGCTGTT	240
15	TCGTACACAG AATGCGGTGCG TTTGATTTTC CAAGGTGCTC GACTTGTACT TTCAACACCA	300
	CCTGCAATAT ATACCTTGCC AGctCCGGCT TGGATCATGC GACATGCATA TTGaACACTT	360
	TCAAGTCCAG ACCCACATTG cCGATCGrTT GTGaCGCCAG TATTGAAGCT TAAGC	415

20

(2) INFORMATION FOR SEQ ID NO: 3298:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3298:

30

	TTAATTGCAG CAGAGCGACT AGCTGATTCA GAGGTGTTAG TTTGTACGGT AATAGGATTC	60
	CCATTTAGGT GCATCGACCA ACTGCCCCGAC GAAAAGCCAT TTTGAAAACC AGAAnGATGC	120
35	CGATTCAAAA ATGGGTGCCA AGATTGAAAA TTTGGACCAA TGGG	164

(2) INFORMATION FOR SEQ ID NO: 3299:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3299:

45

	GTAGATGCCA TTTTCACGTT TCTTAGTTAT TGGCATTTTT TAAATGCGAT GTGTGGCTTC	60
	TACATAACGG GAAATTTTAA GTTTTATGAA TCnACATATC AATTGC	106

50

(2) INFORMATION FOR SEQ ID NO: 3300:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3300:

AAAAGGTGTT ATGAGATTAG TAAATCAnTA GACAAGCAGG TAAATTAAGT GATGTCGCGT 60
CATTTAAGGA AGCGATTAC AATCGAGAAC ACAAAGTACA AC 102

10

(2) INFORMATION FOR SEQ ID NO: 3301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3301:

TTAAAAGTTT GGAGATTATC GTGTCGTCTT CAAGTATGCG TTCATTAATT GATATTGGCG 60
CACCGTATAA CCATGTCAAA GTACCATTTG nAATCAGTCA TTGGCGCATT GGCTGCCCTA 120
GCGTTCA 127

25

(2) INFORMATION FOR SEQ ID NO: 3302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3302:

CCAGCTAGAC GATTGCTAAG GTATTGGATG TTTGAAACGT CCATGGACCC AATTGATTAA 60
TTGGnTGTA CTGGTCAAT GGTATATCC TAAATGCACT GGCCTGCTGG TGTCTTCTG 120
GGCGTTGCTT CGGAAAT 137

40

(2) INFORMATION FOR SEQ ID NO: 3303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3303:

55

ATATAAATTA ACGACGCGTT AATGCAGGCT GATGTGATTT TTATTGGTTT CCCAATTTTC 120
 AAGCTTCCAT CCCTGGTGCT TTGAAAAATG TGTTTGATCT ACTTCCAGTC AATGCGTTTC 180
 5 GTGACAAGGT AATAGGACTT GTAGCGACAG CAGGTTCTAG TAAACATTAT TTAATTCCTG 240
 AAATGCATTT AAAACCAATA TTGAGTTACA TGAAAGCACA TACGATGCAA ACGTATTATT 300
 TATTGAAGAG AAAGATTTTT CAAATCAACA AATTGTCAAT GATGATGTTG TATTTTCGGTT 360
 10 AAAAGCGTTG GCACAATCCA CAATGCGAAC TGCCAAAGT 399

(2) INFORMATION FOR SEQ ID NO: 3304:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3304:

CACCATTATT TACAGGACCT nCGATGACGT GTGGTCCTGT GTTAAGACAT AACATAATAT 60
 25 TCTACCTTTG TAATCAGTAC GGGTTTATCT ATCACAGTAC GG 102

(2) INFORMATION FOR SEQ ID NO: 3305:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3305:

TCAGCGTTAT CAATGAnTGA CTCTAATGCC TTTTACCCA TTTTGTAAA TGGAACATGG 60
 AAGCATAGAG ATGCGrAGTC AGCTAGCGAC TTACCTTGAC GTTTTGCGTA TTCATTCCAG 120
 40 CTTTGTGGr ATGAGCGGAT ATAAGCATCT TTAGATAATG CACCATCAAC TAATGGATAT 180
 TTATGTCCAG TTGGACGCCA GA 202

(2) INFORMATION FOR SEQ ID NO: 3306:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AAGATAGGGA TTTACACCTA TACCTCGTTC CGGGGAAGGG TCGGTGTTCT GAAAAGTTGG 60
 AACTACTCCC G_nCAAAATATT AAATTATGGG AGCGGGAAGG ATCAGGGATT TGACACCTAT 120
 5 GACCTCCATT CCCAGGGAAG GGAATGTGAT T 151

(2) INFORMATION FOR SEQ ID NO: 3307:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3307:

AATTTTCGTTA CCTGCGCCTT CTTTTTGCGG TTTTAAATA AGCGAAAATT TCAGGCGGTA 60
 20 AGACATAACG TCCCAGAATA GCTAGGG 87

(2) INFORMATION FOR SEQ ID NO: 3308:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3308:

ATGATGGCAA AGTCACCAA CTGATTGTGC ACACCAATCC ATCCATCTGC GCTGTAAATA 60
 35 ATGGTTCGCA ATAATTTTAA AATACCTTCC GCTACATTG ATTTAAAGCT GGTGCGCAn 120
 TGGACTAGA 129

(2) INFORMATION FOR SEQ ID NO: 3309:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3309:

GTTCTTTTIA TCGTAGTTGG TGGGACTCCT TATCGGCATC GCGGCTGGAC TCTAGGCGGT 60
 50 GGA_nACGGAC ATTCAAAAGG GATTTAGTTC ATCCAGATG GATTTCAATT TGGGGAATTC 120
 CATTTGGA 128

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3310:

GTACGATTCA GCATAAAGTA CACCACATTT GTCCTACGA CATCTGTAGC TGGTATTGAT 60
 CATGCAATCA TGAATAACGC TAA 83

(2) INFORMATION FOR SEQ ID NO: 3311:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3311:

CTGAGGATAA AGCGTCTCCA AGATAAGTCT AAAGATCATC ATAATGGGCA AAAAAGGTGG 60
 CAGCGATTCTG GTGGCTGGGA ACAAG 85

(2) INFORMATION FOR SEQ ID NO: 3312:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3312:

ATTTTATGTC TAAATGCTGG ACCAACAGTA TTGGCTATTA TTTGGTAACG TGATTACTAC 60
 AAAAAATGGA CCGTTGAGTT CGTGGCACAT GATTGATTTT GTAAGTAAGT ATGATGCACA 120
 TGGGCTnTT 129

(2) INFORMATION FOR SEQ ID NO: 3313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TCACCTAAAA TTAATCAAGG GACTTAACAT TGGCGAGTCA AGGTATTGAT CAAGCTAATG 60

GCACAGTTAA ATGATGCCAA AG 82

(2) INFORMATION FOR SEQ ID NO: 3314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3314:

ATGTTATGGA AGAATATTGA GTTAATTGGC AACGACATTA TACCGGCGAT TAAAAAGCCT 60

TTATCAAAAT AGTGAGGGGC GTCATCA 87

(2) INFORMATION FOR SEQ ID NO: 3315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3315:

TGAACCCGTC GTTGCCCATTT TGCCGGTTCC CGAAAGCCGG CGCCnACGGT TCTCCCTGCC 60

TAAATAGGGG ATGGAATATT AAACCATCTG CACCTGGTTT AACACGCTTT GCAATTGAG 120

TTAAGACATC ATAAGG 136

(2) INFORMATION FOR SEQ ID NO: 3316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3316:

CATTGGCTGT GTCCATTTTT AATCGTTGCG AGTACGTnTA TTAGCAACTT GGAAGTGCCA 60

TTGTTAATTT CAGTGTCTG TTACATTTC ACCATAGTCT TTCACAAT 108

(2) INFORMATION FOR SEQ ID NO: 3317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3317:

ATCTGAAGCT GGGTTTACTA GAGAAGGTAT GTACGTGACA TGAATTACTA ATGGATTTAT	60
TCATCGAGTT ACATCTATAG TTTATTAAAT CAGATACGCC AAAATGChAA TTAGCTTACA	120
AAGATGATGC ATTAAATGCA CG	142

(2) INFORMATION FOR SEQ ID NO: 3318:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3318:

AACATTATGT TAATCAACCT AATGAACGcC TTTATAAATT ACGCTAAACA ATATACAGAT	60
ATGCCGTTTC TTATCATGCT GGATGAAGAT GAAAATGGAT ATAAAGCGGG TCGATTTTTA	120
AGAGCGAGTG ACTTAGGTCA AACAACAGAG CAAGGCGAAT GGAAGCCAGT TATTCATGAT	180
GCAATCAGCG ATAGTTTAGT AGTACCTAAT GGCACAATGG GTCAACGTTG GGAAGAAGGT	240
AAGAAGTGGa ACTTAAAACT AGAAACAGAA GATGGTtTA AAATTAnCCC TACATTATCA	300
ATGACAGAAG GTGGATACGA ATTAGAAACA ATTCAATTCC CATACTTTGA TAGTGATGGA	360
GATGGGATAT CATCGTCCAA TCCnAC	386

(2) INFORMATION FOR SEQ ID NO: 3319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3319:

ACAATGAATG ACATGATTCG AGGTGGACGA CCCCTCCTAT TTTGCATAAA TGCTTTTTGA	60
ATCGCCGTC ATAATGTTTCG TTGnCCAATT AACTCAATAT TCTTCATGAC ATTTTCAAAT	120
GGC	123

(2) INFORMATION FOR SEQ ID NO: 3320:

55

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3320:

10 GCGGAAGTGT CAATTGCCGG TATACAACGT ATTTTAAGAG CTGCAGAACA TnCGGGTGT 60
 AAACGTGTGG TCAATGACTG CCAACTTTGG TGCAGTTGGT TTTA 104

(2) INFORMATION FOR SEQ ID NO: 3321:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3321:

25 GCGCCGGTTT TAACAGGTAA TTTAAACCA AATACTGATA GTAATGCATT AATAGTCAGC 60
 AAAATACAAG TATT 74

(2) INFORMATION FOR SEQ ID NO: 3322:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3322:

40 TCACTCAGGG GGAGATGTCA ATGGGTCAAC ATTATTTGAC AAGGTGTGGA CAGACATGTG 60
 TTATACGGGA AATTGGGCGA CCGCACT 87

(2) INFORMATION FOR SEQ ID NO: 3323:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3323:

55 TGCCAAATGT TCCATAATT TCATTACGAn TCTTAAGTAG GTGGCTATCA TTACGATGCG 60

AATGCGGTCG GAAAGATAAA TAGCTTCATC AATGTCATGC GTCATAAAA TAATAGTTGA 180
 TTGCGTTTTA TGTTTTAGTT GCACTAGTTG ATCCTGAAGT TTATAACGTG TAAATGCATC 240
 5 TAATGCACCT AATGGCTCAT CCATCAATAT AACGTTAGGC TTATGCACAT GCGCTCGACA 300
 TAGTGCCAAA CGTTGTTTCA TACCCCCGGA cAGTTGCTCG GGAAAATGCT TTCCCCTGTC 360
 TTCTAAATCA ACTAATTTAA GCTGTGCGTT AATCTCTTCA 400

10 (2) INFORMATION FOR SEQ ID NO: 3324:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3324:

GAAACCATCG ATTGTAGCAC GAACCATGTT GGATTGGTGT GTTTGnATCC TAATGTATTT 60
 ACTTAAGATA TCAGTGATAC CTGTCTAATT GCAAGTACGG TCAGGA 106

25 (2) INFORMATION FOR SEQ ID NO: 3325:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3325:

35 TCTGAAnTCG CTGTCTGAAT CTGGAATCAC TGTCTGAAAT CCGAAATCGC TAATCTGAAA 60
 TCCTGAAATC CGCTAATCTG AAACCTGGAA GTCGCTGGTC TGGAAGCCCT GAA 113

40 (2) INFORMATION FOR SEQ ID NO: 3326:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3326:

50 TGTCACGTAC TTGCTGTTCA ACAAATACGT CTTACTGGAC GTGCACCTCA TTCTTCATCA 60
 TAGCCTTCTT CATTAACC 78

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3327:

AATTGAAAAT TATCTTACTG CGGTTTTTAG GGGTTTATGT CCCAGCCTCT TACTCnAATT 60
ATATTCAC TA TCCATTAGAC CAAATGGGCC ATTTCCAATA ATCCCGCGGT GGTTTCCGA 119

(2) INFORMATION FOR SEQ ID NO: 3328:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3328:

GTGTTAAAC GTCACGACGT TTGTTTAAAA TGATGCGTCA TAATGTCTAC ACTTTGCTTG 60
CGATCATTCA T 71

(2) INFORMATION FOR SEQ ID NO: 3329:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3329:

CTGACGAACC TTGCATCATT TAACTGTCCA TTAGCTTGAT CAATACCTTG ACTCGCAATG 60
TTAAGTCCTT 70

(2) INFORMATION FOR SEQ ID NO: 3330:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3330:

CCAATCTCG

69

(2) INFORMATION FOR SEQ ID NO: 3331:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3331:

GGACACTAAC ATTAATATGG ACTGGTAATG TTGCTGTAA TAAACTCATA CCAAATCCTG
GGCATCTCTT

(2) INFORMATION FOR SEQ ID NO: 3332:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3332:

CCTTGGGCAC CTTCAATTTG CATATTACGA CGTTTTGCAG CTGGTTCAA TTGGCAATAA
CTACACCTAG TGCAGTTGGA TC

(2) INFORMATION FOR SEQ ID NO: 3333:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3333:

ATAAAATAAT TAGAACTCTA ACATTGGTTT AACTAATGTT TAGACTTTTT GTGGTTTGTA
AAAACAAGTA TATTGA

(2) INFORMATION FOR SEQ ID NO: 3334:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3334:

TGGTAAGTTG AATAAAGTAT TGAAATCGTT GCCAATATCT TTATACCGTT GGTTCCTGGC 60
5 ATTTATTGGG AGGC 74

(2) INFORMATION FOR SEQ ID NO: 3335:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3335:

AGATAGTTAT GCGCAGTTAA AAACGGTGAA ATGTATTTGC AATAATATGC ATATAGGCAC 60
20 CATACGAGTA AGGG 74

(2) INFORMATION FOR SEQ ID NO: 3336:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3336:

TTGAATCATT GTTAAAAATG GAATTAAAGT TGCTAGTATC TGTCGGGTTT TGAAATAGGT 60
CATAGGAGAA AACAGG 76

35 (2) INFORMATION FOR SEQ ID NO: 3337:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3337:

CCAAAGAGGC GTTATTAAGC TATTGATAAA AGTTATGTGA CTAAAAAATG TATTTAAATA 60
AGTAGTACCT AA 72

50 (2) INFORMATION FOR SEQ ID NO: 3338:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 75 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3338:

ATAAGTCGTT CTACCGTATA GCCGTCATTA TTAATCACAA ATAATACCGG TTAAATATGC 60
TGTCTGGTCA TAGTT 75

10

(2) INFORMATION FOR SEQ ID NO: 3339:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3339:

TTCATCAAAG TATTCCAATG GGAGAAAAAG CACAATAACA TTATCACTGG ATGCTAAATC 60
TAAAGGAACC TC 72

25

(2) INFORMATION FOR SEQ ID NO: 3340:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3340:

GTAAAAATAT TTAAATGAAT GTCTTCACTG GAGAACCATT GACAACCTGG TACAAGTGGG 60
ATTATTGGCG TTATTTT 77

40

(2) INFORMATION FOR SEQ ID NO: 3341:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3341:

AACCAAGGAT GGATTGCTAT TTAAATCCTT GGTGCTCTT TATTTTATTT AAATTGTAGA 60
ACCTAGA 67

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3342:

CTGGCAAAAG CACGTTTTAC AAGCATCAAT CCATTAATTA ATAATTCCAT TAAATGTAGA 60
 TTCACAGGGA TATG 74

(2) INFORMATION FOR SEQ ID NO: 3343:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3343:

GTTTGATCAT TAGAGAGATA TAGATATGCC GTAGAAAATA ATATGTCATT TGCGGATATC 60
 ATGGTTAAAG AAGAAATGGA ATTAAGCGGT AAATCACGTG ATGAAGTGCG AGCGaAATGA 120
 AACAAAATTT AGATGTCATG CGAGACGCAT AATCAAAGGG ACGACAGGTG ATGGGGTTGA 180
 AAGTGTAcGG TCTACACTGG TCATGATGCT GCTAAACTAC GTGATTATAA TGAAACACAT 240
 CATGCTTTGT CTGGGATATG AAATGATTGA CGCACAAGGG TGCCATTGCA ACAAATGAAG 300
 TCAATGCTGC CGATGGGTAT TATTTGTGCA CGCCAACAGC TGGTTCCTCG GGTACCATTC 360
 CCGGTGGCAC TTTTAAATTA GAAAAACAC TGGATnGAAC CAGAAGAGCC AATGn 415

(2) INFORMATION FOR SEQ ID NO: 3344:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3344:

TCCTATACCA CCACCGTCAA CAGCTCCTGC CATCGATCGT ACTTTCAATA AGTCCAATAA 60
 TCGCAGTGGT AATTCTAAT ACTA 84

(2) INFORMATION FOR SEQ ID NO: 3345:

(A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3345:

10 CGGGAGGTGT TAAntCTTCA CAAAATGCCG TACTATTCTT TGATGnAATC CATCAAATTA 60
 TCGGTTcAGG TGCCACAGGA AGTGATTcAG GTAGCnAAGG GTTATCTGAT ATTTTGAAAC 120
 CTGCATTaAG TCGTGGTGAG ATTTCTATTA TTGGTGCaAC AACACAAGAT GAATATCGAA 180
 15 ACAATATTCT TAAAGATGCT GCATTAACGC GCAGATTTAA TGAAGTGCTT GTTAATGAAC 240
 CAAGCGCTAA AGATACTGTT GAAATTTTAA AAGGTATTcG CGAAAAATTC GAAGAACACC 300
 ATCAAGTAAA ATTACCAGAT GACGTATTAA AAGCATGTGT TGACTTATCA ATTCAATATA 360
 20 TTCCACAACG ATTATTACCA GATAAAGCAA TCGATGTGTT AGATATTACA GCAGCACATT 420
 TATCnGCGCA AAGnCCAGCT GTCGATAAAG TTGAAACTGG AGAACGAATT TCTG 474

25 (2) INFORMATION FOR SEQ ID NO: 3346:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3346:

35 AAAATTAATA ACTCCTTGGT TATTGATATG CCTAAAGAAG AAGGTACAAT ACAACTAACA 60
 TTAG 64

(2) INFORMATION FOR SEQ ID NO: 3347:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3347:

50 AGGAATAACT TGATATTGAT GATAAAATCG TCAAACGGCA CTAATATTTA AAAACAAAT 60
 GTTTTAAGTT GTTGATTAA AATATTAAT 89

(2) INFORMATION FOR SEQ ID NO: 3348:

55

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3348:

10 ATAACTTGTA CTGCTTCCCA TTAATCACTG TGTCTCTTCA CCAGGAGCTG GCATTCTCTT 60
 AAAGAACANT TCTGATAAAG GTACAATTTC ACCGGGCATA ACTTCAT 107

(2) INFORMATION FOR SEQ ID NO: 3349:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3349:

25 CAACGCATCC TGCACCTTTTA CCTATTCCTG AATCACCAGT AATTAGTACA CCAACACCGT 60
 AAACATCTAC TAAA 74

(2) INFORMATION FOR SEQ ID NO: 3350:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3350:

40 AGATGCACCT ACTTCTAACT GTCGCCAACA TCGCCGCAAT CATTTCAAAA CTACGTTCTG 60
 TA 62

(2) INFORMATION FOR SEQ ID NO: 3351:

45

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3351:

55 GCTGCAAACA ACAAACTATT TTTGATTAAA TTGTGGATAT GATGGTAACC AACCAAGTCT 60

(2) INFORMATION FOR SEQ ID NO: 3352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3352:

ATTGAACGCA AGATTTCGAT ATAGAACATC TAGCGACGTC GATTGCAAG GTTGAACCAT 60
CTACATTAGG TGAGGAA 77

(2) INFORMATION FOR SEQ ID NO: 3353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3353:

TAATCAACAC GAGGAGATGC TATTTAATGT CATCTGACAC AAACAGTTTA GCACATACA 59

(2) INFORMATION FOR SEQ ID NO: 3354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3354:

TTATGTAACC GACGAATGCT GCGATAGTGC TACGCCATCA CCGCCAGCTA ATCCGATTG 59

(2) INFORMATION FOR SEQ ID NO: 3355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3355:

TAACTATACC TTTAGGGTTA CTACCAGCT TAGGTAGGTC ATAACCTTTA ACCACATCT 59

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3356:

AATAACGCTA AACCTAAAAT GCTAAATAAT CCGCCGAACA ACATGCCGTT GTTTGTTGA 59

(2) INFORMATION FOR SEQ ID NO: 3357:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3357:

CCAGAACCAC CCACGCCCTT TGAATATGGG AACTCAAAC GATCTACTGG CTGATGTAAT 60

TACCCCTGTT TTGATTG 77

(2) INFORMATION FOR SEQ ID NO: 3358:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3358:

AAGTTAGGTC TAGGGAACAT CGATAAATTA CCAGTAGTAA ATGCAGTTGA ACAACCAGA 59

(2) INFORMATION FOR SEQ ID NO: 3359:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3359:

CATGACCTTT AAATTGCATA TCTTCTGCAT CAGGTGCATC GCTTTTAAACA ATAACGTCA 59

(2) INFORMATION FOR SEQ ID NO: 3360:

- (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3360:

10 ACGCGACAAC ACCGCCCTCA ACTAAAGTAG AAGCACCGCA ACAAACAGCA AATGCGACA 59

(2) INFORMATION FOR SEQ ID NO: 3361:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3361:

GATTTGATCG AATTGAACGA ACATTGCTT CTCAAACGAT TGCATCTATT AAAGAAGTAT 60

25 GTCTAG 66

(2) INFORMATION FOR SEQ ID NO: 3362:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3362:

GGTTGCACAT CTTTACTAC AAATTCGCT GGTAAAGATG TTGCAAAAGT ATGTCCGT 58

(2) INFORMATION FOR SEQ ID NO: 3363:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3363:

50 CCTTGAAACG GCAACATTTT TGGGTCCTTC TCCATCATTT TATTTAAAAG CGCATTAT 58

(2) INFORMATION FOR SEQ ID NO: 3364:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 58 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3364:

TTGAGAATTT AGGAGGTTAA TGC GTTGATT AAAAGTGGCA AAGCACGTGC ACATACGA 58

10

(2) INFORMATION FOR SEQ ID NO: 3365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3365:

20

GTTTTTTTAT TTTGGATAAA AGGAGCAAAC AAATGGATAT TAACTGGAAA TTGAGATT 58

(2) INFORMATION FOR SEQ ID NO: 3366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3366:

ATTCATCGGT AATGACATTA TTTTACTTT GTAATTTTCAG TAACAGTTGA TCATCATG 58

35

(2) INFORMATION FOR SEQ ID NO: 3367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3367:

45

TAAATTAACA GCCGGATGAA ATGAAAGGTG CTACATGCAC AATCAGTAAT ATCGGTTC 58

(2) INFORMATION FOR SEQ ID NO: 3368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3368:

TACCTACTGG TGAGATTGGC GAACTTGCAA TTAAGGCTAA AAATGTCACG CCAGGATA 58

(2) INFORMATION FOR SEQ ID NO: 3369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3369:

TTAAACGGAG AAGGCTTTAC TTTACATGTT GAGGAAGGTC AAGAAGTTAA ACAAGGTG 58

(2) INFORMATION FOR SEQ ID NO: 3370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3370:

CTGCTAAACT ACGTGATTAT AATGAAACAC ATCATGTCTT TGTCTGGTAT ATGTAAATGA 60

TTGACGGC 68

(2) INFORMATION FOR SEQ ID NO: 3371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3371:

ATTACCAACA GCGAAAATAT TGAAAAGCTG TAAAAAAGCT GGTGCAsmCm TACTTGGATT 60

GAGAATTTAG GAGGTTAATG CGTTGATTAA AAGTGGCAAA GCACGTGCAC ATACGAATAT 120

TGCACCTTATA AAATATTGGG GTAAAAAAGA TGAAGCACTA ATCATTCCAA TGAATAATAG 180

CATATCTGTT ACATTAGAAA AATTTTACAC TGAAACGAAA KCACTTTTAA CGACCAGTTA 240

ACACAGGATC AATTTTGGTT GAATGGTGAA AAGGTTAGTG GCAAAGAATT AGAGAAAATT 300

TCAAAATATA TGGATATTGT CAGAAaTAGA GCTGGCATCG ATTGGTATGC AGAAATTGAA 360

(2) INFORMATION FOR SEQ ID NO: 3372:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3372:

ATTTCAACAA CTTTAAAGCA CGTATAATGA TGATTTTCAG ACTTGTACAA AGGAGAAA 58

(2) INFORMATION FOR SEQ ID NO: 3373:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3373:

AAACCGAGCA GCGCAGTAAA CCTGCAGTAC CTTTATCGCT TCTAGATAAT CCGATTG 57

(2) INFORMATION FOR SEQ ID NO: 3374:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3374:

AGTACGAATA TTACCTTTAT TTAATGGGTG AGCTAAGTTA CTTTTTCATTT CTCGTG 57

(2) INFORMATION FOR SEQ ID NO: 3375:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3375:

GGTGAAGTAT AACTTTGTAA TGGCAGCGCA CTTAATGACT GCCAATAATT GTGACCAACA 60
ACTAACAGAC 70

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3376:

TTCCAAACTT CATTAGGTGA TAGCTTTAAT TTCAAGGCTG GCAATCGCCA TAACAAG

57

(2) INFORMATION FOR SEQ ID NO: 3377:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3377:

TCCTTCAAAG TCAATGGATT TGATCCTCAG AGGACTCAGT GTATCCTCCA AGTGACCTGG

60

CTCGCATCCA

70

(2) INFORMATION FOR SEQ ID NO: 3378:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3378:

ATGAATCATT AAGCCTTTTCG GTGCATATGC TGCAAGACTT TGACCAGCAT GACCAT

56

(2) INFORMATION FOR SEQ ID NO: 3379:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3379:

CCAACGACTG CGCCAATATT AATTGTTGCG CCCATCATAA CGACAGCACC ATCTTC

56

(2) INFORMATION FOR SEQ ID NO: 3380:

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3380:

10 ACAAAAGCAT CAAGCTGTTG AAACAATCAA TGATAGCATT CGAGATTATT TAGTTAG 57

(2) INFORMATION FOR SEQ ID NO: 3381:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3381:

CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA AATAACCGAA GTATTT 56

(2) INFORMATION FOR SEQ ID NO: 3382:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3382:

35 GAACACACAG GCAACCCAAA GCAGTGACGG CGAAANTTGG ATTGATCTTG CAGCATTGAA 60

GAAGATCGCG ATGACTATAC AATCAATATC GAGTAGAAGA CCGAT 105

(2) INFORMATION FOR SEQ ID NO: 3383:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3383:

50 TGTATGTGAA AACTATTTGG CGATATTTTA GTGATGAGCC TCAGTGATCC TGGTTCCTGG 60

TTATCACCTC TGCTAGTTTA GTACCGATGG TCCAAGATTG ATGAGC 106

(2) INFORMATION FOR SEQ ID NO: 3384:

55

(A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3384:

10 TTCTTCGTCA AGATCAATCT CTTCAAGTAC AATCTTTAAT ACCTTCTGCA CCCATTT 57

(2) INFORMATION FOR SEQ ID NO: 3385:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3385:

CGGGCATCTT AAAGCCGATG TTTATCCTGT AATCCTCCAA AAGGAAACAT GTACCTCAAT 60

25 TAGAG 65

(2) INFORMATION FOR SEQ ID NO: 3386:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3386:

CATTTTAAAT TATTTCTATT TGCTTTTAA CCACTTCTCT GACTGCTTCC GAATCATTTT 60

40 TCTTAACTGC A 71

(2) INFORMATION FOR SEQ ID NO: 3387:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3387:

TTAGAAAATG ATAAACGTAA AGCAGTAAGT GCTGAAGAAT ATAAAAAAGC TGACG 55

(2) INFORMATION FOR SEQ ID NO: 3388:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3388:

TCTTCGACAA CTTTAATAAT ATTAGCCAAC GCAGTGTCCC CGCCAAC TTT TGTTCG

(2) INFORMATION FOR SEQ ID NO: 3389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3389:

ATTTATTAAC GATTAATGAC GCTGGCATGC CAATCCAGA TGATCATCGT CGTATC

(2) INFORMATION FOR SEQ ID NO: 3390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3390:

AAATGCTATG TACCCACTTT AGATGAAATT TTAGTAACGT TATGGCCCGA AATGCCAACT

ATTATATTGA

(2) INFORMATION FOR SEQ ID NO: 3391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3391:

CAAACGCAAT AGCTGGTGAC TTAAGTGGG GCACTTGGCA TGTGGATGGC AATACTTCG

(2) INFORMATION FOR SEQ ID NO: 3392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3392:

GCATCTACTG GGAAACGATT ACAAATTGGT GATTTATTAC AAAAGCCAAC TGTAT 55

10

(2) INFORMATION FOR SEQ ID NO: 3393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3393:

20

TTTATAAATA TCCAGTCTG AACGCGATTC CCATAACGGA TCAATGGCAG GATTG 55

(2) INFORMATION FOR SEQ ID NO: 3394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3394:

TGCTTACGCT CAGTGACATA ATCTAATGTG GCACGTAAAG CGCCACCATA CCACC 55

35

(2) INFORMATION FOR SEQ ID NO: 3395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3395:

45

AGTCACCATT TGTTGGTACA GGTTATGGAA CACGTTGCAG CACGTGATTC TGGTGCGG 58

(2) INFORMATION FOR SEQ ID NO: 3396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3396:

CAAATGCATT TAAAACCAAT ATTGAGTTAC ATGAAAGCAC ATACGATGCA AACGT

55

(2) INFORMATION FOR SEQ ID NO: 3397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3397:

TGTTGATGAG TCGTGTTTTA TCTCAAGATG TGTTACTCAA AAAGTTATAG AAGA

54

(2) INFORMATION FOR SEQ ID NO: 3398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3398:

CTTCGTCAAG ATCAATCTCT TCAAGTAAAT CTTTAATACC TTCTGCACCC ATTT

54

(2) INFORMATION FOR SEQ ID NO: 3399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3399:

AATGAAAAGC TAGCTGTAGT TGCAAGAAAA ACTGGCTTAG CGATGGCAGT TGGAT

55

(2) INFORMATION FOR SEQ ID NO: 3400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3400:

(2) INFORMATION FOR SEQ ID NO: 3401:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3401:

TAAAAATCGC GCACTTAAAC CGCTTATGAC AATCATTATT ACCGCAATAT GCTTG 55

(2) INFORMATION FOR SEQ ID NO: 3402:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3402:

GGCACCTCCT TGGATTATTT TTCTTCTACT GTTACTAAGT GCTTAACTTT GTTG 54

(2) INFORMATION FOR SEQ ID NO: 3403:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3403:

GATAAGTCTA ACAAGTGGCA CCCATAATCG ATTAACTAC CGCCACCTTG CAACGTTT 58

(2) INFORMATION FOR SEQ ID NO: 3404:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3404:

TCGTTTTTCGT CCCCAAATTC TGCCAACTTA TTCATGAACT TATCTAGCGC TATTGTTCTT 60

TGTCT 65

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3405:

AAATTTCAGC ACCAATTGTT ATTGGACGAC ACCATTAGA TGCTGGTTCA GTTGC

55

- (2) INFORMATION FOR SEQ ID NO: 3406:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3406:

TCGATTTCAG CGGAACACAT GTAACGTTAG CACAAGCCAT GAACCAATTA GGTGGC

56

- (2) INFORMATION FOR SEQ ID NO: 3407:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3407:

AATTGCTAAT GGTCAAGTAT GGACGTGATC ATTGTTGGTA CTAATTATTG CTGAAACTGT

60

TAAAGATTAG AAGG

74

- (2) INFORMATION FOR SEQ ID NO: 3408:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3408:

TGATTTCACA CTTGATAACG GATACTTCGA AGAGATACAT CAGCAGCGTT CAGCTCAGAT

60

AGTGCTCA

68

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3409:

TATGATTAGA AAAAGGGGAA TTTTATGGA GTATAAGAGT TACTATGATT CGCC

54

- (2) INFORMATION FOR SEQ ID NO: 3410:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3410:

TATCTTTCAT CATTGAAGAA GATCGCGATG ACTATACAAT CAATATCGAG TATA

54

- (2) INFORMATION FOR SEQ ID NO: 3411:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3411:

TTGAAGTGCA CGAATCGAAT TATTGTAAGC AGTAATACTT GCCGGCTTCT TAC

53

- (2) INFORMATION FOR SEQ ID NO: 3412:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3412:

TAGCCGATGG AACCCCATAA CGGTTGCCCT ATAAAAGTAT TGTTTTTGTA TAGTGCTAAA

60

TCA

63

- (2) INFORMATION FOR SEQ ID NO: 3413:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3413:

10

ACTACCATTG CTTGTTCCGG TTTCACAACT GGTTCAGTAT CATTACAAC TGC

53

(2) INFORMATION FOR SEQ ID NO: 3414:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3414:

ATGCTGTTGT AAACGGTAAT ACAACATACC TGCCCAACCC GGTAACGCCA AAAAATGTCC

60

TT

62

25

(2) INFORMATION FOR SEQ ID NO: 3415:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3415:

ACTTAGATCA ATCACATGAT GCCTCACGGA ATCCATTATT TGAAGGTCAT GTTAG

55

(2) INFORMATION FOR SEQ ID NO: 3416:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3416:

TTAGTTCCAG CAATACCTGC TACAGTTGCT GCAGATGCTT CTTTCACCCA TGG

53

50

(2) INFORMATION FOR SEQ ID NO: 3417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs

55

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3417:

TGATTTAGGT GCAAAAATTG TAGGTATCGC TGAGGCTTAC GGTGCATTAC ACGATCCAA 59

10 (2) INFORMATION FOR SEQ ID NO: 3418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3418:

20 CGTGGTCACC ATCACCAATT GCTCGATCTA ATTCACTAAT TCAGATTCAT GTT 53

(2) INFORMATION FOR SEQ ID NO: 3419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3419:

TGGACCTACT GCAATAACTG AACGTCCTGA ATAGTCAACA CGTTTACCAG TAAGT 55

35 (2) INFORMATION FOR SEQ ID NO: 3420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3420:

45 TGTCTCCGGT ACCGTTTGCA CCAGGAATAA AGATGAGCAC GGGTCCTTGT CCG 53

(2) INFORMATION FOR SEQ ID NO: 3421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3421:

AAATTAAGAA AATTCATTGC CAGATAATTT AGATAAATAA TTAAAACTTA GACCATTAC 60
5 CCCAATCCCT GA 72

(2) INFORMATION FOR SEQ ID NO: 3422:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3422:

CATATGTTAA ATGGACTCGC TAGATTTAAG TCGCAATAGT AGCGGCCGTT TCTT 54

20 (2) INFORMATION FOR SEQ ID NO: 3423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3423:

30 CACGTTTCAA ACCTAAAAGA TGCTAAAAAT TTCTCTTAAT TCTTGTGCAA TA 52

(2) INFORMATION FOR SEQ ID NO: 3424:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3424:

ATCGCCTAAC CAAGATGCAC CATCGGTGAT TTTATCGCCT GCCGCTTCAA CCAT 54

45 (2) INFORMATION FOR SEQ ID NO: 3425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AATAGAAAAT GTACGTAGCG GTATGATGAG GATTTCGCAG ACTAGTTTAG GGTCAAGTG

59

(2) INFORMATION FOR SEQ ID NO: 3426:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3426:

CCAACGCCAG ATCCAGAACC AAGTCCAGAC CCAGAACCGG AACCAAGCCC AG

52

(2) INFORMATION FOR SEQ ID NO: 3427:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3427:

CCATATTAAT GGTTATGTTT ATGTGAATGC TTGCTTGCTG GACTTGTCTT TT

52

(2) INFORMATION FOR SEQ ID NO: 3428:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3428:

TAAAACAGAG ATTGATACTG CAGAAGATAA CTGTATCTCT CCATCTACTG TA

52

(2) INFORMATION FOR SEQ ID NO: 3429:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3429:

TGAAAATCCA CAAGTCGCAC GTACAGTGTT TGAAAAGGT ATTATGGCGG CA

52

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3430:

ATAATTCTTC CAAATATATG AAAATGGATT TGTTCTTTT TTATAAAAAT CTTATGCTTT 60
 TTAACATAATT GTAAGA 76

(2) INFORMATION FOR SEQ ID NO: 3431:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3431:

CTGCGGGGGA TAACTGTATC TCTCCATCTA CTGTAAGTC GTATTAGAAC TAAAGCGGCT 60

(2) INFORMATION FOR SEQ ID NO: 3432:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3432:

GGCTTCAGGC TCATTGATAG GTAAAAGTTG CAAAGCCTGC AAAGCGATTG GG 52

(2) INFORMATION FOR SEQ ID NO: 3433:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3433:

TCGCACGATA CGCCTCCGAA TGAAGAAGGT TTATTGTGCG ATTCTTTTAT TGTAAATTT 60
 TAAATTTTT 69

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3434:

GATCGCTATC CATTAGCTAA ATTTAAACGT TCAAACCTCAG GTACATGTTA C

(2) INFORMATION FOR SEQ ID NO: 3435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3435:

TATAGCTACT GCTGCAGCTG CGGCCATTGC AGATGCTGAA CCAACTTCAG C

(2) INFORMATION FOR SEQ ID NO: 3436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3436:

ATTAAAGCCA ACATTAAATTT ATCCACTATT AACATAACG GCTACAGGCT TATTAATGAT

TTATACCTTT

(2) INFORMATION FOR SEQ ID NO: 3437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3437:

TTTGTTTGTT GATTCTTCTC CACCTGTTTC AGGTAGTTCA GATTTCTTAG A

(2) INFORMATION FOR SEQ ID NO: 3438:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3438:

10

GTGAATTCCG TAATTACATT TTAGGCTTGA TTTTCTATCG CTTCTTATCT G

51

(2) INFORMATION FOR SEQ ID NO: 3439:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3439:

TTAAGACAGG TTCCTTATGG GACTCTAACA ACGTATGGTG CTATTGCCAA A

51

(2) INFORMATION FOR SEQ ID NO: 3440:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3440:

35

CACTAGAAGA AACGGATTCA TCAGCTATTG GTATCGATTA CCATACTGCT GTGGA

55

(2) INFORMATION FOR SEQ ID NO: 3441:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3441:

CTTCTGGCAA TAGACCGCA GTTACTGGGG GCAAACCCAG TGTGTAAAAC CGGA ACTACT

60

50

ATGAGGGGCA TGAAAGT

77

(2) INFORMATION FOR SEQ ID NO: 3442:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3442:

GTTCGGTTGT GACAGTCAGT GGACGCGTTA CCAAATGGGC GGGAATTAAA GCAAA

55

10

(2) INFORMATION FOR SEQ ID NO: 3443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3443:

20

ATGAACTTTG GGATAAAGGT GATGCCCAA CTTTCCGTAA CTCATGATGA T

51

(2) INFORMATION FOR SEQ ID NO: 3444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3444:

CAACGCAGCA AAGCGGAGTG GCCCTTTACC TTCACAGAAT AATGGTCTAA T

51

35

(2) INFORMATION FOR SEQ ID NO: 3445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3445:

45

ACCGAGCAGC GCACTAAACC TGCAGTACCT TTATCGCTTC TAGATAATCC

50

(2) INFORMATION FOR SEQ ID NO: 3446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3446:

CCAATGCAAC GATCCAGTTA TTGTGTTGGC GCAATTGATT AATAGTATTC

50

(2) INFORMATION FOR SEQ ID NO: 3447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3447:

GCGCATCATA TCCCATGCA CCGATAAGAT CCTTCTTACC TTCTACAAGT

50

(2) INFORMATION FOR SEQ ID NO: 3448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3448:

GTTCTTACTT CTTTATCGTG GCTCCAACGT GCTCTGTACA TTTTTCCTCA TCTCTCTACT

60

(2) INFORMATION FOR SEQ ID NO: 3449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3449:

CAACACCACC GACACCAGAA GTACCAAGCG AGCCGGAAAC ACCAACACCG

50

(2) INFORMATION FOR SEQ ID NO: 3450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3450:

TTATCACGGT ATATGAGGGG ATTTGAGG

88

(2) INFORMATION FOR SEQ ID NO: 3451:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3451:

TGCAAAACGT TATGAAGTAC AAGTTGATGG AAGCAACAAA GTAAGTGCGn

50

(2) INFORMATION FOR SEQ ID NO: 3452:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3452:

CAGTTAAGTC ACCAGCTATT GCGTTTGGTG ATCTTAAGCA GCGGTGGATT ATCAAGTTTG

60

GGTA

64

(2) INFORMATION FOR SEQ ID NO: 3453:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3453:

TCGTAAACAA TATACTATCT CAACATTTAT TCATCCAATG GAGATAACGT ATTGCGCGGT

60

TTAACAGGTA ATTTAAACCA AATACGGTAG TAATnATTAA TAGATAGCAA ATCAAGTATA

120

AAGAATAAGT A

131

(2) INFORMATION FOR SEQ ID NO: 3454:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3454:

TTAAAAATGC AGTTATGGCC TCTAAAATCG TATTAAGCAT ATTAGCGCCC

50

(2) INFORMATION FOR SEQ ID NO: 3455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3455:

TGCTACATGG CGTTACGGTC AAGATCGTCA ACGATTGATG GGTACAATTG A

51

(2) INFORMATION FOR SEQ ID NO: 3456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3456:

ACAAACTGCC AACGATTGGT CGTGTGAATC ATCCAGTGGA AGAAGCGCAn

50

(2) INFORMATION FOR SEQ ID NO: 3457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3457:

AATCACGTGA GAAGGATACA GCTATTAGTA TCGGTATCAT CGCATTGATT

50

(2) INFORMATION FOR SEQ ID NO: 3458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3458:

(2) INFORMATION FOR SEQ ID NO: 3459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3459:

GGGCCAACAA ATCGGAAACT GCCAATTGGA CGGTTGCCGT CATCAAACCC

50

(2) INFORMATION FOR SEQ ID NO: 3460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3460:

TGCTTCGCT AGAGGATCCG GTATTGCTAG TCAATTACTA CACCATTAA ATTGTGGAAG

60

CAAAGCT

68

(2) INFORMATION FOR SEQ ID NO: 3461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3461:

TGGTCTTCGC AATCCACGGA TATACCTTAG TACCAGGTAA TTGACCACCT T

51

(2) INFORMATION FOR SEQ ID NO: 3462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3462:

AAGCTATTAA TGTAATTTAT CAATTGATTG TGCAACGGAC ATCATCTACA AGACCG

56

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3463:

ATACCAAATG TGAGAAACTG GAGCAGCAAn TTCAATGTGA CCCATTCTTT

(2) INFORMATION FOR SEQ ID NO: 3464:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3464:

TCITTACGGC GTGGTTCTAA TCGCATCTTT TTCAATCTAA GTGCGTTTnT

(2) INFORMATION FOR SEQ ID NO: 3465:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3465:

AAAGAAGATT GGAACGTGTA TTGACGACTG CACCCAGGTA TGGGTGTTTCG CCCGACA

(2) INFORMATION FOR SEQ ID NO: 3466:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3466:

ACATCCGAAA GATGACTTGT TTAaaaaAGC AGAGCATGAT TTGCTTACTA TGATTACACG

CGG

(2) INFORMATION FOR SEQ ID NO: 3467:

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3467:

10 TACCGATGAT TTCCGAGACA TAGACCGGCC TGTCTGGGGG TCAACTGGAA CTTGGTC 57

(2) INFORMATION FOR SEQ ID NO: 3468:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3468:

TGTTCCCTAAT ATTTATGTTG TAAAAATGTA CAATCTAATT AAAGCAATAG TCTTGGGCA 59

25 (2) INFORMATION FOR SEQ ID NO: 3469:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3469:

35

TCCATGATCG TTCAACATTT AAATACACAA CTTAATAAGT ATCGTGTACA AGTTATG 57

(2) INFORMATION FOR SEQ ID NO: 3470:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3470:

CCCTGTTTCAG GCTATCCTCT AAAGTGACGA TATAGAATAG CGATTAATAT CGCGATAGT 59

50

(2) INFORMATION FOR SEQ ID NO: 3471:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3471:

5 TACGCCATCA nCGCCAGCTA ATCCGATTGC GACACCTAAT GCGAAATCAT 50

(2) INFORMATION FOR SEQ ID NO: 3472:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3472:

AACGTCATCA AATGGAAGTA CGTGACGTTT ACTACTCTCA CTATGGCCGT ATGT 54

(2) INFORMATION FOR SEQ ID NO: 3473:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3473:

30 TAATAGGCAT TCCCATTAGG TCGTTCGACA ACTGCAACGC AAGCATTTGA AACAGA 56

(2) INFORMATION FOR SEQ ID NO: 3474:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3474:

TTTAAAGAAT GTCGCGTTAT CTGCGCCCAT TGGATTGACA TACTTCATAC GTATA 55

45 (2) INFORMATION FOR SEQ ID NO: 3475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 50 (D) TOPOLOGY: linear

55

GCCTTTAGGT AAAATGGGCA GAAATGCTAA TCATTTTGGC GCGGAAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 3476:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3476:

AAAnCATTTCG CAATCGACCA TAATTTTTTA TGTAATTCAG CTTGTTGCTG

50

(2) INFORMATION FOR SEQ ID NO: 3477:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3477:

GGAnGACCAT TAATCGATAT CGGTACACAC GCTTTAGATT TAACGTTATG

50

(2) INFORMATION FOR SEQ ID NO: 3478:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3478:

TGCCTCCTTA CGCCATGATG CTTATTCAAA GTAAATTGCT TTGCCGGACT TTGCAGACTG

60

(2) INFORMATION FOR SEQ ID NO: 3479:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3479:

GGTCTTTTCAG CTGCTAACGA GTTCCTGTTA CTGTTTCATGT CTATCACTTT GCGTTCCTC

60

(2) INFORMATION FOR SEQ ID NO: 3480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3480:

CAAGTATCAT ATGGACGGCT CGCCCAACAC AAAACAAGnC CAAGCAAAAC

50

(2) INFORMATION FOR SEQ ID NO: 3481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3481:

ATTAAACAAC ATAGCTCGGC TAATCCTTTA AAGCTTTTGA GTTTTCTGT TGTAGAACAA

60

GA

62

(2) INFORMATION FOR SEQ ID NO: 3482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3482:

TGTGGCTAGC TGTTTCTTTT TTAGGTGCTG TGTAGGAGAT GAACTGATCG T

51

(2) INFORMATION FOR SEQ ID NO: 3483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3483:

GCAGTTTATA AGTAGAGAGA CAGCTGATCA TGAGATAAAA ATGGGTAAAT ATTT

54

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3484:

TTATCTATCA CAGTACGAAT CCCCCAGAGT ACCGATTGTG ACAGCAACTT CTGCG

(2) INFORMATION FOR SEQ ID NO: 3485:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3485:

ATCTCTGGTT CGATTCCCGT CGAGACCGGC ATCATTACAT GTTTATTATG GG

(2) INFORMATION FOR SEQ ID NO: 3486:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3486:

TGTGTCACGA TAATAGGCGT AATATCACTC TTTGGCATGA TTGCCGGATG

(2) INFORMATION FOR SEQ ID NO: 3487:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3487:

TATTTTTGAT CAACTCAAC GCACAAACGA ATGGCCTTTA CCTTCACAGA ATAATGGTCT

AATGTAA

(2) INFORMATION FOR SEQ ID NO: 3488:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3488:

10 TAGGTGGTCA ATTACCTGGT ACTAGGTATA TCCGTGGATT GCGAGGACAA 50

(2) INFORMATION FOR SEQ ID NO: 3489:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3489:

CAATTGTACT TCATAACGTT TTGCATTTTCG CCACCTTCAC CACTATATTT TCCCATGGTC 60

25 (2) INFORMATION FOR SEQ ID NO: 3490:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3490:

35 CTAAACTGAT TGTTTTACGT AACGTTTCAT CGGCTTCTTT CGCTTCTATC 50

(2) INFORMATION FOR SEQ ID NO: 3491:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3491:

TCGATTTACC TTTCATCATT GAAGAAGATC GCCATGACTA TACAATCAAT AT 52

50

(2) INFORMATION FOR SEQ ID NO: 3492:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3492:

AACCTTTTCA CAAATATCAT ATAACTCTTC TAATGGGATA ATCTCTTCAT GT

52

(2) INFORMATION FOR SEQ ID NO: 3493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3493:

GGTTTTAAAC CGTCACGAAC ATCTGGCAAT GCACGAGCAA CGTACATACG TATCTAAAGT

60

TACGCTT

67

(2) INFORMATION FOR SEQ ID NO: 3494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3494:

TACGTTATGT TATGTAAATA ACAGTTAATT ATACCGGTGG TCTGGGTCGA

50

(2) INFORMATION FOR SEQ ID NO: 3495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3495:

CGCTTGTTGT TGTACTTTGG CAGTTCGCGT TGTGGATTGT GCCAGCGCTT TTAAACCGTA

60

(2) INFORMATION FOR SEQ ID NO: 3496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3496:

GGCACCGGCT TCTCTATTGC TTCTTTAGCA TATCTGCAGC TCTCTCAAGG GACATG 56

(2) INFORMATION FOR SEQ ID NO: 3497:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3497:

CACCTTTAGG ATACGCGTCT AACCACTGTG TCGCGTCTCT ATATATCGCT AAACACGTA 59

(2) INFORMATION FOR SEQ ID NO: 3498:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3498:

AAGTAATATC TGAATGCGTA TATTGTCTAA TTTCAAATTC TACAGACATC GACGT 55

(2) INFORMATION FOR SEQ ID NO: 3499:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3499:

AnTGTAACG TCCATCTTCA CATGACAACA ACGATATTTT GACCATCACA 50

(2) INFORMATION FOR SEQ ID NO: 3500:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3500:

(2) INFORMATION FOR SEQ ID NO: 3501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3501:

TGTGTGCCTT TAAGTTGTTG ATGACACGCA TTCACGACAA CAGACATGAC AC 52

(2) INFORMATION FOR SEQ ID NO: 3502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3502:

CTGGCTTCAA TGGCAACTTC TGTACCTGGT ACCAATGGGC GATGACCGAT 50

(2) INFORMATION FOR SEQ ID NO: 3503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3503:

TGTCCGACTT GGCGGnATCG TAATTTAGCG CnTGTAATTC TAAAGGGACC 50

(2) INFORMATION FOR SEQ ID NO: 3504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3504:

AACCTTCATA TTGCTTCTAA TAAGAAACCG AGCAGCGCAC CAAACCTGGC AGTACCTTTA 60

TCGC 64

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3505:

TATTGATGTT GAAAACTGTT ATGTCCTTTC GATGGGCCAA CACnAAATA

(2) INFORMATION FOR SEQ ID NO: 3506:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3506:

GAATATGGTA TCAATGGTAT GCACTAAGGC TTTATGAAAT TCATTAAAA T

(2) INFORMATION FOR SEQ ID NO: 3507:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3507:

CGGTTTTAAT CGGTAAATTA AATATGGATG AGTTTGCAAT GGTGTTTACA GAACATCTAT

TTAA

(2) INFORMATION FOR SEQ ID NO: 3508:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3508:

CAAGGCCTTG TTTTAAAGC AGCTACAGTT GGCAATATGT CCACTCATGT

(2) INFORMATION FOR SEQ ID NO: 3509:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3509:

CAGATGCAAA TTGACATGGT CATCAACATC nGTnCATTA AAGATGGACG

50

(2) INFORMATION FOR SEQ ID NO: 3510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3510:

ACAAGAGGGT CACCCAGCTC GGTGATTCC CACCGCCACA TCATGATATT TATTCATAGA

60

GTTTACGCAC TGTACATGAT TGAATGCGAT AAAG

94

(2) INFORMATION FOR SEQ ID NO: 3511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3511:

ACTCAACAAT GGATATTCTT AACTGAAAA ATGGGTAATG GTGCAAACAT AGTA

54

(2) INFORMATION FOR SEQ ID NO: 3512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3512:

CCGGATGCAC ATTTGATGAC TGAAGTCCGC GATAAAGGGA CAAnAGTCAn

50

(2) INFORMATION FOR SEQ ID NO: 3513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3513:

GCATTAAATT GAAACAATCG GATTTACAAT TTTCTCTTAA TGCTGTCGTC TACACAGC

58

10

(2) INFORMATION FOR SEQ ID NO: 3514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3514:

20

GTGTTTCGTGT TCATGCAAGG TGAATGCGAG TGATCTGTTG GTATGGGCTT TATGCATGGC

60

AATCTG

65

25

(2) INFORMATION FOR SEQ ID NO: 3515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3515:

35

ATGCCACTGA TAATGCnnCT GAACTTATTG ATGACTTCTC ATTAGACTAT

50

(2) INFORMATION FOR SEQ ID NO: 3516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3516:

CGGCGACAAA GAGTAAACAC AGCGGAGGGA CAAAGCCCCGC GACTAGCAAC

50

50

(2) INFORMATION FOR SEQ ID NO: 3517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3517:

5 ATGCCTATGT AGCACCGAGT ACCGATACCG AACACTTAGC TACGCCAGTT C 51

(2) INFORMATION FOR SEQ ID NO: 3518:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3518:

GAGCATnAAG GTGATTTnGA TCGCTATCCG TTAGCTAAAT TTAAACGTTT 50

20 (2) INFORMATION FOR SEQ ID NO: 3519:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3519:

30 GATTGGTATT TAGCTTTAAA TTTATGGTTG GAATAGTAGG TGGCATATAT CGCTGTTAGT 60

ATCG 64

(2) INFORMATION FOR SEQ ID NO: 3520:

35 (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3520:

45 TCTTCAATCT CAGGGGCATC TACTAACATA TCATCCAGTC AATATTGCGT CACATTGTTA 60

ATCGGTTCCG ATC 73

(2) INFORMATION FOR SEQ ID NO: 3521:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3521:

5 TCAAATTGGC AATTGGTACG AATGTCGACT GTACTAACAT CATTAGCTCA TGATTGCCAG 60
GTGATTTCAT GGATG 75

(2) INFORMATION FOR SEQ ID NO: 3522:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3522:

TTCCAATGGG CTTCTGACTT TGGCGGTTTT AGTGCTTGGG TTGCCGGCGG TTTTGGA 57

20 (2) INFORMATION FOR SEQ ID NO: 3523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3523:

30 TGGTGGAGGT TTTGTTTTTT CCGTGTGGT TTTGTTTTTC GTCCTGGTTT CTTTGTTTT 60
TGTGTTCTCT TT 72

35 (2) INFORMATION FOR SEQ ID NO: 3524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3524:

45 ATATCACAAT ATACCGGTTT ATATGCTGTC TAATCATAGT TGAATAGTGA C 51

(2) INFORMATION FOR SEQ ID NO: 3525:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3525:

TAGACCGTCG TGGATAGTTT TGGGTACGGT AACCAATTTA TTTTGAAGAG ACCATCCTC

59

(2) INFORMATION FOR SEQ ID NO: 3526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3526:

TAATAACGTT GCCCTCCCAT GTATATCCTA CCAACATGAC ATCTTGATACA

50

(2) INFORMATION FOR SEQ ID NO: 3527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3527:

TTCCCAACGA GCAGTCGCAT GCGGTACTGC CACGGCATT TGTATGCAGGC CT

52

(2) INFORMATION FOR SEQ ID NO: 3528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3528:

AAAGAAAnGA TnGnnnGnnn GnAnAAAnnn nnCCATnnnn nTAAAAA

50

(2) INFORMATION FOR SEQ ID NO: 3529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CATTAGCCTC ATCCCCTTCG TTTAGACTCG CTATAGATGC ACTAAATGGC GATATATTTT 60

TC 62

5 (2) INFORMATION FOR SEQ ID NO: 3530:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3530:

CACTACCACA AAAATTATAG GTGTTGACCT TCAGGnGCAA GTAGTATGAT 50

(2) INFORMATION FOR SEQ ID NO: 3531:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3531:

30 GAATGCAAAA TCCATTTGTA AGGAnATCGA ATGGTTTAgT AnCTCGTGCA 50

(2) INFORMATION FOR SEQ ID NO: 3532:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3532:

GGTAGAnCnC TGTTTAgTAC TAGGGGCCCC TCTCGGGTTA CCAATTCAGA 50

(2) INFORMATION FOR SEQ ID NO: 3533:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3533:

(2) INFORMATION FOR SEQ ID NO: 3534:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3534:

CGTCAACGAT GTAAAGTAA GCCTTGTCCTA GTTTAATTTA CGAGTGGCGT AA 52

(2) INFORMATION FOR SEQ ID NO: 3535:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3535:

TTAATCCAGA AGTACCGGTG GATTTAGTTA TTGACCACTC AGTTCAAGTG GATAGCTATG 60
CAAATCCAGA AGCTCTTGAA CGTAATATGA AATTAGAATT TGAACGTAAC TATGAACGTT 120
ATCAGTTTTT AAATTGGGCA ACGAAAGCAT TTGATAATTA CAATGCAGTT CCTCCTGCAA 180
CTGGAATAGT TCACCAAGTT AACTTAGAAT ATTTAGCAAG TGTTGTACAT GTTCGTGATG 240
TAGATGGTGA AAAAAGTGA TTTCCAGATA CATTAGTTGG TACTGATTCA CATAACAAC 300
TGATAAATGG TATTGGCGTA CTAGGATGGG GTGTTGGTGG TATTGAAGCT GAAGCTGGAA 360
TGCTTGGACA ACCTTCTTAT TTCCCAATTC CAGAGGTTAT 400

(2) INFORMATION FOR SEQ ID NO: 3536:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3536:

CGTATAGAGT GTCCTACAAC CCCAACAAGC AAGCTTGTTG GTTTGGGCTC TTCCCGTTTC 60
GCTCGCCGCT ACTAAGGGAA TCGAATTTTC TTTCTCTTCC TCCGGGTACT AAGATGTTTC 120
AGTTCTCCGG GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC 180

GCATATCGTC GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC 300
 CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGCTCA CATACGGCTT 360
 5 CGTTTTTCATT ATTTTAAATG CTCATTTACA TAAGTAAACT CTGCTTTAAA ATAATTTAAC 420
 TCATTGTC TG CTAAACGTTT TCTTTTATAA AAAGATTTAA ACGCGTTATT AATCTTGTA 480
 10 GTGTTCTTTC GAACACTAGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACCTCTTA 540
 TTCACTCGGT TTTGCTTGGT AAAATCTATA TTTTACTTAC TTATCTAGTT TTCAATGTAC 600
 AATTTCTTTT TAGTCAAGCG CTCGCATACT GCTTTATTTT CAAAAAATCA AATGCTCATT 660
 15 TACAAAAGTA AACTCCGCTT TAATTTTTCT TAATGCATTG TCTAACAACC GCTTTCTTTA 720
 AAAAGAATAG ATTGTCAAGC GCTCGCATAA GCAATATCAC TTAAACCAA AAATATTTGA 780
 ATGTTAAATA AACATTCAA ACTGAATACA ATATGTCACG TTATTCGCA TCTTCTGAAG 840
 20 AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT 900
 ACCTTGTTAC GACTTCACCC CAATCATTTG TCCACCTTC GACGGCTAGC TCCTAAAAGG 960
 TTA CTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGcGGT GTGTACAAGA 1020
 25 CCCGGGaACG TATTCACCGT AGCATGCTGA TCTACGaTTA CTAGCGtTCC AGCTTCATGT 1080
 AGTCGAGTGC AGACTACCAT CCGGACTGnG GACCAACT 1118

(2) INFORMATION FOR SEQ ID NO: 3537:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3537:

40 GGGGATCCCC AGCCAGAAGA TTTATTCAGT GCGATGATTC GTGAAATTGA AACGCAAGAT 60
 TTCGATATCG AACACCTGGC GACGGCAATT CGTAAmGTTG AAACATCAAC ATTAGGTGAA 120
 45 GAAAGTGAAA ATGACTTTAT CGGTCTGTTC AGCGATATGG ATTTGAGTTC AACGCGACTA 180
 GGTAACAATG TCAAAGAACG TACTGCTTTA ATCTCTAAAG TCATGGTTAA TCTTGACGAC 240
 TTACCATTCTG TTCACAGTGA CATGGAAATT GATATGTTAG GTGATGCATA TGAATTCCTA 300
 50 ATTGGGCGCT TTGnGCGACA CGGGTAAAAA AAGCAGGCGA GTTCTATACA CCACAACAAG 360
 TATCTAAGAT ACTGGCGAnG ATTGTCACAG ACGGTAAAGA TAAATTACGT CACGTGTATG 420
 ACCC 424

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3538:

ATCTCATATG	TTAAAAGGTA	AACAAGGTCG	TTCCCGTCAA	AACTTACTTG	GTAAACGTGT	60
TGACTATTCA	GGACGTTTCA	TTATTGCAGT	AGGTCCAAGC	TTGAAAATGT	ACCAATGTGG	120
TTTACCAAAA	GAAATGGCAC	TTGAACTATT	TAAACCATTG	GTAATGAAAG	AATTAGTTCA	180
ACGTGAAATT	GCAACTAACA	TTAAAAATGC	GAAGAGTAAA	ATCGAACGTA	TGGATGATGA	240
AGTTTGGGAC	GTATTGGAAG	AAGTAATTAG	AGAACATCCT	GTATTACTTA	ACCGTGCACC	300
AACACTTCAT	AGACTTGGTA	TTCAAGCATT	TGAACCAACT	TTAGTTGAAA	GGTCGTGCGA	360
TTCGTCTACA	TCCACTTGTA	ACAACAGCTT	ATAACGCTGA			400

(2) INFORMATION FOR SEQ ID NO: 3539:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3539:

AATAAGTAAG	TTATTTTGTC	TGGTGACTAT	AGCAAGGAGG	TCACACCTGT	TCCCATGCCG	60
AACACAGAAG	TTAAGCTCCT	TAGCGTCGAT	GGTAGTCGAA	CTTACGTTCC	GCTAGAGTAG	120
AACGTTGCCA	GGCAAATGAC	AAATCGGAGA	ATTAGCTCAG	CTGGGAGAGC	ATCTGCCTTA	180
CAAGCAGAGG	GTCGGCGGTT	CGAACCCGTC	ATTCTCCACC	ATTTATTCTT	AGATATAGCC	240
GGCCTAGCTC	AATTGGTAGA	GCAACTGACT	TGTAATCAGT	AGGTTGGGGG	TTCAAGTCCT	300
CTGGCCGGCA	CCATCTTTTG	AGCCATTAGC	TCAGCTGGTA	GAGCATCTGA	CTTTTAATCA	360
GAGGGTCAGA	GGTTCGAATC	CTCTATGGCT	CATTACGATT	TAATTTTAT	ATTTAGCAAA	420
ATAATGCAGA	AGTAGTTCAG	CGGTAGAATA	CAACCTTGCC	AAGGTTGGGG	TCGCGGGTTC	480
GAATCCCGTC	TTCTGCTCCA	TTATTTTGCC	GGGGTGCGG	AACTGGCAGA	CGCACAGGAC	540
TTAAAATCCT	GCGGTGAGAG	ATCACCGTAC	CGGTTGATT	CCGGTCCTCG	GCACCATTTT	600
AGCGCCCGTA	GCTCAATTGG	ATAGAGCGTT	TGACTACGGA	TCAAGAGGTT	ATGGGTTCGA	660

GAGCACTTGG TTTGGGACCA AGGGGTCGCA GGTTCGAATC CTGTCTTCCC GATTACTTCT 780
 TAAATTCCAT TTTATGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 840
 5 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTTATTTTT TACACGATGA ACATTGAAAA 900
 CTGAATGACA ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT 960
 10 TTAGTATTTA TGAGCTAATC AAACATCATA ATTTTTATGG AGAGTTTGAT CCTGGCTCAG 1020
 GATGAACGCT GCGGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT 1080
 TCTCTGaTGT TAGCGGCGGA CGGGTGAGTA ACACGTGGgA TAACCTACCT ATAAGACTGG 1140
 15 GaTAACTTCG GGaAACCGGA GCTAATACCG G 1171

(2) INFORMATION FOR SEQ ID NO: 3540:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3540:

CTCGGCAGTG TGAAATCAAC GACTCGAAGA CACAATGTCT TCTCCCCATC ACAGCTCAGC 60
 30 CTTAACGAGT ACCGGATTTG CCTAATACTC AGCCTTACTG CTTAGACGTG CAATCCAATC 120
 GCACGCTTCG CCTATCCTAC TCGCTCCCCC CATCGATTAA AACGATTATA GGTGGTACAG 180
 GAATATCAAC CTGTTATCCA TCGCCTACGC CTGTCGGCCT CAGCTTAGGA CCCGACTAAC 240
 35 CCAGAGCGGA CGAGCCTTCC TCTGGAAACC TTAGTCAATC GGTGGACGGG ATTCTCACCC 300
 GTCTTTTCGCT ACTCACACCG GCATTCTCAC tCTAAGCGC TCCACATGTC CTTACGATCA 360
 TGCTTCAACG CCCTTAGAAC GCTCTCCTAC CATTGTCCAA AGGCATwCrC ACAGCTTCGG 420
 40 TaATATGTTT AGCCCCGGTA CATTTTCGGC GCagTGTCAC TCGACTAGTG AGCTATTACG 480
 CACTCTTTAA ATGATGGCTG CTTCTnAGCC AACATCCTAG GTTGGTCTGG GGCACGcNAC 540
 ATCCTTTTCC ACTTAACATA TATTTTGGGG ACCTTGGCTG GTGGGTCTGG GGCTGnTTCC 600
 45 C 601

(2) INFORMATION FOR SEQ ID NO: 3541:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3541:

5 GChAGGACCT ThCCAAATTT GAAATCCTTT GACCACnTTT GGGGTAGAGC CCTTTCCChC 60
 GGGGACAAAG TGACCAGGTG GTGCATGGTT GTCGTCAGCT CGTGTCGTGA GATGTTGGGT 120
 TAAGTCCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC ATCATTAACT TGGGCACTCT 180
 10 AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG ACGTCAAATC ATCATGCCCC 240
 TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA AAGGGCAGCG AAACCGTGAG 300
 nTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC TCGACTACAT 360
 15 GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG GTGAATACGT TCCCGGGTCT 420
 TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC CGAAGCCGGT GGAGTAACCT 480
 TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG TGAAGTCGTA ACAAGGTAGC 540
 20 CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATCGGA ACATCTTCTT 600
 CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT GAATGTTTGT TCATTCAAAT 660
 TAATGGGCCT ATAGCTCAGC TGGTTAGAGC GCACGCCTGA TAAGCGTGAG GTCGGTGGTT 720
 25 CGAGTCCACT TAGGCCCACC ATTAATTTAA TACCTATTTG GGGGCTTAGC TCAGCTGGGA 780
 GAGCGCCTGC TTGACGCA GAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTATT 840
 30 TGTACATTGA AACTAGATA AGTAAGTAA ATATAGATTT TACCAAGCAA AACCGAGTGA 900
 ATAAAGAGTT TTAAATAAGC TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAAGAACA 960
 CTCACAAGAT TAATAACGCG TTTAAATCTT TTTATAAAAG AACGTAACTT CATGTAAAG 1020
 35 TTTGACTTAT AAAAATGGTG GAAACATAGA TTAAGTTATT AAGGGCGCAC GGTGGATGCC 1080
 TTGGCACTAG AAGCCGATGA AGGACGTTAC TAACGACGAT ATGCTTTGGG GAGCTGTAAG 1140
 TAAGCTTTGA TCCAGAGATT TCCGAATGGG GAAACCCAGC ATGAGTTATG TCATGTTATC 1200
 40 GATATGTGAA TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC 1260
 CGGAGGAAGA GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCGAAATG G 1311

(2) INFORMATION FOR SEQ ID NO: 3542:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3542:

CGCTAGAGTA GAACGTTGCC AGGCAAATGA CAAATCGGAG AATTAGCTCA GCTGGGAGAG 120
 CATCTGCCTT ACAAGCAGAG GGTGGGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 180
 5 TAGATATAGC CGGCCTAGCT CAATTGGTAG AGCAACTGAC TTGTAATCAG TAGGTTGGGG 240
 GTTCAAGTCC TCTGGCCGGC ACCATCTTTT GAGCCATTAG CTCAGCTGGT AGAGCATCTG 300
 ACTTTTAATC AGAGGGTCAG AGGTTGCAAT CCTCTATGGC TCATTACGAT TTAATTTTIA 360
 10 TATTTAGCAA AATAATGCAG AAGTAGTTCA GCGGTAGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3543:

GTGAGAGTGA CGTTATGTTA TGTAAATAAC AGTTAATTAT ACCGGTGGTC GGGGTCGAAC 60
 25 CGCACTCCAC AAGTGAAGA GaTTTGTAGT CCCGCGCGTC TGCCAATTCC GCCACACCGG 120
 CTTAATGGTA AACAAAAAAC TTCCCTTTGG AAGCAATTAT GGAGCGGAAG ATAGGATTTA 180
 30 CACCTATACC TCGTTCGGG aAGGAACTGg TTcTAAAAGT TGAACTACTC CCGCAAATAT 240
 TAAATTATGG AGCGGAAGAT AGGATTTACA CCTATACCTC ATTCCAGGAA GGAATGTATT 300
 CTAAGAGTTG AAATACTCCC GCATTATTAT TAAATTATGG AGCGGAAGAT AGGATTTGCA 360
 35 CCTATACCTC GTTCCGGGAA GGackTGTTt CTAAAAGTTG AACTACTCCC GCATAAACCT 420
 GGAGGCGGCA ACCGGATTTG AACCGGTGAT AAAGGTTTtG CAGACCTCTG CCTTACCACT 480
 TGGCTATGCg CcAATAACTG GGCTAGCTGG ATTcGAACCA ACGAGTGACG GATmAAAGTC 540
 40 CGTTGCCTTA CCGCTTGGCT ATAGCCCATT AATAATAAGG GCGGCTGAAG GGGATCGAAC 600
 CCTCGAATGT CGGAACCACA ATCCGATGTG TTAACCACTT cACCACAGCC GCCATGGCAG 660
 GGGCAGTAGG AATCGAACCC ACACCAAAGT TTTGGaGACC TCTATTCTAC CGTTGAACTA 720
 45 TGCCCCCTATT aAAAAATaATA AtkGGAGGGG GGCAGATTcG AAnTGCCGAA CCCGAAGGAG 780
 CGGGATTTAC ATTCCGCCGG GTTT 804

(2) INFORMATION FOR SEQ ID NO: 3544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3544:

5 ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60
 GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180
 10 GTGTTGGCTT ATTACCGAGT GGCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240
 CATCGCATAA GTTTGATkAC AAACAAGCTT CCATGACAAA AGTACTGACG AATATCGCAT 300
 TTGCGAAAGT CTCTACAAAT GCCTTTGAGG CACGTCGTTA TGGTTATTTA CGTGGATACA 360
 15 GATACGATTA TTTTCAATAC AGCACAACGT GTCCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 3545:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3545:

25 CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA TCATGCTTCA ACGCCCTTAG 60
 AACGCTCTCC TACCATTGTC CAAAGGnATC nCACAGCTTC GGTAATATGT TTAGCCCCGG 120
 30 TACATTTTCG GCGCAGTGTC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGATGGC 180
 TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCaCA TCCTTTTCCA CTTAACATAT 240
 35 ATTTTGGGAC CTTAGCTGGT GGTCTGGGCT GTTTCCTTT CGAACACGGA CCTTATCACC 300
 CATGTTCTGA CTCCCAAGTT AAATTAATTG GcATTCCGAG TTTGTCTGAA TTCGGTAACC 360
 CGAGAGGGGC cCCTCGTCCA AAcAGTGGCT CTACCTCCAA TAATCATCAn TTGAGGCTAG 420
 40 CCCTAAAGCT AATTCCGAGA GAACCAGTAT CTCCAGTTCG ATTGGAATTC TnCG 474

(2) INFORMATION FOR SEQ ID NO: 3546:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3546:

55

GCAATTCGTA AAGTTGAAAC ATCAACATTA GGTGAAGAAA GTGAAAATGA CTTTATCGGT 120
 CTGTTTCAGCG ATATGGATT T GAGTTCAACG CGACTAGGTA ACAATGTCAA AGAACGTACT 180
 5 GCTTTAATCT CTAAAGTCAT GGTTAATCTT GACGACTTAC CATTTCGTTCA CAGTGACATG 240
 GAAATTGATA TGTTAGGTGA TGCATATGAA TTCCTAATTG GCGCCTTTG GCGACACGGG 300
 TAAAAAAGC AGGCGAGTTC TATACACCAC AACAAAGTATC TAAGATACTG GCGAGATTGT 360
 10 CACAGACGGT AAAGATAAAT ACGTCACGTG TATGACCCAA 400

(2) INFORMATION FOR SEQ ID NO: 3547:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3547:

AACGTTTTCA CTTGCCAAG CCATTTTCTT TTGTGTTTAC TTTTATTTT GACGTTTTAG 60
 25 ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT CGCATCCATT TTTGCCTGG 120
 CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG ACGCTAAGAA CCTTCTTGA 180
 CTTGTGACAA TCGCTTGCTT CTTTCCTCTT CTTGCGCTCT CGCTTACTCA TTTAGCTCTA 240
 30 CTAAACTCGT TGCGCTCTTT TCTCGTTTCG TCAGATTCAA ACGTTTTTCAC TTCGCCAAGC 300
 CATTTTTCTT TGTGTTTGCT TTTTATTTTG ACGTTTTAGA CATAAAAAAA AGAGACCTTG 360
 35 CGGTCTCAAT GCGGCTCATC GCATCCANTT TTTGCCTGGC 400

(2) INFORMATION FOR SEQ ID NO: 3548:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3548:

ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60
 GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120
 50 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180
 GTGTTGGCTT ATTACCGAGT GCGGTTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240

TTGCAAAGTC TCTACAAATG CCTTTGAGGC ACGTCGTTAT GGTTATTAC GTGATACAGA 360

TACGATTATT TTCAATACAG CACAACGTGT CCGAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 3549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3549:

AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC GGTGTGTACA 60

AGACCCGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTAGTAGCGA TTCCAGCTTC 120

ATGTAGTCGA GTTGACAGACT ACAATCCGAA CTGAGAACAA CTTTATGGGA TTTGCTTGAC 180

CTCGCGGTTT CGCTGCCCTT TGTATTGTCC ATTGTAGCAC GTGTGTAGCC CAAATCATAA 240

GGGGCATGAT GATTTGACGT CATCCCCACC TTCCTCCGGT TTGTCACCGG CAGTCAACTT 300

AGAGTGCCCA ACTTAATGAT GGCAACTAAG CTTAAGGGTT GCGCTCGTTG CGGGACTTAA 360

CCCAACATCT CACGACACGA GCTGACGACA ACCATGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3550:

CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 60

TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATAATATTT 120

TGAACCGCAT GGTTCAAAAG TGAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 180

TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG CCGACCTGAG 240

AGGGTGATCG GCCACACTGG AACTGAGACA CCGTCCAGAC TCCTACGGGA GGCAGCAGTA 300

GGGAATCTTC CGCAATGGGC GAAACCTGAC GGAGCAACGC CGCGTGAGTG ATGAAGGTCT 360

TCGGATCGTA AAACCTCTGTT ATTAGGGAAG AACATATGTG 400

(2) INFORMATION FOR SEQ ID NO: 3551:

(A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3551:

10	ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA	60
	ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCACTTTT GAATGTTTAT	120
	TTAACATTCA AATATTTTTT GGTAAAGTG ATATTGCTTA TCGAGCGCT TGACAATCTA	180
15	TTCTTTTAA AGAAGCGGT TGTAGACAA TGCATTAAGA AAAATTAAAG CGGAGTTTAC	240
	TTTTGTAAAT GAGCATTGA TTTTGTAAA ATAAAGCAGT ATGCGAGCGC TTGACTAAAA	300
	AGAAATTGTA CATTGAAAAC TAGATAAGTA AGTAATAAT AGATTTTACC AAGCAAAACC	360
20	GAGTGAATAA AGAGTTTAA ATAAGCTTGA ATTCATAAGA aTAATCGCTA GTGTTGAAA	420
	GAACACTCAC AAGATTAATA ACGCGTTTAA ATCTTTTAT AAAAGANAAC GTTTAGCAGA	480
25	CAATGAGTTA AATTATTTTA AAGCAG	506

(2) INFORMATION FOR SEQ ID NO: 3552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3552:

35	AAGCTGAGGC CGACAGTGGn GCGATGGATA ACAGGTTGAT ATCCTGTAC CACCTATAAT	60
	CGTTTAAATC GATGGGGGA CGCATAGGAT AGGCGACGTG TCGATTGGAT TGCACGTCTA	120
40	AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTGATGGGGA	180
	GAAGACATTG TGTCTTCgAG GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA	240
45	AAATAGGTGC CCGTACCGCA AACCGACACA GGTAGTCAAG ATGAGAATTC TAAGGTGAGC	300
	GAGCGAACTC TCGTTAAGGA ACTCGGCAAA ATGACCCCGT AACTTCGGGA GAAGGGGTGC	360
	TCTTTAGGGT TAACGCCCAG AAGAGCCGCA GTGAATAGGC CCAAGCGACT GTTTATCAAA	420
50	AACACAGGTC TCTGCTAAAC CGTAAGtGAn TGTATAGGGG CTGACGCCTG CCCGGTGCTG	480
	GAAGGTAAAG AGGAGTGGTT AGCTTCTGCG AAcTAcGaAT CGAAGCCCCA GTAAACGGCG	540
55	GCCGTAACTA TAACGGTCCT AAGGTAGCGA AATTCCTGT CGGGTAAGTT CCGACCCGCA	600

5 GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 720
 GATATTGAAA TTCGGCACAG CTTGTACAGG ATAGGTAGGA GCCTTTGAAA CGTGAGCGCT 780
 AcTTaCgTGG aGGCGCTGGT GGGATACTAC CCTAGCTGTG TTGGCTTTCT AACCCGCACC 840
 ACTTATCGTG GTGGGAGACA GTGTCAGGCG GGCAGTTTGA CTGGGGCGGT CGCCTCCTAA 900
 10 AAGGTAACGG AGGCGCTCAA AGGTTCCCTC AGAATGGTTG GAAATCATT C ATAGAGTGTA 960
 AAGGCATAAG GGAGCTTGAC TGCAGACCT ACAAGTCGAG CAGGGTCGAA AGACGGACTT 1020
 AGTGATCCGG TGGTCCGCA TGGGAAGGGCC ATCGCTCAAC GGATAAAAGC TACCCCGGGG 1080
 15 ATAACAGGCT TATCTCCCCC AAGAGTTCAC ATCGACGGGG AGGTTTGGA CCTCGATGTC 1140
 GGCTCATCGC ATCCTGGGGC TGTAAGTCGGT CCCAAGGGTT GGGCTGTTTCG CCCATTAAAG 1200
 CCGTACrmGg CTGGGTTTCA AACGTCGTGA GaCAGTTCGG TCCCTATCCG TCGTGGGCGT 1260
 20 AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 1320
 TACCAGTTGT CGTGCCAACG cATnAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA 1380
 AAcATnCTnA AGCATGAAGC CCCCCTCAAG ATGAGATTTT CCAACTTCGG TTATAAGATC 1440
 25 CCTCAAAGAT GATGAGGTTA ATAGGTTTCA GGTGGAAGCA TGGTGACATG TgGGAGCTGA 1500
 CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACAAA tnCaCTTTTA 1560
 CTTACTATCT AGTTTTGAAT GTATAAATTA CATTATATG TCTGGTGA CT ATAGCAAGGA 1620
 30 GGTACACCT GTTCCCATGC CGAACACAGA AGTTAAGCTC CTTAGCGTCG ATGGTAGTCG 1680
 AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAGTTT TTAAATCAA TTTTGTTAA 1740
 35 AAAATAAAAT GGACAAGATA AAAAAAGTTA TTGACTTAA TGTAAATAAA ATGTATAATT 1800
 AATTCTTGTC GGTAAAGAAA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 1860
 TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT 1920
 40 CATAATTTTT ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA 1980
 CATGCAAGTC GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG 2040
 AGTAACACGT GGATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GGAGCTAATA 2100
 45 CCGGATAATA TTTTGAACCG CATGGTTCAA AAGTGAAAGA CCGTCTTGCT GTCACCTATA 2160
 GATGGATCCg CGCTGCATTA GCTAGTTGGt AAGGtAACGG CTTTACCCA 2209

(2) INFORMATION FOR SEQ ID NO: 3553:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3553:

5 CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC CGAGTGAATA AAGAGTTTTA 60
 AATAAGCTTG AATTCATAAG AAATAATCGC TAGTGTTTGA AAGAACAATC ACAAGATTAA 120
 TAACGCGTTT CCTGTAGGAT GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC 180
 10 CTTGGCACTA GAAGCCGATG AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA 240
 GTAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT 300
 CGATATGTGA ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC 360
 15 CCGGAGGAAG AGAAAGAAAA TTCGATTCCC TTAGTAGCGG CGAGCGAAAC GGGAAGAGCC 420
 CAAACCAACA AGCTTGCTTG TTGGGGTTGT AGGACACTCT ATACGGAGTT ACaAAGGmCG 480
 20 ACATTrGACG AaTCATCTGG gAAAGwTGaT CCAAGGAA 518

(2) INFORMATION FOR SEQ ID NO: 3554:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 587 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3554:

30 AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG 60
 CTAATTCTCC GATTTAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTsGAC 120
 35 TACCATCGAC GCTAAGGAGC TTAACCTCTG TGTTCCGCAT GGAACAGGT GTGACCTCCT 180
 TGCTATAGTC ACCAGACATA TGAATGTAAT TTATACATTC AAAACTAGAT AGTAAGTAAA 240
 40 AGTGATTTTG CTTGCAAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 300
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTGAGGGAT 360
 CTTATAACCG AAGTTGGGAA ATCTCATCTT GAGGGGGGCT TCATGCTTAG ATGCTTTCAG 420
 45 CACTTatCCC GTCCACACAT AGCTACCCAG CTATGCCGTT GGCACGACAA CTGGTACACC 480
 AGAGGTATGT CCATCCCGGT CCTCTCGTAC TAAGGACAGC TCCTCTCAA TTTCTACGC 540
 CCACGACGGa TAGGGaCCGA ACTGtCTCAC GACGTTCTGA ACCCAGA 587

(2) INFORMATION FOR SEQ ID NO: 3555:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 399 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3555:

	GAATCTGAAT CGCTATCTGA ATCCGAGTCA CTGTCGGAAT CTGAGTCACT GTCGGAATCT	60
10	GAATCGCTAT CTGAATCTGA ATCGCTGTCT GAATCTGAAT CGCTGTCTGA ATCTGAGTCG	120
	CTATCTGAGT CGGAATCGCT ATCTGAGTCG GAATCACTGT CGGAATCTGA ATCGCTGTCT	180
	GAGTCGGAAT CACTGTCTGGA GTCAGAATCG CTGTCTGAGT CGGAATCACT GTCGGAATCT	240
15	GAATCGCTAT CTGAATCTGA ATCGCTATCT GAATCCGAGT CACTGTCTGa GTCAGAATCG	300
	CTATCTGGAA TCTGGAGTCA CTGTCGGAAT CTGAGTCACT GGTCTGGAGT CAGAATCGCT	360
20	ATCTGGAATC CGAnGTCATG GTCTGAGTCG GGaATCGCT	399

(2) INFORMATION FOR SEQ ID NO: 3556:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3556:

	ATTCATCTTT CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGTCTT	60
	ACAACCCCAA CAAGCAAGCT TGTTGGTTTG GGCTCTTCCC GTTTCGCTCG CCGCTACTAA	120
35	GGGAATCGAA TTTTCTTTCT CTTCCTCCGG GTACTAAGAT GTTTCAGTTC TCCGGGTGTG	180
	CCTTCTGATA TGCTATGTAT TCACATATCG ATAACATGAC ATAATCATG CTGGGTTTCC	240
40	CCATTCGGAA ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG	300
	TAACGTCCTT CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAATTAAT	360
	CTATGTTTCC ATCCTACAGG AAACGCGTTA TTAATCTTGT	400

45

(2) INFORMATION FOR SEQ ID NO: 3557:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3557:

ACAACTGGTA CACCAGAGGT ATGTCCATCC CGGTCCTCTC GTACTAAGGA CAGCTCCTCT 120
 CAAATTTCTT ACGCCACGA CGGATAGGGA CCGAACTGTC TCACGACGTT CTGAACCCAG 180
 CTCGCGTACC GCTTTAATGG GCGAACAGCA AnCCCTTGGG ACCGACTACA GCCCCAGGAT 240
 GCGATGAGCc GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGAACTCTT GGGGGAGATA 300
 AGCCTGTTAT CCCCggggTA GCTTTTATCC GTTGAGCGAT GGCCCTTCCA TGCGGAACCA 360
 CCGGATCACT AAGTCCGTCT TTCGAcCCTG CTCGACTTGT AGGTCTCGCA GTCAAGCTCC 420
 CTTATGCCCTT TACTCTCTAT GAATGATTTC CAACCATTTCT GAGGGAACtT TGAGCGCCTC 480
 CGTTACCTTT TAGGAGGCGA CCGCCCCAGT CAAACTGCCc GCcTGACACT GTCTACcmCC 540
 ACGATAAGTG GTGCGGGTTm GmAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGCCTn 600
 CCCACTAATA GCGCTCACGT TTCAAAGGCT CCTACCTATC CTGTACAAGC TGTGCCG 657

(2) INFORMATION FOR SEQ ID NO: 3558:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3558:

GAGTCCATGG GTGAAAGAAG CATCTGCAGC AACTGTAGCA GGTATTGCTG GAACTAATAA 60
 TGGTATTACT GTTGACAGCAG GTACTTTCAA CCCTGCTGAT ACAATTCAAG TTGTTGCAAC 120
 GCAAGGACAG CGGAGAGACA GTGAGTGATG AGCAACGTAT nnTnGATTTC ACAGTTGTCTG 180
 CACCACAACC GAACCAAGCG ACTACTAAGA TTTGGCAAAA TGGTCATATT GATATCACGC 240
 CTAATAATCC ATCAGGACAT TTAATTAATC CAACTCAAGC AATGGATATT GCTTACACTG 300
 AAAAAGTGGG TAATGGTGCA GAACATAGTA AGACAATTAA TGTTGTTCGT GGTCAAATA 360
 ATCAATGGAC AATTGCGAAT AAGCCTGACT ATGTAACGTT 400

(2) INFORMATION FOR SEQ ID NO: 3559:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3559:

CGACACAAAA CAAGCCAAGC AAAACAAACG CATATAACGT AACAAACACAT GGAAACGGCC 120
 AAGTATCATA TGGCGCTCGC CAACACAAAA CAAGCCAAGC AAAACAAATG CATACAACGT 180
 5 AACAAACACAT GCAAACGGTC AAGTGTCTATA CGGAGCTCGC CCGACATACA AGAAGCCAAG 240
 TAAAACAAAT GCATACAATG TAACAACACA TGCAGATGGT ACTGCGACAT ATGGGCCTAG 300
 10 AGTAACAAAA TAAGTTTGTA ACTCTATCCA AAGACATACA GTCAATACAA AACATTACGT 360
 ATCTTTACAA CAGTAATCAT GCATTCTATG ATGCTTCTAA 400

(2) INFORMATION FOR SEQ ID NO: 3560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3560:

TTTAGGTTAT ACAGCATTGC AGGCAGGATA CTTATCAATT ACTTATTTAA TCATGGTGTT 60
 25 ATTGATGATT CGAGTTGGTG AAAAATTATT ACAAAAAATG GGTTCTAAGC GACCAATGTT 120
 ATTAGGTACA TTCATTGTGG TCATTGGTAT TGCATTATT TCATTAGTAT TCTTACCAGG 180
 30 CATATTTTAT GTTATCAGTT GTGTCGTAGG ATATTTATGT TTCGGACTAG GCTTAGGTAT 240
 TTATGCAACA CTTTCTACAG ATACAGCTAT TTCGAATGCA CCGTTAGATA AAGTTGGCGT 300
 TGCTTCAGGT ATTTATAAAA TGGCTTCATC ACTTGGTGGG CGCATTCCGT GTCGCAATTA 360
 35 GTGGTGCTGT ATATGCTGGT GCAGTTGCTG CAACGAGCAT TCCATACAGG TGCGATGATT 420
 GCATTTTGGG TTAACGTATT GAATGGGGAA TCCATGGCCA TTTATCGCAA TTTTAATnCG 480
 CGATT 485

(2) INFORMATION FOR SEQ ID NO: 3561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3561:

AAATTATGTG AAGTAAAAGG AGTACGTCCA TGCAAAATTT AGATAAGAAT TTTCGACaTT 60
 55 TATCtCGTAA AGAAAAGTTA CaACAATTGG TTGATAAGCA ATGGTTATCA GAAGAACAAT 120

ATGTCATCGC GCAAGGTGCA TTACCCGTTG GATTATTACC GAATATCATT GTGGACGATA 240
 AGGCATATGT TGTACCTATG ATGGTGAAG AGCCTTCAGT TGTCGCTGCA GCTAGTTATG 300
 5 GTGCAAAGCT AGTGAATCAG ACTGGCGGAT TTAACCGGT ATCTTCTGAA CGTATTATGA 360
 TAGGTCAAAT CGTCTTTGAT GGCCTTGACG ATACTGAAAA ATTATCAGCA GACATTAAAG 420
 10 CTTTAGAAAA GCAAATTCAT AAAATTGCGG ATGAGGCATA TCC 463

(2) INFORMATION FOR SEQ ID NO: 3562:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 643 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3562:

AATTTAAACC CAATTGTCTG GCAAAACGTT TTCCTTTATA AAAAGATTTA AACGCGTTAA 60
 TTAATCTTGG TGCnGGTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT 120
 25 TAAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG 180
 TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA CTGCTTTATT TTCAAAAAT 240
 30 CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTT CTTAATGCAT TGTCTAACAA 300
 CCGCTTTCTT TAAAAAGAAT AGATTGTCAA GCGCTCGCAT AAGCAATATC ACTTTAACCA 360
 AAAAATATTT GAATGTTAAA TAAACATTCA AACTGAATA CAATATGTCA CGTTATTCCg 420
 35 CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC AGCCGCACCT 480
 TCCGATACGG CTACCTTGtT ACGACTTCAC CCCAATCATT TGTCCACCT TCGACGGCTA 540
 GCTCCTAAAA GGTTACTCCA CCGGCTTCGG GTGTTACAAA CTCTCGTGGT GTGACGGGCG 600
 40 GTGTGTACAA GACCCGGGAA CGTATTCACC GTAGCATGCC TCG 643

(2) INFORMATION FOR SEQ ID NO: 3563:

- (i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3563:

GATAAATCCA AATAGTGCAC TATAAAAAAT AATATCTACT AAAGTATCTT TATGTAATCC 60

TTCCATACCA TCGTACACTC AGTGGTCCTA AGTTAAATGC CACAGGATCT ATATAGTTAA 180
 ATACAATACC CATTCAACCT ACTCCTCACT CTTATGACTG TTCTTGATAA TTTCTTCATT 240
 5 TAATCTTTCA CTAAATTCCT CGGCCGTGTT AATGCCCATG ATATTTAATC GATAGTTCAT 300
 TGCAGCGACC TCAATAATTA CCGCAACATT TCTACCAGGT CTTACAGGTA TTGGTTTTTT 360
 10 TTAGTGGnTT TCAGTATCTA AAATACTTAG CGTCTCTTCA 400

(2) INFORMATION FOR SEQ ID NO: 3564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3564:

TCGTCAGCnC nTGTCGTGAG ACGTTGGGTT AAGTCCCCGA ACGAGCGCAA CCCTTAAGCT 60
 TAGTTGCCAT CATTAAAGTTG GGCACCTCTAA GTTGACTGCC GGTGACAAAC CGGAGGAAGG 120
 25 TGGGGATGAC GTCAAATCAT CATGCCCTT ATGATTTGGG CTACACACGT GCTACAATGG 180
 ACAATACAAA GGGCAGCGAA ACCGCGAnGT CAAGCAAATC CCATAAAGTT GTTCTCAGTT 240
 CGGATTGTAG TCTGCAACTC GACTACATGA AGCTGGAATC GCTAGTAATC GTAGATCAGC 300
 30 ATGCTACGGT GAATACGTTT CCGGCTCTTG TACACACCGC CCGTCACACC ACGAGAGTTT 360
 GTAACACCCG AAGCCGGTGG AGTAACTTTT AGGAGCTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3565:

CAAACCATTG GTAGCTATTT GTAACCTTTA TATTGATATT GTTCCTGGAC ATGTTCACTT 60
 GAGAGAGCTT GCAGATATAG CTAAAGAAGC AATTAGAGAA GCCGGTGCCA TTCCATTTGA 120
 ATTCAATACA ATTGGTGTG ATGATGGAAT AGCTATGGGA CATATCGGAA TGCGATATTC 180
 50 TCTACCATCA CGTGAAATTA TTGCAGATGC AGCTGAAACT GTAATTAACG CTCATTGGTT 240
 TGACGGCGTA TTTTACATTC CTAATTGTGA CAAGATTACA CCCGGTATGA TTTTAGCAGC 300

TGCACATGGA AAAGCATTAA CACTTTCATC AATGTTTGAA

400

(2) INFORMATION FOR SEQ ID NO: 3566:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3566:

AAATTACGTA CATATTTAAA GCTGACGGCA CTATGACTGC AGGAACATCT GCCCCACTTT 60
 CTGATGGTGC AGGATTGTGA GTTTTAATGT CTGGAGATAA AGTGAAAGAA CTCGGcGTGA 120
 CACCTATTGC ACGATTTCGTT GGTTTTAAGG CAGTAGGCGT TGACCCGAAA ATTATGGGTA 180
 TTGGGCCTGC ATATGCGATT CCTGAAGTAT TGTCACTCAG CAATCTATCT GTTGAAGACA 240
 TTGATTTGAT CGAATTGAAC GAAGCATTTG CTTCTCAAAC GATTGCATCT ATTAAAGAAG 300
 TAGGTCTAGA TATATCACGT ACGAATGTGA ATGGTGGCGC TATTGCTTka GGTCAATCCAT 360
 TAGGTGCTAC AGGCGCaATG TTAACCGCGC GTTTActTAA TGAAATGGGT AGACGTCCCCG 420

(2) INFORMATION FOR SEQ ID NO: 3567:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3567:

TACGGGAAGT AGCTCAGCTT GGGTAGAGCA CTTGGTTTGG GACCAAGGGG TCGCAGGTTC 60
 GAATCCTGTC TTCCCGATAT ACTGTAATTA TTATGGGGGC TTAGCTCAGC TGGGAGAGCG 120
 CCTGCTTTGC ACGCAGGAGG TCAGCGGTTT GATCCCGCTA GTCTCCACCA TATTATTAC 180
 AACTATATA AGGCGGTGTA GCTCAGCTGG CTAGAGCGTA CGGTTCATAC CCGTGAGGTC 240
 GGGGGTTCGA TCCCCTCCAC CGCCACTATT TATTAGTTGT AAAATTATAT TTAGGACCTT 300
 TAGCTCAGTT GGTAGAGCT AACGGCTCAT AACCGTTCGG TCGCAGGTTC GAGTCCTGCA 360
 GGTCCCATAT AATTTTGGAG GAATACCCAG TCCGGCTGAA 400

(2) INFORMATION FOR SEQ ID NO: 3568:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3568:

TTAGCCAATC CCCATTCTGG ACGTACCTCA CTCCAATCAC TCGCAAACCG CTGCGCTTCT 60
10 TCCACTGGAT GATTACACAG ACCAATCGTT GGCAGTTTGT CCAAACGTTG GCGATTCCGT 120
GTTTCAGAAA TCATCGGCAT CGCGTCATTC AATGATTCAT ATGCATCTAA AGCAATAGAA 180
GATAATGTGT CTGGCACATA TACCCATGCC AACGTATCAG TAGACGTATG ATGTTCTGCT 240
15 ACCGCAAAAA CAGTTGTCTC TGGAnTATAC ACACCTGATT GTTTTAATCC TTGTCTGACA 300
TTTGGACGAT TACATATCAT CGCTAATAAC TTAGCATThA AAACCGCTTG ATGCGCCACC 360
ACAAGCCCCA CATTTCAAGT GATGGCATGG nTGTGGGThn 400
20
(2) INFORMATION FOR SEQ ID NO: 3569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3569:

CCCCGACCTC ACGGGTATGA ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA 60
GTTTGTAAT AATATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG 120
35 CAGGCGCTCT CCCAGCTGAG CTAAGCCCC ATAATAATTA CAGTATATCG GGAAGACAGG 180
ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT ACCAAGCTGA GCTACTTCCC 240
GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC 300
40 TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA 360
TCGAACCGGT ACGTGATCAC TCACCGCAGA TTTTAAGTCC 400
45
(2) INFORMATION FOR SEQ ID NO: 3570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3570:

55

GTTTTTATCC GTTGAGCGAT GGCcNtCCCA TGGGGACCTA CCGGATCACT AAGTCCGTCT 120
 TTTTCGACCCT GCTTCGACTT GTAGGTCTCG CAGTCAAGCT CCCTTATGCC TTTACACTCT 180
 5 ATGAATGATT TCCAACCATT CTGAGGGAAC CTTTGAGCGC CTCCGTTACC TTTTAGGAGG 240
 CGACCGCCCC AGTCAAACCTG CCCGCCTGAC ACTGTCTCCC ACCACGATAA GTGGTGCGGG 300
 10 TTAGAAAGCC AACACAGCTA GGGTAGTATC CCACCAGCGC CTCCACGTaA GyTAGCGCTC 360
 ACGTTTCAAA GGCTCCTACC TATCCTGTAC AAGCTGTGCC GAATTTCAAT ATCAGGCTAC 420
 AGTAAAGCTC CACGGGGTCT TCCGTCCTG TCGCGGGTAA CCTGCATCTT CACAGGTACT 480
 15 ATGATTTTAC CGAGTCTCTC GTTGAGACAG TGCCCAAATC GTTACGCCTT TCGTGCGGGT 540
 CG 542

(2) INFORMATION FOR SEQ ID NO: 3571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3571:

30 ATGCCCCGACC ACATGGAGCT TCCAATCCCA TTGCTCTAAC CAATGAGCTA CTGAACCATA 60
 aTaAAAATGT AAtGATGGCG GTCTCGACGG GAATCGAACC CGCGATCtCn GCGTGACAGG 120
 CAGGCGTGTT AACCCTTACA CTACGAGACC TATAAAATAT TGCGGGAGGC GGATTTGAAC 180
 35 CACCGGACTT CGGGTTATGA GCCCGACGAG CTACCGAACT GCTCCATCCC GCGATAATAA 240
 AAAATAATGG CGGAGGAAGA GGGATTGAA CCCCCGCGGC CCGTTAAGGc CCTGTGCGTT 300
 TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCTCC ATTATTATAG GTAAATCGCT 360
 40 ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC TCCTGCGTGA 420
 CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG AAGAGGGATT 480
 45 CGAACCCCGG CGAGCCGTTA AGCCCCTGTC GGTTTTCAAG ACCGATCCCT TCAGCCGGAC 540
 TTGGGTATTCT CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTkCGA CCGAACGGTT 600
 ATGAGCCGTT AGCTCTAAC 619

(2) INFORMATION FOR SEQ ID NO: 3572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3572:

5 GGTGAAGACA TCACGTATCA AGAAGCATGG GCAGATGAAG AATATCGTGA AGACTTAAAA 60
 GCAGAATTAA TTGATCAAGC GGTACTTCA TTGAGCCACA AGATTATTTC AGTGCGATGA 120
 TTCGTGAAAT TGAAACGCAA GATTTCGATA TAGAACATCT AGCGACGGCG ATTTCGAAAG 180
 10 TTGAAACATC TACATTAGGT GAAGAAAGTG AAAATGACTT TATCGGGCTG TTCAGCGATA 240
 TGGATTTGAG TTCAACGCGA CTAGGTAACA ATGTCAAAGA ACGTACTGCT TTAATCTCTA 300
 AAGTCATGGT TAATCTTGAC GACTTACCAT TCGTTCACAG TGACATGGAA ATTGATATGT 360
 15 TAGGTGATGC ATATGAATTC CTAATCGGGC GCTTTGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 3573:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3573:

25 CAAATCGTAA CTCGCCGGTT CATTCTACAA AAGGCACGCC ATCACCATT AACGGGCTCT 60
 30 GACTACTTGT AAGCACACGG TTTCAGGTTT TATTCTACTC CCCTTCCGGG GTGCTTTTCA 120
 CCTTTCCTC ACGGTACTGG TTTACTATCG GTCCTAGAG AGTATTTAGC CTTAGGAGAT 180
 GGTCTCCCA GATTCCGACG GAATTTACAG TGCTCCGTCG TACTCAGGAT CCACTCAAGA 240
 35 GAGACAACAT TTTCGACTAC AGGATTATTA CCTTCTTTGA TTCATCTTTC CAGATGATTC 300
 GTCTAATGTC GTCCTTTGTA ACTCCGTATA GAGTGTCTTA CAACCCCAAC AAGCAAGCTT 360
 GTTGGTTTGG GGCTCTTCCC ATTTGCTCG CGGCTACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3574:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1051 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3574:

50 TCCCTCAAAG ATGGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC ATGTGGCAGC 60

55

TTTACTTACT ATCTAGTTTT GAATGTATAA ATTACATTCA TATGTCTGGT GACTATAGCA 180
 AGGAGGTCAC ACCTGTTCCC ATGCCGAACA CAGAAGTTAA GCTCCTTAGC GTCGATGGTA 240
 5 GTCGAACTTA CGTTCGCTA GAGTAGAACG TTGCCAGGCA TAATATTAAT CCACAGTAGC 300
 TCAGTGGTAG AGCTATCGGC TGTTAACCGA TCGGTCGTAG GTTCGAGTCC TACCTGTGGA 360
 10 GCCATGGCTC cTtGGTCAAG CGGTTAAGAC ACCGCCCTTT CACGGCGGTA ACACGGGTTC 420
 GAGTCCCGTA GnAGTCATTA TTTTGGAGAA TTAGCTCAGC TGGGAGAGCA TCTGCCTTAC 480
 AAGCAGAGGG TCGGCGGTTC GAACCCGTCA TTCTCCACCA TTTTGATTAT TAAATTATAT 540
 15 GAATAAGCTG GAGGGGTAGC GAAGTGGCTA AACCGGCGG ACTGTAAATC CGCTcCTTCG 600
 GGTTCGGCAG TTCGAATCTG CCCCCCTCCA CCATCTATAT ATTGGGCTAT AGCCAAGCGG 660
 TAAGGCAACG GACTTTGACT CCGTCACTCG TTGGTTCGAA TCCAGCTAGC CCAGCCATTA 720
 20 GAGCCATTAG CTCAGTTGGT AGAGCATCTG ACTTTTAATC AGAGGGTCAG AGGTTCGAAT 780
 CCTCTATGGC TCACTACTTG CACTTTCCAT TTTTGGGAAG TGCttTTTTT TAGGTTCTcC 840
 ACCAAATGTG GTGGGtATAT AATTTAAAGA ACTATTTTTT AAATACAAC TTTAGAGCTT 900
 25 TTATTATTAG GCGGCCAGTC CATTATTGGG CTGGTTGTC TTCTTTTTTT CTCCTTTGtA 960
 CAAGCTGAAA ATCATCATTA TACGTGctTA AAGTGTGAAA TTTCTGTAAC CAAAAGAATn 1020
 30 CACTTGATTA ATTnnATCTA TATAATGCCT C 1051

(2) INFORMATION FOR SEQ ID NO: 3575:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3575:

GTGGAGCGCT TAGAAGTGAG AATGCAAGTG TGAgTAGCGA AAGACGGGTG AGAATCCCGT 60
 CCACCGATTG ACTAAGGTTT CCAGAGGAAG GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA 120
 45 AGCTGAGGCC GACACGTATG GCGATGGATA ACAGGTTGAT ATTCTGTAC CACCTATAAT 180
 CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGAcGTG sCGATTGGAT TGCACGTCTA 240
 50 AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTgATGGGGA 300
 GAAGACATTG TGTCTTCGAG TCGTTgATTT CACACTGCCG AGAAAAGCCT CTAGATAGAA 360
 AATAgGTGCC CGTaCCGCAA AaCCGACACA GGTAGTCCAA GATGnGAATT CTAAnGTGAA 420

55

(2) INFORMATION FOR SEQ ID NO: 3576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3576:

```

TTTGTTCCTT TTTTAATTTA TATATTTAAA ATACACATAT TCAAGAGCTC GAGATATAAG      60
TCAATGTACT AGGCACACAA TTAAATATTG ACAGTAATTA ACCGAACGAA AATGCGCCCC      120
GGGGCCCCAA CATAGAGAAT TTCGAAAAGA AATTCTACAG ACAATGCAAG TTGGCGGGGC      180
CCCAACATAG AAGCTGGCCA ATAGTTAGCT TTCAATAATG TGCAAGTTGG GGTAAGGGCC      240
CCAACACAGA AGCTGGCCAA TAGTCAGCTT TCAATAATGT GCAAGTTGGG GTAAGGGCCC      300
CAACACAGAG AATTTGAAA AGAAATTCTA CAGACAATGC AAGTTGGCGG GGCCCCAACA      360
CAGAAGCTGG GCCAATAGTC AGCTTTTCCA ATAATGTGGC      400

```

(2) INFORMATION FOR SEQ ID NO: 3577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3577:

```

TGCATCTTCA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT      60
TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT      120
ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTTCGTAGC TTCGCAGAAC TAACCACTCC      180
TCTTAACCTT CCAGCACCGG GCAGGCGTCA GCCCTATACA TCACCTTACG GTTTAGCAGA      240
GACCTGTGTT TTTGATAAAC AGTCGCTTGG GCCTATTAC TCGGGCTCTT CTGGGCGTTA      300
ACCCTAAAGA GCACCCCTTC TCCCGAAGTT ACGGGGTCAT TTTGCCGAGT TCCTTAACGA      360
GAGTTCGCTC GCTCACCTTA GAATTCTCAT CTTGACTAAC      400

```

(2) INFORMATION FOR SEQ ID NO: 3578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3578:

5 TAACTTAACA CGACTTCTTA AGTCATTTAG TTTTAATGTT TGATGTGTTT CTGCTAAACC 60
 AATCTCCCAA GGAACACCGG CATGCTGAAT ACTCGTTTTG GGTGAAGCCC TGTACCACCA 120
 TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCACAGA TGCAATGGTA 180
 10 CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT CGCATTTTTTC 240
 AAATCATGTA TCAGTTGCGC TAAATCTTCT ATTGAATAAA TATCATGATG TGGCGGTGGT 300
 GAAATCAGAC CGATACCTGG CGTTGGACCC TCTTGCTCTC GCAATCCACG GATATACCTT 360
 15 AGTACCAGGT AATTGGACCA CCTTCACCAG GCTTTGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3579:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3579:

AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGA GACTAGCGGG ATCGAACCGC 60
 30 TGACCTCCTG CGTGCAAAGC AGGCGCTCTC CCAGCTGAGC TAAGCCCCCA TAATAATTAC 120
 AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC AAGTGCTCTA 180
 CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC CCATAACCTC 240
 35 TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT TTTATTGAAA 300
 ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA TTTTAAGTCC 360
 TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT 400

40 (2) INFORMATION FOR SEQ ID NO: 3580:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3580:

ACGTAAATAA CCATAACGAC GTGCCTCAAA GGCATTTGTA GAGACTTTCG CAAATGCGAT 60

TATGCGATCA GCCATTTCTG CAAGGCCACC GCCACTCGGT AATAAGCCAA CACCTGCTTC 180
 AACAAAGACCG ATATATGTTT CACTTGCAGC GACAACAATA GGTGAGTAAA GTACAAGCTC 240
 5 ACAGCCACCG CCTAAGGCAC GACCTTGAAC AGCTGTGACT ACTGGTTTCA AACTATACTT 300
 CAAACGATTA AAGCTATAAT GTAATTTATC AATTGATTGT GCACGACATC ATCTACAAGA 360
 10 CCGTCTTCCA TGCGCCTTTT TCCATTAAGA AAGGGTTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3581:

ATGTCATTGT TGGTACGGCT TTTCCAGAAG GATTACAAGG CCAAACATT GCACGAACGA 60
 TTGCATTGCG TGCGGATTAT CTGACACGGT ACCGGGTCAA ACAGTGAATC GCTACTGCTC 120
 25 ATCAGGATTA CAAACCATGC GATTGCAGCC AATCAAATTA TGGCTGGTCA AGGAGATATA 180
 CTGTAGCTG GTGCGTTGAA TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA 240
 ACAATCCAAC CTTACAATAT GATGATATAG GTGCGTCATA TCCTATGGGT TTAAGTCTG 300
 30 AAAATGTAGC ATCCCAATTT GACGTATCAC GCGAAGATCA AGATGCTTAT GCTGTCAGAA 360
 GTCATCAACG TGCCTATGAC GCACAACGTG ATGGGTCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3582:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT 60
 TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA GACCTTGCGG 120
 50 TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT 180
 AAGTTGGCTA CCATCGACGC TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT 240
 CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC 300

ATTTTGACGT TTTAGACATA AAAAAAAGAG ACCTTGCGGT

400

(2) INFORMATION FOR SEQ ID NO: 3583:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3583:

15	AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCAAATAGG TATTAAATTA ATGGTGGGCC	60
	TAAGTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT GCGCTCTAAC CAGCTGAGCT	120
	ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA ATACAATATG TCACGTTATT	180
20	CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA AAGGAGGTGA TCCAGCCGCA	240
	CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC ATTTGTCCCA CCTTCGACGG	300
	CTAGCTCCTA AAAAGGTTAC TCCACCGGCT TCGGGTGTTA CAAACTCTCG TGGTGTGACG	360
25	GGCGGTGTGT ACAAGACCCG GGAACGTATT TCACCGTAGC	400

(2) INFORMATION FOR SEQ ID NO: 3584:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3584:

	ACTTATTTGG CGATATTTTA AGTGATGAAG CTTCACTGAT TCCTGGTTCA CTTGGTTTAT	60
40	CACCTTCTGC TAGTTTTAGT AACGATGGTC CAAGATTGTA TGAGCCTATT CATGGATCAG	120
	CACCAGATAT TGCAGGTAAA AACGTTGCCA ATCCATTGG AATGATTCTA TCTTTAGCGA	180
	TGTGTTTACG TGAAAGCTTA AATCAACCAG ATGCTGCAGA TGAATTAGAA CAACATATTT	240
45	ATAGCATGAT TGAACATGGG CAAACGACAG CAGATTTAGG CGGCAAATTG AATACTACTG	300
	ATATTTTCGA AATTCTATCT CAAAAATTGA ATCACTAAGG GGGGAGATGT AAATGGGGTC	360
50	AAACATTATT TGACAAAGTG TGGGACAGAC ATGTGTTATA	400

(2) INFORMATION FOR SEQ ID NO: 3585:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3585:

	ACTGATGACA ATTTTATCTG CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC	60
10	TGTTTTTCGAA ACTAATTTTA CCGCGATATC TGCATCTTTA TTCGCATTTT TCAAATCATG	120
	TATCAGTTGC GCTAAATCTT CTATTGAATA AATATCATGA TGTGGCGGTG GTGAAATCAG	180
	ACCGATACCT GCGGTTGACC CTCTTGCTT CGCAATCCAC GGATATACCT TAGTACCAGG	240
15	TAATTGACCA CCTTCACCAG GCTTGCACC TTGCGCAACT TTAATTTGAA TTTCTTTGGG	300
	CATGTTGTAA ATAATCACTA GTTACACCAA AACGCCCAGA AGCAACTTGT TTAATCGCAC	360
	TTACTTTGGT GGCTCCATC AACTTGTA CTATAACGGT	400

20

(2) INFORMATION FOR SEQ ID NO: 3586:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3586:

	TACAAGTATT ACCATTATCT CAGAGGATT CTAGATAAGG GGCATGGATC ATTTGTCTTC	60
	TTATGAATTT GAGCCAGATA AAGAATCTAT CTTAAGTGTA ATCTTGACCT CAATATGTTG	120
35	AGAGTTTGAT TTACGGAACA ATATTAGACG CAAAAGCAAG TGAGCATGCA ACACGTATGA	180
	CTGCGATGAA AAATGCCACT GATAATGCAA CTGAACTTAT TGATGACTTA TCATTAGAAT	240
	ATAACAGAGC GAGACAAGCA GAAATTACGC AACAAATTAC TGAAATTGTT GGTGGTTCCG	300
40	CAGCGCTTGA ATAATATTTA AAGGAGGAAA ATAGCATGGG AATTGGCCGT GACTCAAGT	360
	TATGGGTCCT GTAATTGATG TTCGATTGTA ACATAACGAG	400

45

(2) INFORMATION FOR SEQ ID NO: 3587:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3587:

55

AGGATTCGAA CCTGCGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120
 CCCGTATAAT TAACGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180
 5 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTATT GAAAATGGTG CCGAGGACCG 240
 GAATCGAACC GGTACGTGAT CACTCACC GC AGGATTTTAA GTCCTGTGCG TCTGCCAGTT 300
 CCGCCACCCC GGCACTATAA AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC 360
 10 CTTGGCAAGG TTGTATTCTA CCGCTGAACT ACTTCTGCAT 400

(2) INFORMATION FOR SEQ ID NO: 3588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3588:

TACTATTGAC ATGTGTGAAC CCTATGTCCG ATTATTTCGC GACCTATTTC CTAATGCAGC 60
 25 TATTATTTTT GACAGATTCC ATATCGTTCA ACATTTAAAT AGAGAACTTA ATAAGTATCG 120
 TGTACAAGTT ATGAATGAAT ACCGTAATAA AAAAGGACCT GATTATACAA TTTTAAAGAA 180
 TAACTGGAAA GTCCTATTGA TGGATACTAG TAAACCATA TTTAGTAAAT ACAGATGGAA 240
 30 TAAATCTTTT AAGGGCTTAT AAACGCTCAT CTGACATTGT AGAATTCATG CTTTCAAAG 300
 ACGATATACT ACGACACTCC TACGAACTTG TCCAGGGATT ACGAAAAGAC CTAAGGTAT 360
 35 GTAATTGGGC CTAAATTTAT TAATCGTTTA AATTCCGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3589:

AGAGCGAACG GACGAGAAGC TTGCTTCTCT GATGTTAGCn GCGGACGGGT GAGTAACACG 60
 TGGATAACCT ACCTATAAGA CTGGGATAAC TTCGGGAAAC CGGAGCTAAT ACCGGATAAT 120
 50 ATTTTGAACC GCATGGTTCA AAAGTGAAAG ACGGTCTTGC TGTCACCTAT AGATGGATCC 180
 GCGCTGCATT AGCTAGTTGG TAAGGTAACG GCTTACCAAG GCAACGATGC ATAGCCGACC 240

AGTAGGGAAT CTTCCGCAAT GGGCGAAAGC TGACGGAGCA ACGnCGCGTG AGTGATGAAG 360
 GTCTTCGGAT CGTAAAACTC TGTATTAGG GAAGAACATA 400

(2) INFORMATION FOR SEQ ID NO: 3590:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3590:

GTTAgGAGAG CGTTCTAAGG GCGTTGAAGC ATGATCGTAA GGACATGTGG AGCGCTTAGA 60
 AGTGAGAATG CCGGTGTGAG TAGCGAAAGA CGGGTGAGAA TCCCTCCACC GATTGACTAA 120
 GGTTTCCAGA GGAAGGCTCG TCCGCTCTGG GTTAGTCGGG TCCTAAGCTG AGGCCGACAg 180
 gTAaGGCGAT GGATAACAGG TTGATATTCC TGTACCACCT ATAATCGTTT TaATCGATGG 240
 GGGGACGCAT AGGATAGGCG AAcGTGcGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG 300
 TATTAGGCAA ATCCGGTACT CGTTaAGGCT GAGCTGTGAT GGGGAGAAGA CATTGwGTCT 360
 TCGAGTCGTT GATTTCACAC TGCCGAGAAA AgCCTCTAGA TAGAAAATAG GTGCCCCGTAC 420
 CGCAAACCGA CACAGGTAAT CCAAGATGAG AATTCTAAGG TGAGCGAGCG AACTCTCGTT 480
 AAGGAACTCG GCAAATGAC CCCGTA ACT 509

(2) INFORMATION FOR SEQ ID NO: 3591:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3591:

ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60
 TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120
 TCGAACCGCT GACCTCCTGC GTGCAAAGCA GCGCTCTCC CAGCTGAGCT AAGCCCCCAA 180
 ATAGGTATTA AATTAATGGT GGGCCTAAGT GGA CTGAAC CACCGACCTC ACGCTTATCA 240
 GCGGTGCGCT CTAACCAGCT GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA 300
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 360

(2) INFORMATION FOR SEQ ID NO: 3592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3592:

TGGGnAACGC AACATCCTTT TCCAACCTAA CATATATTTT GGGACCTTaG CTGGTGGTCT 60
 GGGCTGTTTC CCTTCGAAC ACGGACCTTA TCACCCATGT TCTGACTCCC aAGTTAAATT 120
 AATTGGCATT CGGAGTTTGT CTGAATTCGG TAACCCGAGA GGGGCCCTC GTCCAAACAG 180
 TGCTCTACCT CCAATAATCA TCACTTGAGG CTAGCCCTAA AGCTATTTTCG GAGAGAACCA 240
 GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA GTTCATCCGC TCACTTTTCA 300
 ACGTAAGTCG GTTCGGTCCT CCATTcAGTG TTACCTGAAC TTCAACCTGa CCAAGGGTAG 360
 ATCACCTGGT TTCCGsGTsT ACGACCAAAT AsTAAACGCC CTATTCAGAC TCGCTTTCCG 420
 TanGGCTCCA CATTACTGGn 440

(2) INFORMATION FOR SEQ ID NO: 3593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3593:

TAAACGAACC AATTTTATTT GGTGCACCAC TAGTATTGAA TCCTGTGTTC TTTATTCCAT 60
 TTGTATTAGC ACCAATTGTT AACGTATGGA TTTTCAAACCT TTTCGTTGAA GTGTTAGGAA 120
 TGAATAGTTT TAGTGTGAAT TTACCTTGGA CAACACCAGG TCCATTGGGC ATTATCATGG 180
 GTACAGGTTT TGGTTTATGG TCATTCGTAC TAGCTATTAC TTTGATTGTT GTAGATATTA 240
 TTATnTACTA CCCATTCCCTA AAAGTTTATG ATAGTGAAAT TCTTGATGAA GAAGAAGGAC 300
 GTAAAGAAAG TAATTCAGAT TTAAGAGAAA AAGTTGCAGC AAACCTTTGA TACGAAAAAA 360
 GCTGATTCAA TTTTAGCGGC AAGTGGTGTA TCAGACGATG 400

(2) INFORMATION FOR SEQ ID NO: 3594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3594:

	AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG	60
10	TGCCTTCTGa TATGCTATGT ATTCACATAT CGATAACATG ACATAACTCA TGCTGGGTTT	120
	CCCCATTCGG AAATCTCTGG ATCAAAGCTT aCTaCAGCTC CCCAAAGCAT ATCGTCGTTA	180
	GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA	240
15	TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT	300
	TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAAATAA TTAACTCAT TGCTGCTAA	360
	ACGTTTTCTT TTATAAAAAG ATTTAAaGC GTTAaTAATC CTCTCGCTC	409

20

(2) INFORMATION FOR SEQ ID NO: 3595:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3595:

30

	AATATAAGCC CTGGATCATA CATGACCTGT ATTTGGGCAA TCCCTTCTGC TACATCTTCT	60
	GCCCACTCAT TCAATATTTG TTTTGCAATA TCATCACCTT CTTCAGCTGC TTCAAACAAT	120
35	ACTGGCACAT GTGTGCTTCT CGTAAATCCT CCGGCAATCA TCGGCTTTTT CAATGCACTC	180
	GTTGCAGCAC GTTGCTCAAA CGTTGTATTT TCAGTTGGAC GATACAATAA ATACCCAACT	240
	TCATTTGCCT TATGAAGCTC ACCATTATCA ATATGACCTT GGATTATTCT TGTACGCACC	300
40	CCCAATGGCC TGGTACCAAG CGTCCATACA AAAGATCCGT TCTGGCTTGG ATATTGGATG	360
	GTAATTTCCA ATTCGGCCTA GTTAATGGCA GCGGTTTTAA	400

(2) INFORMATION FOR SEQ ID NO: 3596:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 596 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3596:

55

CTGCCGAACC CGAAGAGCGG ATTTACAGTC CGCCGCGTTT AGCCACTTCG CTACCCTCCA 120
 GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG ACGGGTTCGA CCGCCGACCC 180
 5 TCTGCTTGTA AGGCAGATGC TCTCCAGCT GaGCTAATTC TCCAAAATAA TGA CTCTCTAC 240
 GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTCT TAACCGCTTG ACCAAGGAGC 300
 CATGGCTCCA CaGGTAGGAC TCGAACCTAC GACCGATCGG TTAACAGCCG ATAGCTCTAC 360
 10 CACTGAGCTA CTGTGGaTTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 420
 TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 480
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 540
 15 AGTAAAGTG ATTTTGCTTC GCAAAACATT TATTTTGATT AAGTCTTCGA TCGATT 596

(2) INFORMATION FOR SEQ ID NO: 3597:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3597:

TCATCTTGAG GGGGGCTTCA TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 60
 30 TACCCAGCTA TGCCGTTGGC ACGACAAC TGACACCAGA GGTATGTCCA TCCCGGTCCT 120
 CTCGTACTAA GGACAGCTCC TCTCAAATTT CCTACGCCCA CGACGGATAG GGACCGAACT 180
 GTCTCACGAC GTTCTGAACC CAGCTCGCGT ACCGCTTTAA TGGGCGAACA GCCCAACCCT 240
 35 TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT 300
 CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG 360
 40 CGATGGCCCT TCCATGCGGA ACCACCGGAT CAATAAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3598:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 397 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3598:

AACCAACGGC AGCAACTACA TGACCTAATT CTTGTGCTGA CTCTACATTT AGTAGCTCTA 60

CACTTCAATT GTACCAATCA ATCGTTGACG ATCTTGATCG TAACGCCATG TAGCAATACC 180
 ACGATACTGT CCGTCACGAC TCGCGTATGC ATGCGCACTT GCTTCTGCAC CACGCGTATC 240
 5 ATTTCCCTGTT GCTAAACAA CAGCATGTAT GCCATTCTATA ACACCTTTAT TATGTGTTGC 300
 TGCACGATGA ATATCTACTT GGGCCAATAC AGAAGCACGT TCCATCGTTT GcaACCTCTT 360
 CTCCAGTTCT CTCGCCCTT GGCTAAATCT TTAACAT 397
 10

(2) INFORMATION FOR SEQ ID NO: 3599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3599:

AACCCITGGG ACCGACTACA GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT 60
 CCCCCTCGAT GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCAGGGTA GCTTTTATCC 120
 25 GTTGAGCGAT GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG 180
 CTCGACTTGT AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTTT 240
 CAACCATTCT GAGGGAACCT TTGAGCGCCT CCGTTACCTT TTAGGAGGCG ACCGCCCCAG 300
 30 TCAAAGTCC CGCCTGACAC TGTCTCCAC CACGATAAGT GTGCGGGTTA GAAAGCCAAC 360
 ACAGCTAGGG TAGTATCCCA CCAGCGCCTC CAACGTAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3600:

ATCTGAATCT GAGTCGTTGT CTGAGTCCGA ATCGCTATCT GAATCTGAGT CGCTATCTGA 60
 GTCTGAGTCG CTATCTGAAT CTGAGTCGCT GTCTGAATCT GAATCACTGT CTGAGTCTGA 120
 50 GTCGCTGTCT GAGTCTGAAT CGCTGTCAGA ATCTGAGTCG CTATCTGAGT CTGAATCTGA 180
 ATCACTGTCT GAGTCCGAAT CGCTATCTGA ATCTGAATCG CTATCTGAGT CTGAGTCGCT 240
 ATCCGAATCT GAGTCGCTAT CTGAGTCTGA GTCGCTATCC GAGTCTGAAT CGCTGTCTGA 300

GGTCTGGAAT CTGAnTCGCT AACTGAAATC TGAGTCGCTA

400

(2) INFORMATION FOR SEQ ID NO: 3601:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3601:

ATTTAATACC TATTTGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 60
 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTATTTGTA CATTGAAAAC TAGATAAGTA 120
 AGTAAATAT AGATTTTACC AAGCAAAACC GAGTGAATAA AGAGTTTTAA ATAAGCTTGA 180
 ATTCATAAGA AATAATCGCT AGTGTTTCGAA AGAACATCCA CAAGATTAAT AACGCGTTTA 240
 AATCTTTTAA TAAAAGAACG TAACTTCATG TTAACGTTTG ACTTATAAAA ATGGTGGAAA 300
 CATAGGTTAA GTTATTAAGG GCGCACGGTG GGATGCCCTG GCACTAGAAG CCGATGAAGG 360
 GnCGTTACTA ACGACGATAT GCTTTGGGGA GCTGTAAGTA 400

(2) INFORMATION FOR SEQ ID NO: 3602:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3602:

GCTGTCTGAG TCGGAATCAC TGThGGAGTC AGAATCGCTG TCTGAGTCGG AATCACTGTC 60
 GGAATCTGAA TCGCTATCTG AATCTGAATC GCTATCTGAA TCCGAGTCAC TGTCTGAGTC 120
 AGAATCGnTA TCTGAATCTG AGTCACTGTC GGAATCTGAG TCACTGTCTG AGTCAGAATC 180
 GCTATCTGAA TCCGAGTCAT TGTCTGAGTC GGAATCGCTC GCTGAGTCGG AATCGCTTGC 240
 TGAATCTGAA TCACTCGCTG AGTCTGAATC ACTTGCTGAA TCTGAATCAC TCGCTGAATC 300
 TGAACCACTA TCTGATGTAG GAATCACTAC CCGAATCTGA AnCGCTATCT GAATAAGAAT 360
 CGCTGCCAGA TCTGAACCTG GGGTCAGAAT CTGAAT 396

(2) INFORMATION FOR SEQ ID NO: 3603:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 529 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3603:

	TTTCTTATCT GTAATTTTAT CGTAAGATTT TTTCGCAATG AGATTGGAT CGTnTTTGTC	60
10	CACTACAATA TCTAATAGTT TTACTTTAAG TCCAGCATTC ACAAAAAGTG CTGCCAGTTG	120
	AGCGCCCAT TGTGCTGCGC CAAGAACGGT TACTTTATTA ATTGTCATAG TGATTCCTCC	180
	AATTAGTTG AGGATAAGAT AACCATTAAAG ATAATTGGAA TAACGTTGCT ATTTTATAAA	240
15	ATTAATTAAG TATCTTTGAC AGTCATCTTA GCCTCTTATT TAAGGaAAAA GCTTTATGCT	300
	TAAAATAAGT CTTTTTTAGT GAAATTAATG CATCTCATAT AATTATTTGC TATTTATACG	360
	AAAGCmGaAT CTCCAGTCaA AGCGCGTCCA ATTACTAAGG CATTAAATTC ATGTGTACCT	420
20	TCGTACGTGT AAATCGCTTC TGCATCAGAG AAGAAACGTG CAATATCATA ATCGTCAGCT	480
	AGTATGCCAT TACCACCTGT AATACCGCGG CCCATAGCTA CtnTCTCAC	529

25

(2) INFORMATION FOR SEQ ID NO: 3604:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3604:

35	CACAAGATAA GCATTGTAGA TGTGGATGCT TTAAGTGGGC AAGCGATTGG TCGTCCTAAA	60
	ACAGGTACAT ATGCGCTATC TGACCTAGTC GGTTTAGATA TTGCAGTGTC TGTAATTAAA	120
	GGCATGCAAC AAGTACCTGA AGAAACACCT TATTTTCATG ATGTCAAAT TGTAATACG	180
40	TTGTTTGACA ATGGCGCACT CGGACGTAAA ACGAAACAAG GATTTTACAA AAAGGATAAA	240
	GAAACTAAAG CTCGACTTGT TTACGATGTT GAAAAACAAG ATTATGTACC TGTATCGCAA	300
45	CCACAATTAC CAATTTTAAA TGAATTTAAT AAAGACTTAG TGCaTAACCT TGATACCATA	360
	TTCCAATGCG CAAGACGAGC GGGGACTATT TTTATGGGG	399

(2) INFORMATION FOR SEQ ID NO: 3605:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3605:

5 ATCACTTGAG GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTCGATT 60
 GGAATTTCTC CGCTACCCTC AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCCT 120
 CCATTCAGTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA 180
 10 CGACCAAATA CTAAACGCCC TATTCAGACT CGCTTTCGCT ACGGCTCCAC ATTTACTGCT 240
 TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCAGCCAT 300
 TAACGGGCTC TGGACTACTT GTAAGCACAC GGTTCAGGT TCTATTTAC TCCCCTCCG 360
 15 GGGTGGCTTT TCACCTTCC CTCACGGTAA TGGGTTCACT 400

(2) INFORMATION FOR SEQ ID NO: 3606:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3606:

25 AAATCCTGCG GTGAGTGATC ACTAACCCGG TTCGATTCCG GTCCTCGGCA CCATTTTCAA 60
 TAAAAACATA TGCGCCCGTA GCTCAATTGG ATAGAGCGTT TGA CTACGGA TCAAGAGGTT 120
 30 ATGGGTTCGA CTCCTATCGG GCGCGTTAAT TATACGGGAA GTAGCTCAGC TTGGTAGAGC 180
 ACTTGGTTTG GGACCAAGGG GTCGCAGGTT CGAATCCTGT CTTCCCGATA TACTGTAATT 240
 35 ATTATGGGGG CTTAGCTCAG CTGGGGAGAG CGCCTGCTTT GCACGCAGGA GGTCAGCGGT 300
 TCGATCCCGC TAGTCTCCAC CATATTATTT ACAAACIATA TAAGGCGGTG TAGCTCAGCT 360
 GGCTAGAGCG TACGGTTCAT ACCCGTGAGG TCGGGGGTTC 400

(2) INFORMATION FOR SEQ ID NO: 3607:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3607:

50 GGGTGTGCTT CTGATATGCT ATGTATTCAC ATATCGATAA CATGACATAA CTCATGCTGG 60
 GTTTCCTT CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 120

TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTAA CATGAAGTTA CGTTCTTTTA 240
TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTCTT TTCGAACACT AGCGATTATT 300
5 TCTTATGAAT TCAAGCTTAT TTAAGCTCT TTATTCACCTC GGTTTTGCTT GGTAAAATCT 360
ATATTTTACT TACTTATCTA GTTTnCAATG TACAATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3608:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3608:

20 TAGTTTTCAA TGTACAAATA ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 60
TGCAAAAGC CGCTCTCCCA GCTGAGCTAA GCGCCCAAT AGGTATTAAA TTAATGGTGG 120
GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCCTCT AACCAGCTGA 180
25 GCTATAGGCC CATTAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240
ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300
GCACCTTCCG ATACGGCTAC CTGTGTACGA CTTACCCCA ATCATTGTGTC CCACCTTCGA 360
30 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTGGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3609:

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3609:

AGGGCACTCT TACTGGGCGT GTTAAATTAC TAANTTCAAT CAGCAGAAGA ACTAGGACAT 60
45 GGCGCTTTTA AAATTATTGA AACACATGCA TAAAAGATG TACAAGCAGT ATTGGGTTTT 120
CATAATGACC CATCGGCTTC GGTAGGTACA TTTGCAATCA AAACAGGGGC AATTACATCA 180
GCAGTAGATC GTTTTGAGTT TCATATTAAA GCGTGGGTG GTCATGCTGC AAACCAGAAC 240
50 AATGCAACGA TCCAGTTATT GTGTTGGCGC AATTGATTAA TAGTATTCAA TCCATAGTTA 300
GTAGAAATCT ATCTGCGTTT GATGAAGCGG TAGTAACAAT TGGACAAATA TCATGTGGTA 360

(2) INFORMATION FOR SEQ ID NO: 3610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3610:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120
 CCCATTCCGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240
 TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT 300
 TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAATGA ATTTAACTCA TTGTCTGCTA 360
 AACGTTTTGC TTTTATAAAA AGATTTAAAC GCGTTGATTT 400

(2) INFORMATION FOR SEQ ID NO: 3611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3611:

GAGCTAGGCC GGCAATATGT AAGAATAAAT CGTGGAGAAT GACGGGTTTC AACCGCCGAC 60
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 120
 GGCAACGTTT TACTCTAGCG GAATAAGTT GNACTACCAT CGACGCTAAG GAGCTTAACT 180
 TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240
 TAATTTATAC ATTCAAACT AGATAGTAAG TAAAGTGAT TTTGCTTCGC AAAACATTTA 300
 TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC ACATGTCACC ATGCTTCCAC 360
 CTCGAACCTA TTAACCTCAT CATCTTTGAG GGATCTTAAT 400

(2) INFORMATION FOR SEQ ID NO: 3612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3612:

5 ACCCAGCTCG CGTACCGCTT TAATGGGCGA ACAGCAATCC CTTGGGACCG ACTACAGCCC 60
 CAGGATGCGA TGAGCCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120
 GAGATAAGCC TGTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC CTTCCATGCC 180
 10 GAACCACCGG ATCACTAAGT CCGTCTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAGTCA 240
 AGCTCCCTTA TGCCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACCTTTGA 300
 15 GrGCCTCCGT TACCTTTTAG GAGGCGACCG CCCAGTCAA ACTGCCCCGCC TGACACTGTC 360
 TCCCACCACG ATAAGTGtnc GGGGGTTAGA AAGCCAACAC 400

(2) INFORMATION FOR SEQ ID NO: 3613:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3613:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCaA 60
 30 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 120
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 180
 TTTAAAATAA TTAACTCAT TGTCTGCTAA ACGTTTTCTT TTATAAAAAG ATTTAAACGC 240
 35 GTTATTAATC TTGTGAGTGT TCTTTGGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 300
 TATTTAAAC TCTTTATTCA CTCGGTTTTG CTGGGTAAAA TCTATATTTT ACTTACTTAT 360
 40 CTAGTTTTCA ATGTACAAAT AATGGTGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC 420
 TTATCAGGCG TGCGCTCTAA CCAGCTGAGC TATAGGCCA TTTTTTTGaA TGTTAAATAA 480
 ACATTCA 487

(2) INFORMATION FOR SEQ ID NO: 3614:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAT AATATGGTGG 60
 AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG 120
 5 CTAAGCCCC ATAATAATTA CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT 180
 GGTCCCAAAC CAAGTGnTCT ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT 240
 AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC TCTATnCAAT TGAGCTACGG 300
 10 GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA TCGAACCGGT ACGGTGATCA 360
 CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GChAGTTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3615:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3615:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AACTCGTTG CGCTCTTTTC TCGTTTCGTC 60
 AGATTCAAAC GTTTTCACCT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120
 30 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCTACTCTA 180
 GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT 240
 TGCTCTTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 300
 35 TCTTTTCTCG TTTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT 360
 TTACTTTTTA TTTTGACGTT TAGGCATAAA AAAAGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 3616:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3616:

TnGTGTCTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT 60
 ATTCACTCGG TTTTGCTTGG KAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA 120
 55 CAATTTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC TTAAACCAA AAATATTTGA 180

AAGATGTTCC GAATATATCC TTAGAAAGGA GGnGATCCAG CCGCACCTTC CGATACGGCT 300
 ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 360
 5 TTACTCCACC GGCTTCGGGT GTTACAACT CTCGTnGGTG TGACGGGCGG TGTGTACAAG 420

(2) INFORMATION FOR SEQ ID NO: 3617:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3617:

CACTAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 60
 20 GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT TTCTTTTATG 120
 TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT TAAATAAACA 180
 25 TTCAAAACTG AATACAATAT GTCACATTAT TCCGCATCTT CTGAAGAAGA TGTCCGAAT 240
 ATATCCTTAG AAAGGAGGTG ATCCAGCCGC ACCTTCCGAT ACGGCTACCT TGTACGACT 300
 TCAnCCCAAT CATTTGTCCC ACCTTCGACG GCTAGCTCCT AAAAGGTTAC TCCACCGGCT 360
 30 TCGGGTGTTA CAAACTCTCG TGGTGTGACG GCGGGTGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3618:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3618:

GATATACGCT ATGGCTGGAG CAGTGTGGCC AAATGGCGGA AGACAAACGT TTAATGCGAT 60
 45 ATACTTAGCG CAAAATATTG GTGTGGCTGT CGGTGCTGCA ATGGGCGGCT TTGTCCGAGA 120
 ATTTAGCTTT AACTATATCT TTTTAGCCAA TCTTATTATG TAIGTTGTGT TTGCGCTTGT 180
 CCGGTTAACn AATTTAATAT TGAAATTAAT GCGAAAGTTA AATATCCAAC TCATTTAGAT 240
 50 ATTACTGGTA AAAAGAATAA AGCAAGATTT ATTTCAITAG TACTAATTTG TGCAATGTTT 300
 GCAATTTGTT GGGTTGCATA TATTCAATGG GGAGTCTACA ATCGCTTCAT TTTACACAAT 360
 55 CTATTAATAT TTCAATGGGC ACAATATAGT GTTTTATGGG 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3619:

TCGCACGCCT TCGCCTATCC TACTGCGTCC CCCCATCGAT TAAACGATT ATAGGTGGTA 60
 CAGGnAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCG GCCTCAGCTT AGGACCCGAC 120
 TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC 180
 ACCCGTCTTT CGCTACTCAC ACCGGCATT CACTTCTAA GCGCTCCACA TGTCCTTACG 240
 ATCATGCTTC AACGCCCTTA GAACGCTCTC CTACCATTGT CCAAAGGAAA TCCACAGCTT 300
 CGGTAATATG TTTAGCCCCG GTACATTTTC GGCAGTGT CACTCGACTA GTGAGCTATT 360
 ACGCACTCTT TAAATGATGG CTGCTTCTAA GCCAACATCC 400

(2) INFORMATION FOR SEQ ID NO: 3620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3620:

TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA 60
 CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTTGA 120
 GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT CCACACATAG CTACCCAGCT 180
 ATGCCGTTGG CACGACAACT GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA 240
 AGGACAGCTC CTCTCAAATT TCCTACGCCC ACGACGGATA GGGACCGAAC TGTCTCACGA 300
 CGTTCTGAAC CCAGCTCGCG TACCGCTTTA ATGGGCGAAC AGCCCAACCC TTGGGACCGA 360
 CTACAGnCCC AAGGATGCGA TGAGCCGACA TCGAGGTGCC 400

(2) INFORMATION FOR SEQ ID NO: 3621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3621:

5 CCACACCCGc AAATGGTGag CCATAGcAGG ATTcGgaACC TCTGcACCCT CTGATTAAAA 60
 GTCAGcATGC TCTACCAACT GaGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 120
 ACCCCCAACC TACTGATTAC AAGTCAGTTG CTCTACCAAT TGAGCTAGGC CGGCAATATG 180
 10 TAAGAATAAA TGGTGGAGAA TGACGGGTTC GAACCGCCGA CCCTCTGCTT GTAAGGCAGA 240
 TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC 300
 GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA 360
 15 ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTAATTTA TACATTCAAA 420
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGT 475

(2) INFORMATION FOR SEQ ID NO: 3622:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3622:

30 TGGACGAAAC TTTATATCGA TCAATTTCTA TCGAGTTGGA CAATGCCGAA GCGTGACAAA 60
 AGTTTTTACC ATGCATGGTT GCATTTAGCG CAACATGACC ATAGTTTTAC TAAAGCACAG 120
 CGCnCAAGTG ATTAAAGGCT TACCCAATGA TCCTGAAATG ACGATAGAGT CAGTATTAAC 180
 35 TCATTTTTCA ATAGATCAGG AAGACTACCA AGCTTATGTT GAAGGACATC TTTTGGCGTT 240
 ACCGGGTTGG GCAGGTATGT TGTATTACCG TTCACAACAG CATCACTTTG AACAAACATTT 300
 GTTAACGGAT TATTTGGCAA TTCGGTTAGT TGTCGAACAA TTGCTAGTTG GTGGATGAGT 360
 40 TTTAAGTCAG TCGCTAAAGA TTGTGGAAG TAAGATCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3623:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3623:

55 TAGATGCTTT CASACTTATC CCGTCCACAC ATAGCTACCC AGCTATGCCG TTGGACGACA 60

ATTCCTACG CCCACGACGG ATAGGGACCG AACTGTCTCA CGACGTTCTG AACCCAGCTC 180
 GCGTACCGCT TTAATGGGCG AACAGCCAAC CCTTGGGACC GACTACAGCC CCAGGATGCG 240
 5 ATGACCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG GAGATAAGCC 300
 TGTTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC TTCCATGCGG GAACACCGGA 360
 10 TCACTAAGTC CGTCTTTCGA CCCTGCTCGA CTTTGTAGGn 400

(2) INFORMATION FOR SEQ ID NO: 3624:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3624:

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCTG AACCGCCGAC 60
 CCTCTGCTTG TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 120
 25 GGCAACGTTT TACTCTAGCG GAAnTAAGTn GnACTACCAT CGACGCTAAG GAGCTTAACT 180
 TCTGTGTTCTG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240
 30 TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAACATTTAT 300
 TTTGATTAAG TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC 360
 TCGAACCTAT TAACCTCATC ATCTTTGAGG GGATCTTATA 400

(2) INFORMATION FOR SEQ ID NO: 3625:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3625:

TTAAAGAACG CTAATAACTG ATCGTAACCA CTATATATAT TGTGTGACC TCTAACAGCA 60
 TAATGTCTAA ATGTTTGTGG GATATATTGA AGCAATCCTT TTGCTGGATT GCCCTGTAAA 120
 50 ACGTTGATGT CTCTAAGCGA ACTAGATTGA GTTATACCTG CATTTCTCTC TGATTCGTGT 180
 TGAATCAAGC TAATGATATT TCCTACGTCA GCCGAAGTAA CATTACACC CATTCGTTTT 240
 55 GCTGCACGAC GTATATCGCC TGCCCAAGCA GATGCAGCCT TATTAACACC TGAACCACTT 300

CCTGGATGCG ACCCTTGCAT CAnTTGGGAA ATGTAnGTGT

400

(2) INFORMATION FOR SEQ ID NO: 3626:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3626:

GATTGTGGTT CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCCTTATT ATTAATGGGC 60
 TATAGCCAAG CGGTAAGGCA ACGGACTTTG ACTCCGTCAC TCGTTGGTTC GAATCCAGCT 120
 AGCCCAGTTA TTGGCGGCAT AGCAAGTGGT AAGGCAGAGG TCTGCAAAAC CTTTATCACC 180
 GGTTCAAATC CGGTTGCCGC CTCCAGGTTT ATGCGGGAGT AGTTCAACTT TTAGAACACG 240
 TTCCTTCCCG GAAGAGGTAT AGGTGCAAAT CCTATCTTCC GCTCCATAAT TTAATAATAA 300
 TGCGGGAGTA TTTCAACTCT TAGAATACAT TCCTTCCTGG AATgAGGTAT AGGTGTAAAT 360
 CCTATCTTCC GCTCCATAAT TTAATATTTG cGGGAGTAGT TCAACTTTTA GAAACAGCTC 420
 CTTCCCGGAA CCGAGGTATA GGTGTAAATC CTATCTTCCG C 461

(2) INFORMATION FOR SEQ ID NO: 3627:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3627:

TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG 60
 AACGTAAGTT GGCTnAnATC GACGCTAAGA ACCTTTCTTG ACTTGTGACA ATCGCTTGCT 120
 TCTTTCCTCT TCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 180
 TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT TTGTGTTTGC 240
 TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT 300
 CGCATCCATT TTTTGCCTGG CAACGTCTTA CTCTAGCGGA ACGTAAGTTC GACTACCATC 360
 GACGCTAAGG GAGCTTAACT TCTGTGTnCG GGCATGGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3628:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3628:

10 ATGCTTTTCAG CACTTATCCC GTCCACACAT AGCTACCCAC CTATGCCGTT GGCACGACAA 60
 CTGGGTACAC CAGAGGTATG TCCATCCCGG TCCTCTCGTA CTAAGGACAG CTCCTCTCAA 120
 ATTCCTACG ACCCAGCAGC GATAGGGACC GAACTGTCTC ACGACGTTCT GAACCCAGCT 180
 15 CGCGTACCGC TTTAATGGGC GAACAGCCCA ACCCTTGGGA CCGACTACAG CCCCAGGATG 240
 CGATGAGCCG ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACCTTTG GGGGAGATAA 300
 GCCTGTTATC CCCGGGGTAG CTTTTATCCG nTGAGCGATG GGCCTTCCAT GCGGnACCAC 360
 20 CCGnTTACTA AGTCCGTCCT TCGAnCCTGC TCGACTTGTA 400

(2) INFORMATION FOR SEQ ID NO: 3629:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3629:

35 TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA TCAATGGCAG GATTGAAAGG 60
 ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGT TTTTCATACC AAGTCGCTGC 120
 CGGCAAAACA ATGTCAGAAT ATAACGGTGT TGCCGTCATT CTGAAGTCTA AAGAGACCAC 180
 40 TAAATCTAAC TTACCTGTTG TTTCTTCACG CCACGTAATT TCTTCTGGCT TTTTCATCTC 240
 ATTTGGTGTA GCTAATAACC CTGATTTTGT GCCAAGTAAA TGCTTCATAA AGTATTCTTG 300
 ACCTTTTGCA GAACTTGAAA TTAAGTTTGA ACGCCATATA AATAATGATT TTGGATGATT 360
 45 CTnTTTCAAA TCAGGATCTT CTATTGCAAA TGGGGTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3630:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 589 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TTTAAGTTGT nGATTTAAAA TATTAAATAA GTGTAAATTT GACTATTGAn ATTCkrACaA 60
 ATACATATTA AAATAATATT TGTTGAATTA ATTGAGTTAG GAAATTTATT TTTTAGAAAT 120
 5 AAAATAATTA AAAATAATTC TTGACTTACA AAAACTTACG AGTTATAATT AAATCTTGTA 180
 AGTGACAAAC GAACATTGAA AACTGAATGA CAATATGTCA ACGTTAATTC CAAAAACGTA 240
 ACTATAAGTT ACAAACATTA TTTAGTATTT ATGAGCTAAT CAAACATCAT AATTTTTATG 300
 10 GAGAGTTTGA TCCTGGCTCA GGATGAACGC TGGCGGCGTG CCTAATACAT GCAAGTCGAG 360
 CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 420
 15 TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATrATATTT 480
 TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 540
 TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATA 589

(2) INFORMATION FOR SEQ ID NO: 3631:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3631:

CCAACTGAGC TAATGGCTCT TCCATGGTGC CGGCCAGAGG ACTTGAACCC CCAACCTACT 60
 GATTACAAGT CAGTTGCTCT ACCAATTGAG CTAGGCCGGC AATATGTAAG AATAAATGGT 120
 35 GGAGAATGAC GGGTTCGAAC CGCCGACCCT CTGCTTGTA GGCAGATGCT CTCCCAGCTG 180
 AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTCTG 240
 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTTCGGC ATGGGAACAG GTGTGACCTC 300
 40 CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT TCAAACTAG ATAGTAAGTA 360
 AAAGTGATTT GCTTCGCAAA ACATTTATTT TGATTAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3632:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3632:

TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 120
 AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT 180
 5 CAAGCTTATT TAAAACTCTT TATTCACITCG GTTTTGCTTG GTAAAATCTA TATnTTACTT 240
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCGCTGACC 300
 10 TCCTGGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAn GCCCCCAhAT AGGTATTAAA 360
 TTAATGGGGG GGCCTAAGTG GACTCGAACC ACCGACCTCA 400

(2) INFORMATION FOR SEQ ID NO: 3633:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3633:

ATATGTCAAC GTTAATTCCA AAAACGTAA CTATAAGTTA CAAACATTAT TTAGTATTTA 60
 25 TGAGCTAATC AAACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAG GATGAACGCT 120
 GGCGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT TCTCTGATGT 180
 30 TAGCGGCGGA CGGGTGAGTA ACACGTGGAT AACCTACCTA TAAGACTGGG ATAACCTCGG 240
 GAAACCGGAG CTAATACCGG ATAATATTTT GAACCGCATG GTTCAAAAGT GAAAGACGGT 300
 CTTGCTGTCA CTTATAGATG GATCCGCGCT GCATTAGCTA GTTGGTAAGG TAACGGCTTA 360
 35 CCAAGGChAC GATGCATAGC CGACCTGAGA nGGTGATCGG 400

(2) INFORMATION FOR SEQ ID NO: 3634:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3634:

TGAGCTAGGC CGGCAATATG TAAGAATAAA TGGTGGAGAA TGACGGGTTT GAACCGCCGA 60
 50 CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAAACTGCC 120
 TGGCAACGTT CTACTCTAGC GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA 180
 55 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 240

TATTTTGATT AAGTCTTCGA TCGATTAGTA TTCGTCAGCT CCACATGTCA CCATGCTTCC 360
 ACCTCGAACC TATTAACCTC ATCATCTTTG AGGGATCTTA 400

(2) INFORMATION FOR SEQ ID NO: 3635:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3635:

TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT TTAGCTCTAC 60
 TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 120
 ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTGTAGAC ATAAAAAAA GAGACCTTGC 180
 GGTCTCAAAT GCGGCTCATC GCATCCATT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 240
 CGTAAGTTGG GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT 300
 CTTTCCTCTT CTTGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCTCTTT 360
 TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TTCGCCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3636:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3636:

TACTTATCTA GTTTTCAATG TACAATTTCT TTnTAGTCAA GCGCTCGCAT ACTGATTTTC 60
 AAAAAATCAA ATGCTCATTT ACAAAGTAA ACTCCGCTTT ATTTTCTTA ATGCATTGTC 120
 TAACAACCGC TTTCTTTAAA AAGAATAGAT TGTCAAGCGC TGCATAAGC AATATCACTT 180
 TAACCAAAAA ATATTGAAT GTTAAATAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240
 ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300
 GCACCTTnCG ATACGGCTAC CTTGTTACGA CTTACCCCA nTCATTTGTn CCACCTTCGA 360
 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTGGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3637:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3637:

AGCGCTCGCA TAAGCAATAT CACTTTAACC AAAAAATATT TGAATGTTA AATAAACATT 60
 CAAAACTGnA ATACAATATG TCACATTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA 120
 TATCCTTAGA AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT 180
 CACCCCAATC ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT 240
 CGGGTGTTAC AAATCTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC 300
 ACCGTAGCAT GCTGATCTAC GATTACTAGC GATTCCAGCT TCATGTAGTC GAGTTGCAGA 360
 CTACAATCCG AACTGAGAAC CACTTATGGG ATTGCCTnAC 400

(2) INFORMATION FOR SEQ ID NO: 3638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3638:

TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC GGAAGTAAGT CGAnCTACCA 60
 TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA 120
 TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAC TAGATAGTAA GTAAAAGTGA 180
 TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 240
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 300
 AACCGAAGTT GGGGAAATCT CATCTTGAGG GGGGCTTCAT GCTTAGATGC TTTCAGCACT 360
 TATCCCGTCC ACACATAGCT ACCCAGCTAT GCCGTGGCA 400

(2) INFORMATION FOR SEQ ID NO: 3639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

ATGTCTCTAA CGCCTTTAAT AGTATTGAAC ACAATTGGGA AAAAGCAGC GATAAAAATA 60
 ATCGCAATCG CTGGCAAACCT ACCAATACCA AACCATAGAA CAACAAATGG TGCCCATGCT 120
 5 ATCGGAGATA TCGGCCTAAT CAATTGAAAT AGCGGTTCTGA TAGCGTTGTA TAGCCAACGA 180
 TTCCTTCCAA GCAAGAAGCC CAATGGAATA GCAACCAACA ATGCGACAAC AAAGCCCGCT 240
 ACAAATCTCC ATAACTAAT TGCTAAATGT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 300
 10 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 360
 ATAaTGACCA TTTCCCAaT GCCTAAGAAA aTAATAAATG TGATAATAGG TAATATAAAT 420
 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 480
 15 AGTCATCCAT ATGCAGGTGG ATTAAACAAA TGATGTTGTT TTACCAngTC GTAATTTCTT 540
 GATAGCCGGA T 551

20 (2) INFORMATION FOR SEQ ID NO: 3640:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3640:

30 CACTAAACTA AATTAATGAA GTGCCTTATG TATAAAAATT ATAACCTGAT CCAACTTACA 60
 CTACCAATAG AAACCTCTGT TAGAATTCCT CAAATTGATA TTTCGCGATA TGTTAATGAA 120
 ATTGTTGAAA CGATACCTGA TAGCGAATTC GATAAATTC GACATCATCG TGGCGCAACA 180
 ICCTATCATC CAAAAATGAT GTTAAAAATC ACCTTATATG CATATACTCA ATCTGTATTT 240
 ICTGGTCGTA GAATAGAGAA ATTACTTCAT GACAGTATTC GAATGATGTG GTTAGCTCAA 300
 AATCAAACAC CTTCTTATAA AACTATTAAT CGTATTAGAG TGAATCCTAA TACTGATGCG 360
 TTAATTGAAT CTTTATTTAT CCACTTTCAT AGTCAATGTT 400

(2) INFORMATION FOR SEQ ID NO: 3641:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3641:

GATTGTCCTT TGGcAATGGT AGGAGAGCGT TCTAAGGGCG TTGAAGCATG ATCGTAAGGA 120
 CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CGAAAGACGG GTGAGAATCC 180
 5 CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC 240
 CTAAGCTGAG GCCGACAGnG TAGGCGATGG ATAACAGGTT GATATTCTTG TACCACCTAT 300
 AATCGTTTTA ATCGATGGGG GGrCGCATAG GATAGGCGAA CGTTGCGATT GGATTGCACG 360
 10 TCTAAGCAGT AAGGCTGGAG TATTAGGCAA ATCCGGTA 398

(2) INFORMATION FOR SEQ ID NO: 3642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3642:

TAATGTCTAC ACTTTGCTTG CGATCATTCA TTTTAAAGCC AGACTTTTTA TAATCTTGTA 60
 25 CAAATGCTTG CGCTACATCC TTGTGTTGAT CAAGCAATTC CCCTCTCAGT ACTAGCACAC 120
 AGCAATACGC ATCAGGtATA ACGTCATCAC CATGTTTCAA AGTCTTACCT TTGCCTAACT 180
 TTTcACCCAG TGCACCGAAT GGTTCGGCTA CAGAATACCC TGTaATTCTG TGTTCACTCA 240
 30 ATGCGGCTGG CATTCTGCT GCGGACATTT CATGATAGCT AAAATGCCCC GGTTTAATCT 300
 TTAATTGTTT ACGTAATTCC TCAAGTAAAA GATAATGTGt TGAATAACgA TGTGGtATAC 360
 CAAATGGkA ATCATCGCCA TTAtTATTAA ATTCaTTTAA GTGCATACCT TTTTGTCCCA 420
 35 TAATGACATT GCCTTCATG 439

(2) INFORMATION FOR SEQ ID NO: 3643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3643:

ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60
 50 TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120
 TCGAACCGTG ACCTCCTGCG TGCAAAGCAG GCGCTCTCCC AGCTGAGCTA AGCCCCCAAA 180

GCGTGCGCTC TAACCAGCTG AGCTATAGGC CCATTAATTT GAATGAACAA ACATTCAAAA 300
 CTGAATACAA TATGTCACGT TATCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT 360
 5 TAGAAAGGAG GTGATCCAGC CGCACCTTnC GATACGGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3644:

GCGAAACTGT ACGGAGCAAC GCCGCGTGAG TGATGAAGGT CTCGGATCG TAAAACTCTG 60
 TTATTAGGGA AGAACATATG TGTAAGTAAC TGTGCACATC TTGACGGTAC CTAATCAGAA 120
 AGCCACGGCT AACaCGTGCC AGCAGCCGCG GTAATACGTA GGTGGCAAGC GTTATCCGGA 180
 ATTATTGGGC GTAAAGCGCG CGTAGGnGTT TTTTAAGTCT GATGTGAAAG CCCACGGnTC 240
 25 AACCGTGGAG GGTCAATTGGA AACTGGAAAA CTTGAGTGCA GAAGAGGAAA GTGGAATTCC 300
 ATGTGTAGCG GTGAAATGCG CAGAGATATG GAGGAACACC AGTGGCGAAG GCGACTTTCT 360
 GGTCTGTAAC TGACGCTGAT GTGCGAAACG TGGGGATCA 399

(2) INFORMATION FOR SEQ ID NO: 3645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3645:

TATTATACTT TACATTTCTC GTTTCGTCAG ATTCAAACGT TTTCAC TTCG CCAAGCCATC 60
 TTCTTTTG TG TTTGCTTTTA TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT 120
 45 CAATGCGGCT CATCGCATCC ACTTTTTTGCC TGGCAACGTT CTA CTCTAGC GGAACGTAAG 180
 TnCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 240
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATnAT ACATTCAAAA CTAGATAGTA 300
 50 AGTAAAGTG GATTTTGCTT CGCAAAACAT TTATTTTGA TTAAGTCTTC GATCGGATTA 360
 GTATTCGTCA GCTCCACATG TCACCATGGC TTCCACCTCG 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 758 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3646:

AGATAAGTAA GTAAATATA GATTTTACCA AGCAAAACCG AGTGAATAAA GAGTTTTAAA 60
 TAAGCTTGAA TTCATAAATA ATCGCTAGTG TTCGAAAGAC ACGAnCAAGA TTAATAACGC 120
 GTTTAAATCT TTTTATAAAA GAACGTAAC TCATGTTAAC GTTTGACTTA TAAAAATGGT 180
 GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC CTTGGCACTA GAAGCCrATG 240
 AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA GTAAGCTTTG ATCCAGAGAT 300
 TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT CGATATGTGA ATACATAGCA 360
 TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA GAAAGAAAAT 420
 TCGATTCCCT TAGTAGCGGC GAGCAnAACG GGAAGAGCCC AAACCAACAA GCTTGCTtGg 480
 GGGTnTGTaG GACACTCTAT ACGGATTACA AAGGACGACA TTAGACGAAT CATCTGGaAA 540
 GATGAATCAA AGAAGGTAAT AATCCTGTAG TCGAAAATGT TGTCTCTCTT GAGTGGATCC 600
 TGaGTACGAC GGAGCACGTG AAATTCCGTC GGAATCTGGG GAGGaCCATC TCCTAAGGCT 660
 AAATACTCTC TAGTGACCGA TAGTGGAACC aGTaCCGTGA GGGAAAGGTg AAAAGCACCC 720
 gGAAGnAGT TGAAATaGAA ctGGAAACCG TGTGCTTA 758

(2) INFORMATION FOR SEQ ID NO: 3647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3647:

ACAAACTCCG AATGCCAATT AATTTAACTT GGGAGTCAGA ACATGGGTGA TAAGGTCCGT 60
 GTTCGAAAGG GAAACAGCCC AGACCACCAG CTAAGGTCCC AAAATATATG TTAAGTGGAA 120
 AAGGATGTGG CGTTGCCCAG ACAACTAGGA TGTTGGCTTA GAAGCAGCCA TCATTTAAAG 180
 AGTGCGTAAT AGCTCACTAG TCGAGTGACA CTGCGCCGAA AATGTACCGG GGCTAAACAT 240
 ATTACCGAAG CTGTGGATTG TCCTTTGGnA TGGGTAAGGA GAGCGTTCTA AGGGCGTTGA 300

AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAAGGTT

400

(2) INFORMATION FOR SEQ ID NO: 3648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 521 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3648:

15 GTCATTGGAA ACTGGAAC TTAGTGCGAG AAGAGGAAAG TGAATTCCA TGTGTAGCGG 60
 TGAAATGCCG AGAGATATGG AGGAACACCA GTGGnCGAAG GCGACTTTCT GGTCTGTAAC 120
 TGACGCTGAT GTGCGAAACG TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC 180
 20 GTAAACGATG AGTGCTAAGT GTTAGGGGGT TTCCGCCCCCT TAGTGCTGCA GCTAACGCAT 240
 TAAGCACTCC GCCTGGGGAG TACGACCGCA AnGTTGAAAC TCAAAGGAAT TGACGGGGAC 300
 CCGCACAAGC GgTGGaGCAT GTGGTTTAAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC 360
 25 TTGACATCCT TTGACAACTC TAGAGATAGA GCcTTCCCT TCGGGGGACA AAGTGACAAG 420
 TGGTGCGTGG TGTCGTCAAC TCCTGTCGTT GAGATGTTGG GGTAAnTCCC CGCAAnGAGC 480
 GCACCCTTAA GCCTTAGTTT nCATCATTAA GTTGGGCACT C 521

(2) INFORMATION FOR SEQ ID NO: 3649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3649:

CCAAAGTTCA TCTTTTACGA ATGAGAAATA GGTGTTGCAT ATTCAATGGT CTCATCTTGT 60
 TTATAAAAGC CACCATCTAA ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC 120
 45 ATACGTGTTT TAACACGTTT GTATCCCATT GCATCCCATA ATTGGAATGG ACCAAGTTTC 180
 CAGTTGAACC CCCAGACAAG CGCACGGTCT ATGTCTCGGA AATCATCGGT AGCTTTAGGT 240
 ACATTGATAG CAGAGTAATA GAAATTATTA CGTAATGTCT CCCATAAAAA TAGTCCCGCT 300
 50 TCGTCTTGcG CATTGAATAT GGTATCAAKg TTATGCACTA aGTCTTTATT AAATTCATTT 360
 AAAATTGGTA ATTGTGGTTG CGATACAGGT ACATAATCTT 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3650:

GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTTCGAA CCCCCGCGGn CCGTTAAGGC 60
 CCTGTGCGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC ATTATTATAG 120
 GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC 180
 TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG 240
 AAGAGGGATT CGAACCCCCG CGAGCCGTTA AGCCCTGTC GGTTCCTCAAG ACCGATCCCT 300
 TCAGCCGGAC TTGGGTATTTC CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTGCGA 360
 CCGAACGGTT ATGGAGCCGT TAGCTCTAAn CAACTTGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3651:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3651:

TGGCGCTGTG CTTTAGTAAA ACTATGGTCA TGTGCGCTA AATGCAACCA TGCATGGTAA 60
 AAACCTTGCT CACGCTTCGG CATTGTCCAA CTCGATAGAA ATTGATCGAT ATAAAGTTTC 120
 GTCCATTTAA TCATTGACG ATTCACITGT TCGCTAAGTG GCTCACCTTG TTCATCTATT 180
 ATTGCATCAC TCATCGGACG TACATCATAG TGATGATATG ATTCAGCCAT ATCACGTTTT 240
 GATTTTTCTA ATAGTAGATC AGCAACAACA TCAACATTTG AATGATTCAT ATATGATGGC 300
 AGGTACGTCT TTAAATGTTT TAATGTTATC AATATAAAGA TGATGTAGTG TTGCGGGATA 360
 TGTAGTGAnG TTCAAGTAAC ATATCAGTAA CAAGTTGATT 400

(2) INFORMATION FOR SEQ ID NO: 3652:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3652:

CATTGTCCAA AGGACAATCC ACAGCTTCGG TAATATGTTT AGCCCCGGTA CATTTTCGGC 60
 5 GCAGTGTAC TCGACTAGTG AGCTATTACG CACTCTTTAA ATGATGGCTG CTTCTAAGCC 120
 AACATCCTAG TTGTCTGGGC AACGCCACAT CCTTTTCCAC TTAACATATA TTTTGGGACC 180
 TTAGCTGGTG GTCTGGGCTG TTTCCCTTTC GAACACGGAC CTTATCACCC ATGTTCTGAC 240
 10 TCCCAAGTTA AATTAATTGG CATTCCGAGT TTGTCTGAAT TCGGTAACCC GAGAGGGGCC 300
 CCTCGTCCAA ACAGTGCTCT ACCTCCAATA ATCATCACTT GAGGGCTAGC CCTAAAGCTA 360
 ATTTCCGAGA GAACCAGCTA TCTCCAGGTT CGATGGAATT 400

(2) INFORMATION FOR SEQ ID NO: 3653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3653:

GGTTCCGGTCC TCCATTCACT GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG 60
 TTTCGGGTCT ACGACCAAAT ACTAAACGCC CTATTCAGAC TCGCTTTCGC TACGGCTCCA 120
 30 CATTACTGTC TTAACCTTGC ATCAAATCGT AACTCGnCGG TTCATTCTAC AAAAGGCACG 180
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTTCA 240
 TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 300
 35 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 360
 CGTACTCAAG nATCCACTCA AGAGAGACAA CATTTTCGAC 400

(2) INFORMATION FOR SEQ ID NO: 3654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3654:

AAAGGTCCTA AATATAATTT TACAACAAAT AAATAGTGGC GGTGGAGGGG ATCGAACCCC 60
 CGACCTCACG GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC TTATATAGTT 120

GCGCTCTCCC AGCTGAGCTA AGCCCCCATA ATAATTACAG TATATCGGGA AGACAGGATT 240
 CGAACCTGCG ACCCCTTGGT CCCAAACCAA GTGCTCTACC AAGCTGAGCT ACTTCCCGTA 300
 5 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGnTCT 360
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3655:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3655:

20 TATTGAAGCC TGAGTCAACA CGTACGCAAA TCGATCAAAT CATCGATGAA GCGAAACATA 60
 CAATTTTAAA TCTGTATGTG TGAATCCAAC ACATGTTAAA TATGCAGCAG AGCnnCTAGC 120
 TGATTCAGAG GTGCTCGTTT GTACGGTAAT AGGATTCCCA TTAGGTGCGT CGACAACTGC 180
 25 AACGAAAGCA TTTGAAACAG AAGATGCAAT TCAAAATGGT GCAGATGAAA TTGACATGGT 240
 CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 300
 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGGAT TATTGAGACG GTATTGTTGG 360
 30 GACCATGACG AAATTGTAAA AGCGAGTGGA ATTAACCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3656:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 530 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3656:

GATGAGTCGC TGnCTGATCT GAACGCTGTC TGAGnCCGAA CGCTACTGAA CTGAGTCGCT 60
 45 GTCTGAGTCT GAATCGCTAT CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTGTCTGA 120
 GTCTGAGTCG CTGTCTGAGT CTGAATCGCT ATCTGAATCT GAGTCGCTGT CTGAGTCTGA 180
 GTCGCTATCT GAGTCTGAGT CGCTGTCTGA ATCTGAGTCG CTGTCTGAAT CTGAATCGCT 240
 50 GTCTGAGTCT GAATCGCTAT CTGAGTCTGA ATCGCTATCT GAGTCTGAAT CACTGTCTGA 300
 GTCCGAGTCA CTGTCTGAAT CTGACTCACT ATCTGATTCT GAGTCGCTAT CTGATTCTGA 360

ATCTGAACCT GAGTCGCTGT CTGAGCCTGA AGTCACTGGT CTGAATCCGA ATCCGGATCC 480
 GGGTCTGGGG CTTGGGTTCC GGTTCCTGGGT CTGGGACTTG GGTTCTGGGA 530

(2) INFORMATION FOR SEQ ID NO: 3657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3657:

GTTTAACTA CGCAAGACAT CGAAGAAGCT GACGGTGTCA TAATTGCAGC TGATAAACAA 60
 GTTGATCTGT CCCGATTTGT TGGTAAACGG TTGATTAATG AAAATGTTTCG CGAAGGGATT 120
 CATAATCCGA GAGGTCTAAT TCAACGTATC ATTAATCAAG ATGCGCCTAT TTATCAATCT 180
 GAAACAAATT ATCATTGCAA AGATCGCGGT AAGTCTAAAA ATGGTATTCA AATGGTGTAT 240
 CAACATTTAA TGAACGGTGT ATCGTTTATG GTTCCTTTTA TCGTAGTTGG TGGACTCCTT 300
 ATCGCCATCG CGCTGGACTC TAGGCGGTGA ACGACATCAA AAGGATTAGT CATCCCAGAT 360
 GGATTCATTT TGGGAAATCC ATTGGAATAC ATTGGGTAGT 400

(2) INFORMATION FOR SEQ ID NO: 3658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3658:

GAAGAAGTTT ATGAAACGGT TATGAATAAG CCATACACTA GATATCCAGT GTACGAGGGA 60
 GATATTGATA ACATTATTGG GGTGTTTCAT TCTAAATATC TGTTGGCTTG GAGTAATAAA 120
 AAAGAAAATC AAATTACAAA CTATTCAGCT AAGCCATTAT TTGTGAATGA ACACAATAAA 180
 GCTGAATGGG TATTACGTAA GATGACTATT TCTAGAAAAC ATTTAGCAAT TGTGTTGGAC 240
 GAATTTGGTG GTACTGAAGC GATAGTGTCA CATGAAGACT TAATTGAAGA ATTATTAGGT 300
 ATGGaAATTG AAGATGAGAT GGaTAAAAAG GAAAAAGAAA AACTTTCTCA ACAGCAAATT 360
 CmATTTCaAC AACGGAAAAA TCGCmACGTA TCTATATAAG GnGCGAACAG CTATGTGGTA 420
 ATAAGAATCG ACTTACTCAA ATGTTAAGTA TTGAATATCC AATTATACAA GCAGGTATGG 480

TAGGCGCGGT TACTTTAATA CGCAGCAATT GGAAGATGAA ATAGATTATG GTACGCCAAT 600
 TAACGTCAAA TTCTTTTGGC GTAAATGTCT TTGGTACCAA GTCAACAATC ATATACCAGT 660
 5 AGTCAAAT 668

(2) INFORMATION FOR SEQ ID NO: 3659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3659:

AAAAGAATGG TAAGTTGAAT AAAGTATTGA AATCAATTGC CAATATCTTT ATACCGTTGA 60
 TTCCTGnATT TATTGGAGCT GGATTAATTG GTGGTATTGC AGCAGTACTG AGTAACTTAA 120
 TGGTGGCAGG CTATATTTCA GGTGCTTGGG TTACGCAACT TATAACAGTA TTTAATGTCA 180
 TTAAAGACGG TATGTTAGCA TACTTAGCTA TTTTCACTGG TATTAATGCG GCTAAAGAAT 240
 TTGGTGGCAG ACCAGGACTT GGTGGCGTGA TTGGTGGTAC AACGTTATTA ACGGGTATTG 300
 CTGGTAAAAA TATTTTAATG AATGTCTTCA CTGGAGAACC ATTGCAACCT GGACAAnGTG 360
 GGATTATTGG CGTTATTTTG CCGTTTGGAA TTTAAGTAAT 400

(2) INFORMATION FOR SEQ ID NO: 3660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3660:

CTGAGCTAAT GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GAACCCCCAA CCTACTGATT 60
 ACAAGTCAGT TGCTCTACCA ATTGAGCTAG GCCGGCAATA TGTAAGAATA AATGGTGGAG 120
 AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 180
 AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTCGGACT 240
 ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT 300
 GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AAAC TAGATA GTAAGTAAAA 360
 GTGATTTTGT TTTGCAAAA CATTTATTTT GGATTAAGTC 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3661:

```

10  TGATGTTTGA TTAGCTCATA AATACTAAAT AATGTTTGTA ACTTATAGTT ACGTTTTTTG      60
    GAATTAACGT TGACATATTG TCATTCAGTT TTCAATGTTT ATTTTCTTA CCGACAAGAA      120
    TTAATTATAC ATTTTATTAA CATTTAAGTC AATAACTTTT TTTATCTTGT CCATTTTATT      180
15  TTTTAACCAA AATTGATTA AAAAAGTCC TGGCAACGTT CTACTCTAGC GGAACGTAAG      240
    TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA      300
    CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA      360
20  AGTAAAAGTG ATTTTGChTC GCAAACATTT ATTTTGATTA      400
  
```

(2) INFORMATION FOR SEQ ID NO: 3662:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3662:

```

    CGCTCAACGT CTGCCTTCGT AATGGCTTTT GTAGAAATTC TAACTAAATA ATTTCGAATG      60
35  CTATCATTGA TTGTTTCAAC AGCTTGATGC TTTTGTCAA GCTTTTGTAT CAATTTTTTA      120
    TCGTCTTTTG TAATTTGCGG AATGTCTTCA AACATTGATA AGACAATCTG ACCCACATTT      180
    TGTAATTCTT TTTGAGTTTC TTGTAATGCA ACACCAGGTG CGTGATAAAC AAGATCTTTG      240
40  TTTAAGTGCT GAGGTTTATA GTCATCAGCA ATATCTTTAC CTGGGACAAG CTTTGTAACA      300
    ATCCATGCTA AACCTGCTAC AAATGGTAAT TGAATCAAAG TATTTGTTAT GTTGAAGATA      360
    CCATGTGATA CTGCAATCGT CATCGCTGGT TTTAAGTGCC ATAAATCTTG TAACAAACTA      420
    ATCAAATGAA TCACAACTGG CAAGAAAATT GTGAAGATAA TTACCCCGAT TAAGTTAAAG      480
    ATGACGTGTA CAAGCGCCGC ACGTTTTGCA GCGATTGAGC CGGCTAAACT AGCTAAGATA      540
50  GCTGTAATCG TGGTACCAAT GTTATCGCCT AGTAACACAG GGAkGCTGC GTTTAAGCTA      600
    ATTAAATCTT GTTGATAAAA TTCTTGTAAG ATACCAATCG TCGCACTTGA ACTTTGAACT      660
  
```

AGCATTAAAT TGGCTTnAAA TC

742

(2) INFORMATION FOR SEQ ID NO: 3663:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3663:

ATGAATTCAA GCTTATTTAA AACTCTTTAT TCACTCGGTT TTGCTTGGTA AAATCTATAT	60
TTTACTTACT TATCTAGTTT TCAATGTACA ATTTCTTTTT AGTCAAGCGC TCGCATACTG	120
CTTTATTTTC AAAAAATCAA ATGCTCATTT ACAAAGTAA ACTCCGCTTT AATTTTCTT	180
AATGCATTGT CTAACAACCG CTTTCTTTAA AAAGAATAGA TTGTCAAGCG CTCGCATAAG	240
CAATATCACT TTAACCAAAA AATATTTGAA TGTTAAATAA ACATTCAAAA CTGAATACAA	300
TATGTCACGT nATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT TAGAAAGGAG	360
GTGATCCAGC CGCACCTTCC GATACGGGCT ACCTnGTnAC	400

(2) INFORMATION FOR SEQ ID NO: 3664:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 636 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3664:

AACTAATAGT TCACTTTTAC TTTTTTCTTT TTCATTATTA TCCATTATTT TTTCACCGCC	60
AAAACGAATT TCATGATGTT AATTTAAATG TTCTATGACA AAATTAAGCA ACGATGTTtT	120
ATATTTATTT CCAACTATGT CTAGATTAAA TTTCTAAAAA TAKACATCAT TTAAAAGGAG	180
CTTGGGACAT AAATCAATGT CCTAGGGTCT ATAATATTAT AAtGCTAGTA GTTGACTGAA	240
TGAAAATGCG CTTGCAACAA GCTTTTTTCA ACTCTAGTCA GGGGCCCCAA CACAGAGAAT	300
TTCGAAAAGA AATTCTACAG GCAATGCGAG TTGGGGGTGTG GGCCCCAACA CAGAGAATTT	360
CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGTGGG CCCCACACA GAGAATTTCG	420
AAAAGAAATt CTACAGGCAA TGCGAGTTGG GGTGTGGGCC CCAACATAGA GAAATGGaTT	480
CCCAaTTTCT ACAGACAATG CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC	540

TACAATAATG nGCAAGTTGG CGGGGnCCCC AACACA

636

(2) INFORMATION FOR SEQ ID NO: 3665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3665:

TATCATTTC	TGTTGCTAAA	ACAACAGCAT	GTATGCCATT	CATAACACCT	TTATTATGTG	60
TTGCTGCACG	ATGAATATCT	ACTTGGGCCA	ATACAGAAGC	ACGTTCCATT	CGTTTGGCAA	120
CCTCTTCTCC	AGTTCTCTCG	CCCCTTGCTA	AATCTTTAAC	ATCAATTTTCG	CCTTGAACCT	180
TAACAACGGA	CGCTGTTGCA	TGATTGGATA	AAATACTCAT	TAAAATGTCG	CTTTGGGAAA	240
CTCATTTTTT	AAAAATGCAG	TTATGGCCTC	TAAAATCGTA	TTAAGCATAT	TAGCGCCCAT	300
AGCATCTTTC	GTATCAACAA	ATACTTTTAA	AGATAGTAAC	TGtTGtTCAG	GrAATGTakC	360
matCGCTATA	CGtTGGTAAc	CACCACCACG	CGCTTTAATA	GGAA		404

(2) INFORMATION FOR SEQ ID NO: 3666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3666:

GTGGTTCAG	TAGCAATTAT	TGAACGATAT	TAGGCTATCT	AGTCGGCATA	TTTGTA AAAC	60
AAGATCCAAT	TAAATATCAA	CAGGAATAAC	GAATAATATA	AAAGAGGTTG	GGACATAAAT	120
CCCTAAAAAA	ACAGCAGTAA	GATAATTTTC	AATTAGAAAA	TATCTTACTG	CTGTTCTCTA	180
TTTATACAAT	ACTTCGTATT	GAATGGCTTC	GCTTTCCTAG	GGTGCCGTCT	CAGCCTCGGT	240
CTTCGACTGG	CACTGCTCCC	TCAGGAGTCT	CGCCATTAAT	ACTACGTATT	AACGTGTAAT	300
TTTACTTTGA	AATACTTTAA	AAAAATAAGA	CACTTTGCCC	AACTTGCACA	TAAATGTAAA	360
ATTCAATAAA	ATAAATTCT	GTGTTGGATC	CCTnCGTATA			400

(2) INFORMATION FOR SEQ ID NO: 3667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3667:

	CCAACAAATC TGTCTGTGCG ATCGCCTTTG TCGTTCCAAA TAAATATGTA CAAACGAATC	60
10	CACCAGCATA CGCnCCAAGT AATCCTGCAA TATAACCTAA ATACATATTA TCTGAGATTA	120
	ATGGTAATAG TGACACACCA CTTGGGCCCTA TTGCTTTGGC ACCAATATGT CCAATTCCAC	180
	CTATTACAGC GCCACCAATA CCACCACCAA TACAAGCAGT TAAGAAAGGT CGACCTAATG	240
15	GCAAAGTCAC ACCATAGATT AATGGTTCTC CGATACCTAG GGAAACCAAC TGGCAATGCA	300
	CCTTTTAAAG TATTACGTAA TGTGTGTGTG CGGTTTACAT CTTACCCAAA GTGCTAATGC	360
20	GGGCACCTAC TTGGTCCCAG CACCAGCCAT CGCTGCAATT	400

(2) INFORMATION FOR SEQ ID NO: 3668:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3668:

	ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG CTATGTATTC ACATATCGAT	60
	AACATGACAT AACTCATGAC TGGGTTTCCC CATTCGGAAA TCTCTGGATC AAAGCTTACT	120
35	TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG	180
	CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA AACGCGTTAT	240
40	TAATCTTGTG AGTGTTCCTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT	300
	AAAACCTCTT ATTCACTCGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT	360
	TTTCAATGTA CAATTTCTTT TTAGTCAAGC GCTCGCATAA	400

45

(2) INFORMATION FOR SEQ ID NO: 3669:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3669:

GAGCGCTACT TACTGGnAGG CGCTGGTGGG ATACTACCCT AGCTGTGTTG GCTTTCTAAC 120
 CCGCACCCT TATCGTGGTG GGAGACAGTG TCAGGCGGGC AGTTTGACTG GGGCGGTCGC 180
 5 CTCCTAAAAG GTAACGGAGG CGCTCAAAGG TTCCCTCAGA ATGGTTGGAA ATCATTGATA 240
 GAGTGTAAG GCATAAGGGA GCTTGACTGC GAGACCTACA AGTCGAGCA GGTGAAAGA 300
 10 CGGACTTAGT GATCCGGTGG TTCCGCATGG AAGGGCCATC GCTCAACGGA TAAAAGCTAC 360
 CCCGGGGGAT AACAGGCTTA TCTCCCCCAA GAGTTCACAT 400

(2) INFORMATION FOR SEQ ID NO: 3670:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3670:

ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATCTTTC 60
 25 TTTGTGTTTG CTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTTG CGGTCTCAAT 120
 GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGC 180
 30 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTGCGC ATGGGAACAG GTGTGACCTC 240
 CTTGCTATAG TCACCAGACA TATGAATGTA AATTATACAT TCAAACTAG ATAGTAAGTA 300
 AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAACT CTTCCGATCG ATTAGTATTC 360
 35 CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCCGAACCT 400

(2) INFORMATION FOR SEQ ID NO: 3671:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3671:

CACCCGAAGA TATTGCTCAG ACAAAGTCAT CATATACAGG AAAGTATTTA AAAGAAGTAC 60
 50 TTGAACGAGA TAAACAAAAT ACTGAAGATA AATAAGATTA AAAGAAGTGA AGGATGTTAT 120
 AAATTTATCC TTCGCTTCTT TTTATTAATT TAGTAATGAA TAGTAGAAAG AAAAGATGCG 180
 TAAAAAGAAT TATGTTAAGA TAGGGTCAAT CTAGAGTAGT TAAACATAAA TCGAACTGGG 240

TTAGCCACAG CTATTGTGTA CTAAAAATA GGAATGCATG AGTGCACCnA nAGGnAGAAT 360
 ACTAATTTCC AAAGAAAAAG TATTCCTTAT GTTGGGGCCC 400

(2) INFORMATION FOR SEQ ID NO: 3672:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3672:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAG ATTCCATTCTG AGAAAGAACG 60
 TAAATTTAAT cCTGATTTAG CmCCaGGGAC aGAAAAAGTA mCmAGaGAAG GACaAAAAGG 120
 TGAGAAGACA ATaACGACAC CAACACTAAA AAATCCATTA ACTGGAGTAA TTATTAGTAA 180
 AGGTGAACCA AAAGAAGAAA TCACAAAAGA TCCGATTAAT GAATTAACAG AATACGGACC 240
 AGAAACGATA ACACCAGGTC ATCGAGACGA ATTTGATCCG AAGTTACCAA CAGGAGAGAA 300
 AGAAGAAGTT CCAGGTAAAC CAGGAATTAA GAATCCAGAA ACAGGAGACG TaGTTAGACC 360
 ACCGGTCGAT AGCGTAACAA AATATGGACC TGTAAGGA GACTCGATTG TAGAAAAAGA 420
 AGAGATTCCA TTCAAAACGT AAATTTAATC CGGATTTAGC A 461

(2) INFORMATION FOR SEQ ID NO: 3673:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3673:

CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCATCTG GTTTTGCTTG GTAAATCTA 60
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA 120
 ACCGCTGACC TCCTGCGTGC AAAGCAGGCG CTCTCCAGC TGAGCTAAGC CCCCAAAAG 180
 GTATTAAATT AATGGGGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG 240
 TGCGCTCTAA CCAGCTGAGC TATAGGCCCA TTAATTTGAA TGAACAAACA TTCAAACTG 300
 AATACAATAT GTCACGTTAT TCCGCATCTT CnGAAGAAGA TGTTCGAAT ATATCCTTAG 360
 AAAGGAGGTG ATCCAGCCGC ACCTTCCGAn ACGGCTACCT 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3674:

ACATGAAGAC TTAATTGAAG AATTATTAGG TATGGAAATT GAAGATGAGA TGGATAAAAA	60
GGAAAAAGAA AAACCTTCTC AACAGCAAAT TCAATTTCAA CAACGGAAAA ATCGCAACGT	120
ATCTATATAA GGAGCGAACA GCTATGTGGG AATAAGAATC GACTTACTCA AATGTTAAGT	180
ATTGAATATC CAATTATACA AGCAGGTATG GCAGGAAGTA CGACACCGAA ATTAGTTGCA	240
TCAGTAAGTA AACAGTGGTG GGTAGGCAC AATAGGCGCG GTTACTTTAA TACGCGCCAA	300
TTGGAGATG GAGATGATT ATGTACGCCA TTAACGTCAA ATCTTTTGG CGTAAATGTC	360
TTTGTACCAA GTCAACAATC ATATACCAGT AGTCCAAAT	400

(2) INFORMATION FOR SEQ ID NO: 3675:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3675:

AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA ACCGCCGACC	60
CTCTGCTTGT AAGGCAGATG CTCTCCAGC TGAGCTAATT CTCCGATTTA AAACCTGCCTG	120
GCAACGTTCT ACTCTAGCGG AACGTAAGTT CGACTACCAT CGACGCTAAG GAGCTTAACT	180
TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG	240
TAATTTATAC ATTCAAAAT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA	300
TTTGTATTAA GTCCTCGTCG TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT	360
CGGACCTATT AACCTCATCA ACCTTGAGGG ATCTTATAAA	400

(2) INFORMATION FOR SEQ ID NO: 3676:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3676:

5 TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG ACATGTGGAG 60
 CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCCAAAGACG GGTGAGAATC CCGTCCACCG 120
 ATTGACTAAG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC CTAAGCTGAG 180
 10 GCCGACAGCG TAGGCGATGG ATAACAGTTG ATATTCCTGT ACCACCTATA ATCGTTTTAA 240
 TCGATGGGGG GACGCATAGG ATAnGCGAAn GTGCGATTGG ATTGCACGTC TAAGCAGTAA 300
 GGCTGAGTAT TAGGCAAATC CGGTACTCGT TAAGGCTGAG CTGTGATnGG GAGAAGACAT 360
 15 TGAGTCTTCG AGTCGTTGAT TTCACACTGC CGAGAAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3677:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3677:

AAAGCGCCAC ATGGTGCCAA GTCTGGAGTT AATCCAGCAA TTGCTTGTTT TAAGCTATTA 60
 30 TATTTTCTT CTACTTTTGT TTTTCTGCG GCAATTTGTT GGTGAGTCGC ATCACCATTG 120
 TTAATAACAT TTTGTGCATT TGTGATTCT GTTTGACCCG CACGTTTAGC ATTTTCATAT 180
 GCTTGGATTG ATGATTGTGT CATACCATCA GTAGTTACTG ATTTATTGAT TTCTTCATCA 240
 35 AGTTTCGTCT TAGCAGTTTT TAAAGCACTA TTATCAGCTA AAGGTACTAA TTGGATTAAAT 300
 TGCTTGCGTT AATCGCTCAT TGACACGATT TACATTTGTT AACGCAGATT GCACTTCTTG 360
 TACTGTTCTT AATGGGCTTT TGAATAATA GCATTAGCGC 400

40 (2) INFORMATION FOR SEQ ID NO: 3678:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 648 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3678:

ACAGTCAATT GntCTACCAA TTGAGCTAGG CCGGTTAAGA AATGGTTCCA GGACAGAGTC 60
 GAATGCCGAC ACATGGAGCT TCAATCCATT GCTCTAACCA ACTGAGCTAC TGAACCATAA 120

AGGCGTGTTA ACCGCTACAC TACGAGACCT ATAAAATATT GCGGGAGGCG GATTTGAACC 240
 ACCGTACTTC GGGTTATGAG CCCGACGAGC TACCGAACTG CTCCATCCCG CGATAATAAA 300
 5 AAATAATGGC GGAGGAAGAG GGATTCTGAAC CCCC GCGGCC CGTTAAGGCC tGTCGGTTTT 360
 CAAGACCGAT CCCTTCAGCC GGACTTGGGT ATTCTCCAT TATTATAGGT AAATCGCTAT 420
 10 TAATTATAAA ATTAAATGGC GGTCTCGACG GGAATCGAAC CCGCGATCTC tGCGTGACAG 480
 GCAGGCGTGT TAAyCGCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA 540
 ACCCCCGCGA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGGACTT 600
 15 GGGGTATTCC TCCAAAATTA TATGGGACCT TGCAGGACTC GAACCTGC 648

(2) INFORMATION FOR SEQ ID NO: 3679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3679:

CTGATCCCGT TGTGCTTCAC ACCCGATAGA TAGGGATTTA CAGATAAATT CAGGTCTCTT 60
 CCACGTCATA TTTGGACCCA TCGAAAATTC GGGTTCTCAA ATCATCGAAC ATAACAAAAG 120
 30 AAGCTAAGCA ACATGTAGGC CGTTGTCACT TAACTTCTTG TTTTCCGAT GACAGCTTCT 180
 ATTTAGAGAA TGTCATGATT ATTTTATATT CACTTCAATG TTATCAATAT TAGTGCCATC 240
 35 TATGACATCT GCCATGCGAT TTTCTTGTA TTTTGTGTC AATTCAAACG TGTACTTTCC 300
 ACCGTTTTTC ATTTTAATAA CAATTTTACC TGAACCAACG TTACCGTACA GATTATTTTT 360
 TTCAATAAGT TGTTTTCTCA ATTTAAAATC AAGTTCTTTC 400

(2) INFORMATION FOR SEQ ID NO: 3680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3680:

TCAATGCGGC TCATCGCATT CATTTCTTGT CTAGCAACGT TCTACTCTAG CGGAAnTAAG 60
 TTAGCTACCA TCCTCGCTAA GAACCTTTCT TGACTTGTA CAATCGCTTG CTTCTTTCCT 120

TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240
 TTGACGTTTT AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA 300
 CTCTAGCGGA AGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC TTGTGACAAT 360
 CGCTTGGCTT CTnTCCTCTC CTTTCGGnTCT CGGCTTACTC 400

(2) INFORMATION FOR SEQ ID NO: 3681:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3681:

TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 60
 TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT TTGTGTTTAC 120
 TTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTCA CGGTCTCAAC TTGCCTGGCA 180
 ACGTTCTACT CTAGCGGAAC GTAAGTTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT 240
 TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT 300
 AAACGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 360
 TTTTCTTTG TGGTTTACTT TTTATTTTGA CGGTTTAGGC 400

(2) INFORMATION FOR SEQ ID NO: 3682:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3682:

TTGAACATGT TGAATCTAAT GAAATTCCTG TTCGTCGTCT AGTTGAAGAG AACGGCGTTG 60
 AGCATGAAGG TGAATTAGAT CGCTATCCAT TAGCTAAATT TAAACGTTCA AACTCAGGTA 120
 CATGTTACAA CCAACGTCCA ATCGTTGCAG TTGGAGATGT TGTTGAGTAT AACGAGATTT 180
 TAGCAGATGG ACCATCTATG GAATTAGGAG AAATGGCATT AGGTAGAAAC GTATAGTTGG 240
 TTTTCATGACT TGGGACGGTT ACAACTATGA GGATGCCGTT ATCATGAGTG AAAGACTTGT 300
 GAAAGATGAC GTGTATACTT CTATTCATAT TGAAGAGTAT GAATCAGAAG CACGTGATAC 360

(2) INFORMATION FOR SEQ ID NO: 3683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3683:

```

TTGGAATTTT TCCGCTACCC TCAGTTCATC CGCTCACTTT TCAACGTAAG TCGGTTCCGGT      60
CCTCCATTCA GTGTTACCTG AACTTCAACC TGACCAAGGG TAGATCACCT GGTTCGGGT      120
CTACGACCAA ATACTAAACG CCCTATTCAG ACTCGCTTTC GCTACGGCTC CACATTTACT      180
GCTTAACCTT GCATCAAATC GTAACGCGC GGTTCATTCT ACAAAGGCA CGCCATCACC      240
CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCCTTC      300
CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGGTTTCA TATCGGTCAC TAnGAGAGTA      360
TTTAAGCCTT AnGAGATGGT CCTCCCAGAT TCCCGACGGG      400

```

(2) INFORMATION FOR SEQ ID NO: 3684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3684:

```

GATnTATGAT GAAAAACTAT CTGACTGCTG TTTCACTTTT TATAAGACTT CTGAATGTCT      60
TCACTTATAC TTCTAGTCAC AGATtnAAAT AATCAAAAGT GCACATTATT AAAATATCAA      120
TTTCACACTC AATGCGGCTC ATCGCATTCA TTCTTTGTCT AGCAACGTTT TACTCTAGCG      180
GAACGTAAGT TAGCTACCAT CCTCGCTAAG AACCTTTcTT GACTTgTGAC AATCGCTTGC      240
TTCTTTCTCT TCCTTCGGCT CTCGCTTACT CATTTAGCTC TACTAAACTC GTTGCGCTCT      300
TTTCTCGTTT CGTCAGATTc AAACGTTTTT ACTTCGCCAA GCCATTTTTTc TTTGTGTTTA      360
CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA CTTGCCTGGG      420
CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG TCGCTAAAGA CCTTTCTTGA      480
CTTGtGACAA TCGCTTGCTT CtnTCCTCTC CTTGCGCTCT CGGTACT      528

```

(2) INFORMATION FOR SEQ ID NO: 3685:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3685:

10 AAATTATGGT CGATTGCGAA TGATTTAAGA GGGAnCATGG ATGCGAGTGA ATTCCGTAAT 60
 TACATTTTAG GCTTGATTTT CTATCGCTTC TTATCTGAAA AAGCCGAACA AGAATATGCA 120
 GATGCCTTGT CAGGTGAAGA CATCACGTAT CAAGAAGCAT GGGCAGATGA AGAATATCGT 180
 15 GAAGACTTAA AAGCAGAATT AATTGATCAA GTCGGTTACT TCATTGAGCC ACAAGATTTA 240
 TTCAGTGCGA TGATTCTGTA AATTGAAACG CAAGATTTTCG ATATAGAGCA TCTAGCGACG 300
 GCGATTGCGA AAGTTGAAAC ATCTACATTA GGTGAnGAAA GTGAAAATGn CTTTATCGGG 360
 20 CTGTTTCAGCG ATATGGATTT GAGTTCAACG CGGCTAGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3686:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 403 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3686:

TTAAATTATT GGTCTATCGG TTCTTGGGGT GGCCATGGTA TCTGTTCACT CTTCGGTGGT 60
 35 GCAGTTGCGA CAACTATGGG TTGGAGATGG ATTTTCATCT TCTCAATTAT CGTTGCCGTA 120
 CTTTCAATGT TACTCATCAA AGGGACGCCT GAAACGAAAT CAGAAATTAC CAATACACAT 180
 AAATTTGACG TTGCAGGGCT AATTGTTCTA GTAGTTATGT TGCTAAGTTT AAACGTTGTC 240
 40 ATTACTAAAG GTGCAGCACT TGGTTACACA TCATTATGGT TCTTTGGTTT GATTGCAATC 300
 GTAATTGTAG CATTCTTTAT TTTCTTAAAT GTTGAGAAAA AAGTAGATAA TCCACTTATT 360
 GATTTTAAAT TATTgAAAAT AAACCATATA CAGGTGCAAC GGT 403

45

(2) INFORMATION FOR SEQ ID NO: 3687:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TATGAGCCCG ACGAGCTACC GAACTGCTCC ATCCCGCGAT AATAAAAAAT AATGGCGGAG 60
 GAAGAGGGAT TCGAACCCCC GCGGCCCGTT AAGGnCTGT CGGTTTTCAA GACCGATCCC 120
 5 TTCAGCCGGA CTGGGTATT CCTCCATTAT TATAGGTAAA TCGCTATTAA TTATAAAATT 180
 AAATGGCGGT CTCGACGGGA ATCGAACCCG CGATCTCCTG CGTGACAGGC AGGCGTGTTA 240
 ACCGCTACAC TACGAGACCA TTAGTAAAC GGAGGAAGAG GGATTCTGAAC CCCC GCGAGC 300
 10 CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC CGGACTTGGG TATTCCTCCA 360
 AAATTATATG GACCTTGCA GACTCGAACC TGCGACCGAA CGGTATGAGC CGTAGCnCTA 420
 ACCACTGGGC TAAAGTCCTA ATATAATTT 449

(2) INFORMATION FOR SEQ ID NO: 3688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3688:

AAAACGTCGT AATATGCAA TTGAAGGTGC CAAGGTTGTT ATTCAAGGTT TCnATAATGC 60
 CGGAAGTTTC TTAGCTAAAT TCTTATATGA TTTAGGTGCA AAAATTGTAG GTATCTCTGA 120
 30 TGCTTACGGT GCATTACAG ATCCAAATGG CTTAGATATA GATTATTTAT TAGACCGTCG 180
 AGATAGTTTT GGTACGGTAA CAAATTTATT TGAAGAAACA ATCTCAAATA AAGAATTGTT 240
 TGAATTAGAT TGTGACATT TAGTACCAGC GGCTATTTC AACC AAATTA CAGAAGACAA 300
 35 TGCACATGAT ATTAAAGCTA GTATCGTTGT TGAAGCTGCT AATGGACCTA CAACACCAGA 360
 AGCAACACGT ATTTTAACTG AACGTGGTAT ATTATTAGTT 400

(2) INFORMATION FOR SEQ ID NO: 3689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3689:

CACGCTTATC AGGCGTGGC TCTAACCAGC TGAGCTATAG GCCCATTAAT TTGAATGAAC 60
 AAACATTCAA AACTGAATAC AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTC 120

CGACTTCACC CCAATCATTT GTCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC 240
 CGGCTTCGGG TGTTACAAAC TCTCGTGGTG TGACGGGCGG TGTGTACAAG ACCCGGGAAC 300
 5 GTATTCACCG TAGCATGCTG ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT 360
 TGCAGACTAC AATCCGAACT GAGAACTT TATGGGGAA 400

(2) INFORMATION FOR SEQ ID NO: 3690:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 553 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3690:

Gcncggtttt aggcccattc ggttaccccc ntTCCATAAA TGGTGCCCGG CCAGAGGACT 60
 TGAACCCCCC AACTTACTGA TTACAAGTCA GTTGCTCTAC CAATTGAGCT AGGCCGGCTA 120
 AGAAATGGTT CAGGACAGAG TCGAACTGCC GACACATGGA GCTTCAATCC ATTGCTCTAC 180
 25 CAACTGAGCT ACTGAACCAT AATAAAATG TAATGATGGC GGTCTCGACG GGAATCGAAC 240
 CCGCGATCTC tGCGTGACAG GCAGGCGTGT TAACCGCTAC ACTACGAGAC CTATAAAATA 300
 TTGCGGGAGG CGGATTTGAA CCACCGaCtT CGGGTTATGA GCCCACGAG CTACCGAACT 360
 30 GCTCCATCCC GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTGAA CCCCCGCGGC 420
 CCGTTAAGGC CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 480
 ATTATTATAG GTAnATCGCT ATTAATTATA AnATTAAAAT GGCGGTCTCG ACGGGAATCG 540
 35 AACCCGCGGA TCT 553

(2) INFORMATION FOR SEQ ID NO: 3691:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3691:

TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 60
 50 GTTGGCTACC ATCGACGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 120
 TCTTCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT 180

TTTGACGTTT TAGACATAAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 300
 ATTTTTTGCC TGGCAACGTT CTA CTCTAGC GGAACGTAAG TTCGGACTAC CATCGACGCT 360
 5 AAGGGAGCTT AACTTTCTGT GTTCGGGCAT GGGGAACAGG 400

(2) INFORMATION FOR SEQ ID NO: 3692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3692:

TCGAATACTG TCATGAAGTA ATTTCTCTAT TCTACGACCA GAAAATACAG ATTGAGTATA 60
 20 TGCATATAAG ATGTTTTTTAA CATCATTTTT GGATGATAGG ATGTTGCACC ACGATGATGT 120
 CTGAATTCAT CGAATTCCTA TCAGGTATCG TTTCAACAAT TTCATTAAACA TATCGCGAAA 180
 TATCATTTTG AGAATTCTAA CGAATTTCTT ATTGGTAGTG TAAGTTGGGG TCATGTTATA 240
 25 ATTTTATAC ATAAGGCACC TCTTTAATTT AGTTTAGTAG TATTTATTAA ATTATACGAG 300
 GGACCCAACA CAGAAAATTC ATTTTATTGa ATTTTACATT TATGTGmCAA GTTGGGaAAA 360
 ATGTCTTATT TTTTCAAAGT ATTTAAAAGT AAAaTTACAT GTTAATACGT 410

(2) INFORMATION FOR SEQ ID NO: 3693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3693:

ACTTCATATA ATTTATGAAA TAAACCTGTC AATTTTGGAT TGATTATGCT TTGTGATTCT 60
 TTTTATTTCT GCGTAATAAC GCTAAACCTA AAATGCTAAA TAATCCGCCG AACACATGC 120
 45 CGTTGTTTGT TGATTCTTCT CCACCTGTTT CAGTAGTTCA GATTTCCTAG ATTGTGCTTT 180
 TTTAGTTGGT ACCACTGcTT TAACCTTTTC ATTGATTTCa ATAACAGGTG TTA CTACTTT 240
 ACCTTGTTCC ACTGGTTTAG AAGGTTTTTT AGGTTCTTCT TTAGCAGGTG GTaTTGGTTT 300
 50 ACCAGGTTCA GTTGGTACCT CTGGCGTTGG CGGTGTGGT GTTCCGGCT CGCTTGGTAC 360
 TTCTGGTGTC GGTGGTGTG GGTGTTnCC GGCTTCGCTT GGTACTTCTG GGTGTTCCGT 420

(2) INFORMATION FOR SEQ ID NO: 3694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3694:

GCATCGTTGC CTTGGTAAGC CGTTACCTTA CCAACTAGCT AATGCAGCGG GAGTCCATCT 60
 ATAAGTGACA GCAAGACCGT CTTTCACTTT TGAACCATGC GGTTCAAATn ATTATCCGGT 120
 ATTAGCTACG GTTCCCCGAA GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC 180
 ACCCGTCCGC CGCTAACATC AGAGAAGCAA GCTTCTCGTC CCGTTCGCTC GACTTGCATG 240
 TATTAGGCAC GCCGCCAGGT TCCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG 300
 ATGTTTGATT AGCTCATAAA TACTAAATAA TGTTTGTAAC TTATAGTTAC GTTTTTTGGG 360
 AATTAACGTT GGACATATTG TCATTCCAGT TTTCAATGTT 400

(2) INFORMATION FOR SEQ ID NO: 3695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3695:

ACCTAATATA TAGACAGGTT CATCACTTAA TGACTTTGCA AGTTCGGCAA TGTCTGTGTC 60
 GTCGCGTTTG ACACGATAAT CACTGTCAGG GTTTGAAGCG GAATCAGGGA GTGGTTCAGT 120
 TAACTCGCTT TCTCCATAAT CACGACGATC AACGGCTACA ACAGTAAAAT GGTCTTTTAA 180
 CTGTTCTGCA AGAGGCAGAA AAATGTCTCC GGTACCGTTT GCACCAGGAA TAAAGATGAG 240
 CACGGGTCCT TGTCCGACTT GGTGGTATCG TAATTTAGCG CCTTGTAATT CTAAAGTTTC 300
 CATATTCAAT GACCTCCATT TGTTAATTGT TAGGTGATAA ACCTAATAAT TTAGCACCAT 360
 TTGGTATAAC TTAATTTCTn CTTTTCCTTC ATCnGGTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3696:

5 TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG 60
 CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT 120
 CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 180
 10 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 240
 CATTTTTATA AGTCAAACGC TCACATACGG CTTCGTTTTT ATTATTTTAA ATGCTCATTT 300
 ACATAAGTAA ACTCTGCTTT AAAATAATTT AACTCATTGT CTGCTAAACG TTTTCTTTTA 360
 15 TAAAAAGATT TAAACGCGTT GATTAA_nCTG TGAGTGTCTT 400

(2) INFORMATION FOR SEQ ID NO: 3697:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3697:

CACTTTAACC AAAAAATATT TGAATGTAA ATAAACATTC AAAACTGAAT ACAATATGTC 60
 30 ACGTTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 120
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 180
 TTGCACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 240
 35 TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA 300
 TTACTA_nCGA TTCCA_nCTTC ATGTAGTCGA GTTGCAGACT ACAATCCGAA CTGAGAACAA 360
 CTTTATGGGA TTGCTTGAC CTCGCGGTTT CGCT_nCCCTT 400

40 (2) INFORMATION FOR SEQ ID NO: 3698:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3698:

AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60

55

CCCCATTCCG AAATCTCTGG ATCAAAGCTT ACTTACAGCT CCCCAAAGCA TATCGTCGTT 180
 AGTAACGTCC TTCATCGGCT TCTAGTGCCA AGGCATCCAC CGTGCGCCCT TAATAACTTA 240
 5 ATCTATGTTT CCATCCTACA GGAAACGCGT TATTAATCTT GTGAGTGTTT TTTCGAACAC 300
 TAGCGATTAT TTCTTATGAA TTCAAGCTTA TTTAAAACTC TTTATTCACT CGGTTGTGCT 360
 TGGnAAAATC TATATTTTAC TTACTTATCT AGGTTTCAAT 400

(2) INFORMATION FOR SEQ ID NO: 3699:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3699:

TTTATGGCAT ACACGCATCA TAATACAGCC CAACACCACT AATGGTGCAG TTGCAAATCC 60
 AAATTCCTCC GCTCCAAGCG CACATGCGTA CGCTACATCT TTACCAGTTA ATAACTTACC 120
 25 GTCTGTTTCT AACTTAACAC GACTTCTTAA GTCATTTAGT TTTAATGTTT GATGTGTTTC 180
 TGCTAAACCA ATCTCCCAAG GAACACCGGC ATGCTGAATA CTCGTTTTGG GTGAAGCCCC 240
 TGTAnCACCA TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCCAAGA 300
 30 TGCAATGGTA CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT 360
 CGCATTTTTT AAATCATGTA TCAGTTGCGC TAAATCTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3700:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3700:

CGACGTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGT TCGGCATGGG AACAGGTGTG 60
 ACCTCCTTTG CTATAGTCAC CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG 120
 TAAGTAAAAG TnATTTTGCT TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG 180
 50 TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT 240
 TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTCnG GGGGGGCTTC ATGCTTAGAT 300

GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA

400

(2) INFORMATION FOR SEQ ID NO: 3701:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3701:

15 AACCAAGCCC AATAATGGAC TGGCCGCCTA ATAATAAAG CTCTAAAAGT TGTATTTTAA 60
 AAATAGTTCT TTAAATTATA TACCCACCAC ATTTGGTGGG GAACCTAAAA AAAAGCACTT 120
 CCCAAAAATG GAAAGTGCAA GTAGTGAGCC ATAGAGGATT CGAACCTCTG ACCCTCTGAT 180
 20 TAAAAGTCAG ATGCTCTACC AACTGAGCTA ATGGCTCTAA TGGCTGGGCT AGCTGGATTC 240
 GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA 300
 TAGATGGTGG AGGGGGGCGAG ATTCGAACCTG CCGAACCCGA AGAGCGGnTT TACAGTCCGC 360
 25 CGCGTTTAGC CAnTTCGnTA CCCCTCCAGn TTATTCATAT 400

(2) INFORMATION FOR SEQ ID NO: 3702:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3702:

TTTAAGTCCT GTGCGTCTGC CAGTTCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA 60
 CGGGATTGCA ACCCGCGACC CCAACCTTGG CAAGGTGTT ATTCTACCGC TGAACACTT 120
 40 CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA AGgTTAGaTC CTAAGTCTAG 180
 TGCGTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG 240
 45 ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGGCTCT TCCATGGTGC 300
 CGGCCAGAGG ACTTGGAACC CCCAACCTAC TGGATTACAA GTCAGTTGGC TCTACCAATT 360
 GAnGCTAAGG CCGGCAATAT GTTAAGnATn AATGGTGGAG 400

50 (2) INFORMATION FOR SEQ ID NO: 3703:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3703:

	CAACTAATAA ATAGTGGCGG TGGAGGGGAT CGAACCCCCG ACCTCACGGG TATGAACCGT	60
10	ACGCTCTAGC CAGCTGAGCT ACACCGCCTT ATATAGTTTG TAAATAATAT GGTGGAACT	120
	AGCGGGATCG AACCGCTGAC CTCCTGCGTG CAAAGCAGgC GCTCTCCCAG CTGAGCTAAG	180
	CCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCG AACCTGCGAC CCCTTGGTCC	240
15	CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGCGC CCGATAGGAG	300
	TCGAACCCAT AAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG CTAACGGGCG	360
	CATATGTTTT TAATTGAAAT GGTGCCCGAG GACCGGAATG	400

20

(2) INFORMATION FOR SEQ ID NO: 3704:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3704:

30

	CTAACGCCTA CGCGTTACAT GAAAAACGGA GAACAAGCAG AACAATTATT ACGTCAGCTT	60
	ATAGAAAAAG ATGAAGCACT AGCTAAGTAT GTCATGGTTT GTGATGAAAC AGCTTGGTGG	120
35	TCATATATGG GTCAAGATAA TGATATTTTC AAAGATCAAT TAGGTCATCT AACTGTTTCT	180
	CTAAGAAAGT ATCCCGAAGT GCTAGCCAAA AATGATACGC AACAGCTAGT GTCAATGGCA	240
	GCACTCGCGG CAAATGATCG CACTTTATAT CAAATGATTT GTGGAAAAGA TAATATTTCT	300
40	AAAAATGATG TCATGACGTT ATTTGAAGAT ATCGCGCAAG TCTTTTAAA GGTAACACTA	360
	TCATTTATGC AATACGGCGC ATTACCCAGA GTTGCATGGT	400

(2) INFORMATION FOR SEQ ID NO: 3705:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3705:

55

TGACGGGGAC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT TCGAAGCAAC GCGAaGaACC 120
 TTACCAAATC TTGaCATCCT TTGaCAACTC TAGaGATAGA GCTTTCCCCT TCGGGGGTAC 180
 5 AAAGTGACAG GTGGTGCATG GTTGTCTGTC GCTCGTGTCTG TGAGATGTTG GGTAAAGTCC 240
 CGCAACGAGC GCAACCCTTA AGCTTAGTTG CCATCATTAA GTTGGGCACT CTAAGTTGAC 300
 10 TGCCGGTGAC AAACCGGAGG AAGGTGGGGA TGACGTCAA TCATCATGCC CCTTATGATT 360
 TGGGgCTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGT GAGTCAAGCA 420
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGACTAC ATGAAGCT 478

(2) INFORMATION FOR SEQ ID NO: 3706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3706:

25 ATCTTAAGTC TTTGGTGAAC CGTTTTGTAG AATTAAATAA TATTACAGAG CCGCTAGCAG 60
 TAACGATCCA AACGAATTTA CCACCATCAC GTGGATTAGG ATCGAGTGCA GCTGTCGCGA 120
 30 TTGCTTTTGT TCGTGCAAGT TATGATTTT TAGGGAAATC ATTAACGAAA GAAGAACTCA 180
 TTGAAAAGGC TAATTGGGCA GAGCAAATTG CACATGGTAA ACCAAGTGGT ATTGATACGC 240
 AAACGATTGT ATCAGGCAAA CCAGTTTGGT TCCAAAAAGG TCATGCTGAA ACGTTGAAAn 300
 35 CTCAAAGTTT AGACGGCTAT ATGTTTGTTA TAGAnACTGG TGTGAAAGGT TCACCAAGAC 360
 AAGCAGTAGA AGATGTTCCA TAAACTTTGG TGAGGACCCT 400

(2) INFORMATION FOR SEQ ID NO: 3707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3707:

50 GTCGAACTGC CGACACATGG AGCTTCAATC CATTGCTCTA CCAACTGAGC TACTGAACCA 60
 TAATAAAAAT GTAATnnTGG CGGTCTCGAC GGGAAATCGAA CCCGCGATCT CCTGCGTGAC 120
 AGGCAGGCGT GTTAACCGCT ACACTACGAG ACCTATAAAA TATTGCGGGA GGCGGATTTG 180

TAAAAAATAA TGGCGGAGGA AGAGGGATTC GAACCCCGC GGCCCGTTAA GGCCCTGTCG 300
 GTTTTCAAGA CCGATCCCTT CAGCCGGA CT TGGGTATTCC TCCATTATTA TAGGTAAATC 360
 5 GCTATTAATT ATAAAATTAA ATGGCGGTCT CGACGGGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3708:

GTTCGCCCCAT TAAAGCGGTA CCAGCTGGG TTCAGAACGT CGTGAGCAG TTCGGTCCCT 60
 20 ATCnGGGGTG GCGTAGGAA ATTTGAGAGG AGCTGTCCTT AGTACGAGAG GACCGGGATG 120
 GACATACCTC TGGTGTACCA GTTGTCTGTC CAACGGCATA GCTGGGTAGC TATGTGTGGA 180
 CGGGATAAGT GCTGAAACAT CTAAGCATGA AGCCCCCTC AAGATGAGAT TTCCCAACTT 240
 25 CGGTTATAAG ATCCCTCAAA GATGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC 300
 ATGTGGAGCT GACGAATACT AATCGATCGA AGACTTAATC AAAATAAATG TTTTGCGAAC 360
 30 AAAATCCACT TTTACTTACT ATCTAGTTTT GAATGTATAA 400

(2) INFORMATION FOR SEQ ID NO: 3709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3709:

AATTTTATGG GCCCTTTATG GACTTTATAT TmCCTAAAAT ACTATTAAGA AGTCCTGAAA 60
 AATTCACATT AGCAGTTGGA TTGTTCAACT TTATTAATGA TAAGTATGCA AATAATTTCA 120
 45 CAGTGTTTGC AGCAGGGGCA ATTATGATTG CAGTACCTAT AGCAATCGTA TTCTTGTTCT 180
 TGCAACGCTA TTTAGTATCA GGTTTAACAA CAGGTGCGAC AAAAGGTTAG TTTGAAATT 240
 50 GGAGTGGGCC AGAATTGATA AAGAACCACT AATGACGATA AAGATTAAAA GGAGGACGTT 300
 ATGATGACGA TTAAAGTTGG AATCATTGGG TGTGGTGGTA TTGCGAATGG CAAGCACATG 360
 CCAAGTTTAC AAAAAGTTGA AAATGTTGAA ATGATCGCAT TTGTGACGTG GACTTTCGAA 420

(2) INFORMATION FOR SEQ ID NO: 3710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3710:

```

AGTGCTCTAC CAAGCTGAGC TACTTCCCGT ATAATTAACG CGCCCGATAG GAGTCGAACC      60
CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT      120
TTATTGAAAA TGGTGCCGAG GACCCGAATC GAACCGGTAC GTGATCACTC ACCGCAGgAT      180
TTTAAGTCCT GTGCGTCTGC CAGTTCGGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA      240
CGGGATTCTGA ACCCGCGACC CCAACCTTGG CAAGGTGTa TTCTACCGCT GAACTACTTC      300
TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GcTkAGaTCC TgAAGTCTAG      360
TGCGTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG      420
ACCCTCTGGA TTGAAAAGTh CAGATGCTCT GACCAACTGG AGCTAATGGC TCTTCCCATG      480
GTGGCCGGCC AGAAGGACTT GGAACCCCCA ACCTGATGGA TTTACAATTC AGTTGGCTCT      540
AACCAATTTG AGCTAAGGC                                         559
  
```

(2) INFORMATION FOR SEQ ID NO: 3711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3711:

```

AACCTTTTAG GAGCTAGCCG TCGAAGGTGG GACAAATGAT TGGGGTGAAG TCGTAACAAG      60
GTAGCCGTAT CGGAAGGTGC GGCTGGATCA CCTCCTTTCT AAGGATATAT TCGGAACATC      120
TTCTTCAGAA GATGCGGAAT AACGTGACAT ATTGTATTCA GTTTTGAATG TTTGTTTCATT      180
CAAATTAATG GGCCTATAGC TCAGCTGGTT AGAGCGCACG CCTGATAAGC GTGAGGTCGG      240
TGGTTCGAGT CCACTTAGGC CCACCATTA TTTAATACCT ATTTGGGGGC TTAGCTCAGC      300
TGGGAGAGCG CCTGCTTTGC ACGCAGGAGG TCAGCGGTTG GATCCCCTA GTCTCCACCA      360
TTATTGTGAC ATTTGAAAAC TAGATAAGTA AGTAAAATAT                                         400
  
```

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3712:

TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG 60
 CGAnnTCATG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GCCTGAAACC nnGTGATCTA 120
 CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTGA 180
 AAAGTGAGCG GATGAACTGA GGGTAGCGGA GAAATTCCTAA TCGAACCTGG AAATAGCTGG 240
 TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGG ATTATTGGAG GTAGAGCACT 300
 GTTTGGACGA GGGGCCCCCTC TCGGGTTACC GAATTCAGAC AACTCCGAA TGCCAATTTA 360
 ATTAACTTG GGGAGTCAGA ACATTGGGTG ATAAGGTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3713:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3713:

TTTTTAAGTC TGATGTGAAA GCCCACGGCT CAACCGTGAA GGGTCATTGG AACTGGAAA 60
 ACTTGAGTGC AGAAGAGGAA AGTGGAATTC CATGTGTAGC GGTGAAATGC GCAGAGATAT 120
 GGAGGAACAC CAGTGGCGAA GGCGACTTTC TGGTCTGTAA CTGACGCTGA TGTGCGAAAC 180
 GTGGGGATCA nACAGGATTA GATACCCGGT AGTCCACGCC GTAAACGATG AGTGCTAAAG 240
 TGTTAGGGGG TTCCGCCCCC TTAGTGCTGC AGTAAACGCA TTAAGCACT CCGnCTGGGG 300
 AGTACGnCCG CAAGTTGGAA ACTTCAAAGG AATTGACGGG GGACCCGCAC AAGCGTTGGG 360
 AGCATGTGGT TTAATTTTCA AGCAACGGAG AGGAACCTGA 400

(2) INFORMATION FOR SEQ ID NO: 3714:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3714:

5 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60
 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAACGTAAnT CGACTACCAT 120
 CGACGCTAAG GAGCTTAACT TCTGTGTTCT GCATGGGAAC AGGTGTGACC TCCTTGCTAT 180
 10 AGTCACCAGA CATATGAATG TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT 240
 TTTGCTTCGC AAAACATTTA TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC 300
 cAtGTCACCA TGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAGG GATCTTATAA 360
 15 CCGAAGTTGG GAAATCTCAT CTGAGGGGG GCTTCATGTC TTAGCATTTC AGTCACTTAT 420
 GCCCG 425

(2) INFORMATION FOR SEQ ID NO: 3715:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3715:

30 GTCCCTGCTG TTCCTATCAT ATAAATGATA GATTCAAATA GATTGTAGG TTTGTCATGC 60
 CCAGTTACAA GTTGC GTTAT CGTAGACACT AACATTAATA TGACTGGTAA TGTGCTGTT 120
 AATAAACTCA TACCAAATCC TGGCATCTCT TGATCCGTAA ATTCTTTTTG TGCACCTAAC 180
 35 GCTGAAATAT CGCCTTCTCG TGTATACGCA GACGGAATCA TTTTTGTGC ACTTTGTTAA 240
 ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATAACA GTAATACATC 300
 TCCAACATTT GCCTTTAATT CTTTTCGAG ACTACCGGTC CTGGGATGTG GTGGTAAAAA 360
 40 GCCATGTGTC ACTGATAAAG CTGTTACCAT AnGTAGTCCT 400

(2) INFORMATION FOR SEQ ID NO: 3716:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3716:

55 TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCATCGG TTTTGCTTGG TAAAATCTAT 60

GCAATATCAC TTTAACCAAA AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA 180
 ATATGTCACA TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA 240
 5 GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG 300
 TCCACCTTC GACGGCTAGC TCCTAAAAGG TTAATCCACC GGTTCGGGT GTTACAAACT 360
 10 GTTCGTGGTG TGACGGGGCG GTGTGTTACA AGACCCGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3717:

AAAGGACGAC ATTAGACGAA TCATCTGGAA AGATAATTCA AAGAAGGTAA TAATCCTGTA 60
 GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGGTACGAC GGAGCACGTG AAATTCGGTC 120
 25 GGAATCTGGG AGGACCATCT CCTAAGGCTA AATACTCTCT AGTGACCGAT AGTGAACCAG 180
 TACCGTGAGG AAAGGTGAAA AGCACCCCGG AAGAGATTGA AATAGAACCT GAAACCGTGT 240
 30 GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTGTAG AATGAACCGG 300
 CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA GCCGTAGCAn AAnnTGTTC 360
 GAATAGGGCG TTTAGTATTT TGGTCGTAGC CCGAGAACCA 400

(2) INFORMATION FOR SEQ ID NO: 3718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3718:

TAATTCATCT GCAGCATCTG GTTGATTTAA GCTTTCACGT AAACACATCG CTAAAGATAG 60
 AATCATTCCA AATGGATTGG CAACGTTTTT ACCTGCAATA TCTGGTGCTG ATCCATGAAT 120
 50 AGGCTCATAA AATCTTGGAC CATCGTTACT AAAACTAGCA GAAGGTGATA AACCAAGTGA 180
 ACCAGGAATC ACTGAAGCTT CATCACTTAA AATATCGCCA AATAAGTTTT CACATACGAT 240
 GACGTCAAAT TGTTTTGGnA TTTGTGATTA AATGCATACT ACAAGCATCA ACAAATAAGT 300

TTTACTAGAA GCTAATACAT TTCCTTATCA ACGGATGThA

400

(2) INFORMATION FOR SEQ ID NO: 3719:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3719:

15	ATTTAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAANTA AGTnGAGCTA CCATCGACGC	60
	TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC	120
	CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT	180
20	TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT	240
	CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA	300
	GTTGGGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT	360
25	CCACACATAG CTACCCAGCT AGCCGTTGGC ACGACAAngG	400

(2) INFORMATION FOR SEQ ID NO: 3720:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3720:

	CGTTACACCT TCCAATAAAT TTGCTGTTGC TGGATAAGGA GAAATATTGA TATATTGTCT	60
40	TAAATTACTA TAATGCCAAT TTAAGTCTGG ATGATTTGTT AAGACACCAA TAGGATTATC	120
	TTTTATAACC ACTTCACCCT CTTTAAATGA AACTTCGACT GTATGTCCAG TTGCATCGGA	180
	AACATGATAA TGCAATGGCG GAACTTCACC GATGTCATTT AAATATACAG CTACAACATG	240
45	TATTTGGGAT GCTTGTTGTT TCATATCTTC AATGCTTGTT GTATATCCCA AAATCCATGT	300
	CACAATTTCA TTTTGCGTAA TATTCATCGC GTCCGCTTTG TGTGTTGGAT CCATATGGAA	360
50	CTATAACCTC GGGAAATATT GTGGTTGAAA TGGGCACGCC	400

(2) INFORMATION FOR SEQ ID NO: 3721:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3721:

	AGTCAGTTTA TAGCGATTGC TGGACTGACA GTACTTGTGC CATTATTGCC AATTTATATG	60
10	GCATCACTAC AAAATCTATC AGTCGTAGAA ATACAGTTGT nGAGTGGTAT AGCGATTGCT	120
	GCTCCAGCTG TAACGACGAT GATAGCTTCG CCGATATGGG GGAAGCTAGG TGATAAGATC	180
	AGCCGAAAT GGATGGTGT T AAGAGCGTTA CTTGGTTTGG CGGTATGCTT ATTTTAAATG	240
15	GCATTGTGTA CGACACCATT ACAGTTTGTA CTTGTGGAGG TTATTGCAGG GACTATTTGG	300
	TGGTGTGTGTT GATGCATCAA GTGCGTTTGC GAGTGCAGAA GGCGCCACTG AnAGATCGTG	360
	GGAAAGGTAT TAGGAAGACT GCAAATTnCA GTTCACGCGCA	400

20

(2) INFORMATION FOR SEQ ID NO: 3722:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3722:

	TCTAAAAGTT GAACTACTCC CGCATAAACC TGGAGGCGGC AACCGGATTT GAACCGGTGA	60
	TAAAGGTTTT GCAGACCTCT GCCTTACCAC TTGGCTATGC CGCCAATAAC TGGGCTAGCT	120
35	GGATTGGAAC CAACGAGTGA CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAT	180
	TAATAATAAG GCGGGCTGAA GGGGATCGAA CCCTCGAATG TCGGAACCAC AATCCGATGT	240
	GTTAACCACT TCACCACAGC CGCCATGGCA GGGGCAGTAG GAATCGAACC CACACCAAAG	300
40	GTTTTGGAGA CCTCTATTCT ACCnTTGAAC TATGCCCCTA TTAAAATGAT AAATGGAGGG	360
	GGGCAGATTC GAACTGCCGA ACCCGAGGGG CGGATTTTAC	400

45

(2) INFORMATION FOR SEQ ID NO: 3723:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3723:

55

GGTTCAAGTC CTCTGGCCGG CACCATTtTtT GGAGGGGTAG CGAATGGCTA AACGCGGCGG 120
 ACTGTAAATC CGCTCCTTCG GGTTCGGCAG TTCGAATCTG CCCCCCTCCA TTTATTATTT 180
 5 TTAATAGGGG CATAGTTCAA CGGTAGAATA GAGGTCTCCA AAACCTTTGG TGTGGGTTTCG 240
 ATTCTACTG CCCCTGCCAT GCGGGCTGTG GTGAAGTGGT TAACACATCG GATTGTGGTT 300
 10 CCGACATTCG AGGGTTTCGAT CCCCTTCAGC CGCCTTATTA TTAATGGGCT ATAGCCAAGC 360
 GGTAAGGCAA CGGACTTTGA CTCCGTCACT CGTTGGTTTCG 400

(2) INFORMATION FOR SEQ ID NO: 3724:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3724:

25 CACTTTAGCA AATGGTGACA AAGTCCGTAT TGCTACAATT TTTGACTTAA TGGCAAGTCA 60
 ATATGGCGTG CGTCGTTTTG ATCATAAATT AGAATCAAAA GGATACGACG ATGCAGAATC 120
 AAAATATACA CCTGCTTGCG AAGAAGCCAT TTCAGGCGTA AAACAAAGTG TTnGTCATTC 180
 30 AAGTAGCGAA AGAATTTGCG CAAAACGCTA TCGATACTGA AGGGCGTTCA ATGATTATCA 240
 TGGGTGCGGG TATTAAACCAT TGGTTTAACT CAGATACGAT TTATCGTTCC AATCTTAAAC 300
 TTAGTTATGT TATGTGGCTG TCAGGTGTGA ATGGTGGCGG TTGGGGCTCA CTATGTGGGG 360
 35 ACAAGAAAAA TGTCGTCCGA TTGAAGGATG GAGTACTGTC 400

(2) INFORMATION FOR SEQ ID NO: 3725:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3725:

45 CGCTATCTGA ATCTGAATCG CTATCTGAAT CTGAGTCGTT GTCTGAGTCC GAATCGCTAT 60
 50 CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTATCTGA ATCTGAGTCG CTGTCTGAAT 120
 CTGAATCACT GTCTGAGTCT GAGTCGCTGT CTGAGTCTGA ATCGCTGTCA GAATCTGAGT 180
 CGCTATCTGA GTCTGAATCT GAATCACTGT CTGAGTCCGA ATCGCTATCT GAATCTGAAT 240

CCGAGTCTGA ATCGCTGTCT GAGTCTGAGT CGCTGTCTGA ATCTGAATCG CTATCTGAGT 360
 CTGAGTCGCT GTckGAATgC GCTGTCTGAA TCTGAGTCGC TATGCTGAAT GCTGAGTnCG 420
 5 CTATGTGAGT CTGAATGCCG TGTGCAGAAT CTGAGTGCCG TCATCTGATG TTTCTT 476

(2) INFORMATION FOR SEQ ID NO: 3726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3726:

ATACGACCAC TGTTTAATGC GTCCATTAAA TCTGGCCAAT TATTGAATTT AACTAATTCT 60
 20 AGTTTATATT TCGGATGATT GTATTGTGAT AATAATTTTT TAGTCATCAT CAAATTAGCT 120
 GAATGTGTAA TCGGCAAATA TCCAATTTTA ATCACTTGCT GATTTTGGGC ATTTTLAGAC 180
 CGTTCITTAG ACGTCCTTTG CCAATCACAT CCTGTAATTA TAAAGATTCC AATGATGACG 240
 25 ATTATGCTTA ACCTTTTCAT CGTCACTCAC TCCTTATAAA TAATATTCAG GTTCAACTTG 300
 ATGATGATTC AATGCAAnGT TTCCATAATT TCATTACGAA TCTTAAGTAG GTGGCTATCA 360
 30 TTACGGACTG CGTGGATGTG AnGCTGTAAA TTCCATAnTG 400

(2) INFORMATION FOR SEQ ID NO: 3727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3727:

ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 60
 ATGGGCGAAC AGCAAACCTT TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC 120
 45 GAGGTGCCAA ACCTCCCCGT CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG 180
 GGTAGCTTTT ATCCGTTGAG CGATGGCCCT TCCATGCCGA ACCACCGGAT CACTAAGTCC 240
 50 GTCTTTCGAC CCTGCTCGAC TTGTAGGTCT CGCAGTCAAG CTCCCTTATG CCTTTACACT 300
 CTATGAATGA TTTCCAACCA TTCTGAGGGA ACTTTGAGCG CCTCCGTTnC CTTTTAGGAG 360
 GCGAACGGCC CCAGTTCAAA CTGCCCCCCT GAACACTGTC 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3728:

TTGAAAAGTC ATATCAAAGC GCACATGTTT TTAAGCGTCG TCGAACACCT ATCGTGAAAG	60
GTGTGTCATT TGAGTGTCCA ATCGGTGCGA CGATTGCGAT TATCGGAGAA AGTGGTAGCG	120
GTAATCGAC GTTGAGTCTA TTGATATTAG GTATTGAGAA ACCGGATAAA GGTGTGTGTA	180
CCTTAAATGA TCAACCGATG CATAAGAAGA AAGTGAGACG TCATCAAATT GGTGCTGTAT	240
TTCAAGATTA TACGTCATCA TTACATCCAT TTCAGACTGT TAGAGAAATC TTATTTGAAG	300
TGATGTGTCA ATGTGATGGA CAACCTAAAG AAGTTATGGA AGTCCAAGCA ATTACATTGT	360
TGGAAGAAGT CGGTCTATCT AAGGCATACA TGGGATAAAT	400

(2) INFORMATION FOR SEQ ID NO: 3729:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3729:

ATCGAACCCC CGACCTCAGC GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC	60
TTATATAGTT TGTAATAAT ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG	120
TGCAAAAGC CGCTCTCCA GCTGAGCTAA GCCCCATAA TAATTACAGT ATATCGGGAA	180
GACAGGTTTC AACCTGCGAC CCCTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC	240
TTCCCGTATA ATTAACGCGC CCGATAGGAG TCGAACCCAT AACCTCTTGA TCCGTAGTCA	300
AACGCTCTAT CCAATTGAGC TACGGGCGCA TATGTTTTTA TTGAAAATGG TGCCGAGGAC	360
CGGAATCGAA CCnGTAGTGA ATCACTCACC GCAGATTTTA	400

(2) INFORMATION FOR SEQ ID NO: 3730:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3730:

5 ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT 60
 CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACTTAAT CTATGTTTCC 120
 ACCATTTTAA TAAGTCAAAC GTTAACATGA AGTTACGTTT TTTTATAAAA AGATTTAAAC 180
 10 GCGTTATTAA TCTTGTGAGT GTTCTTTTCGA ACACTAGCGA TTATTTCTTA TGAATTCAAG 240
 CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT TTACTTACTT 300
 ATCTAGTTT CAATGTACAA ATAATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT 360
 15 GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC 400

(2) INFORMATION FOR SEQ ID NO: 3731:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 401 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3731:

25 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 60
 30 TGGAGAATGA CGGGTTCGAA CCGCCGACCC TCTGCTTGTA AGGCAGATGC TCTCCCAGCT 120
 GAGCTAATTC TCCGATTTAA AACTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC 180
 GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTTCGG CATGGGAACA GGTGTGACCT 240
 35 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA TTCAAACTA GATAGTAAGT 300
 AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAA GTCTTCGATC GATTAGTATT 360
 CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCGAACCTA T 401

(2) INFORMATION FOR SEQ ID NO: 3732:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3732:

50 CATTATTAAAC GGCTATGGTT TAACTGAAGC ACCTCTTGTA CTTGTTAATA CACCGGAAAA 60
 TTCAAAACGT AAGCCAATGA GTATTGGTAA AGCAGTCATG TTCGTTGATG CACGTATCCT 120

AAATGTCACG CCAGGATATT GGAATAAACC AGCAGAGACT GCCAAAGCAT TTCATGGTCG 240
 ATATTTATTA ACTGGTGA CT TAGCGAgATG GACAACGATG GCGATATATT TATTATTGAC 300
 5 CGCAAAaAAG AaTTAATCAT AACTGGTGGc GAAAATGTCT TACCATCCGa gTCGAAAtGC 360
 TTaCtGaGCA TCCACTAGTA GACCGGTGTG TGGTCGT 397

(2) INFORMATION FOR SEQ ID NO: 3733:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3733:

20 AAGTAACAAT CGTTCACCGT CGTGATGAGT TACGTGCACA GCGTATTTTA CAAGATAGAG 60
 CATTCAAAAA TGATAAAATC GACTTTATTT GGAGTCATAC TTTGAAATCA ATTAATGAAA 120
 AAGACGGCAA AGTGGGTTCT GTGACATTAA CGTCTACAAA AGATGGTTCA GAAGAAACAC 180
 25 ACGAGGCTGA TGGTGTATTC ATCTATATTG GTATGAAACC ATTAACAGCG CCATTTAAAG 240
 ACTTAGGTAT TACAAATGAT GTTGGTTATA TTGTAACAAA AGATGATATG ACAACATCAG 300
 TACCAGGTAT TTTTGCAGCA GgGATGTTT GCGACAAAGG TTACGCCAAA TTGTCACTGC 360
 30 CACGGCGATG GTAGTATGCC AGCGCAAGTG CCACGGAATG 400

(2) INFORMATION FOR SEQ ID NO: 3734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3734:

GCCGTTTACT GTGGCTTCGA TTCGTAGCTT CGCAGAAGCT AACCACCTCCT CTTAACCTTC 60
 45 CAGCACCGGG CAGGCGTCAG CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT 120
 TTGATAAACA GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGCGTTAA CCCTAAAGAG 180
 CACCCCTTCT CCCGAAGTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTGCTCTG 240
 50 CTCACCTTAG AATTCTCATC TTGACTACCT GTGTGGGTTT GCGGTACGGG CACCTATTTT 300
 CTATCTAGAG GCTTTTCTCG GCAGTGTGAA ATCAACGA cT CGAAGACACA ATGTCTTCTC 360

TAGACGTGCA ATCCAATCGG CAACGCTTCG CCTAATCCTA ACTGGCGGTC CCCCCCnAT 480

(2) INFORMATION FOR SEQ ID NO: 3735:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3735:

15	CGATCCCTTC AGCCGGACTT GGGTATTCTT CCAAATTAT ATGGACCTTG CAGACTCGAA	60
	CCTGCGACCG AACGGTTATG AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA	120
	TAATTTTACA ACTAATAAAT AGTGGCGGTG GAGGGGATCG AACCCCCGAC CTCACGGGTA	180
20	TGAACCGTAC GCTCTAGCCA GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG	240
	TGGAGACTAG CGGGATCGAA CCGCTGGACC TCCTGCGTGC AAACAGnCGC TCTCCAGCT	300
	GAGCTnAAGC CCCATAATA ATTACAGTAT ATCGGGAAGA CAGGATTCGA ACCTGCGACC	360
25	CCTTGGTCCC CAAACCAAGT GGTTTnACCA AGTTGAGCTA	400

(2) INFORMATION FOR SEQ ID NO: 3736:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3736:

	TGAGCCCGAC GAGCTACCGA ACTGCTCCAT CCGCGATAA TAAAAAATAA TGGCGGAGGA	60
40	AGAGGGATTG GAACCCCGCG GGCCCGTTAA GGCCCTGTCG GTTTTCAAGA CCGATCCCTT	120
	CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC GCTATTAAAT ATAAAAATTAA	180
	ATGGCGGTCT CGACGGGAAT CGAACCCGCG ATCTCCTGCG TGACAGGCAG GCGTGTTAAC	240
45	CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTGAACCC CCGCGAGCCG	300
	TTAAGCCCCCT GTCGGTTTTT AAGACCGATT CCTTCAGCCG GACTTGGGTA nTnTCCAAA	360
50	ATTATATGGA CCTTGCAGGA CTCGAACTGC GAnCGAACGG	400

(2) INFORMATION FOR SEQ ID NO: 3737:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3737:

	TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC	60
10	AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC	120
	CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT	180
	TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
15	TTTTAAGTCC TGTGCGTCTG CCAGTTCGCG CACCCCGGCA CTATAAAAAT GGAGCAGAAG	300
	ACGGGATTTC AACCOCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACACTTT	360
20	CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA	400

(2) INFORMATION FOR SEQ ID NO: 3738:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3738:

	AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG	60
	CTAATTCTCC GATTTAAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AATCGGAnCT	120
35	ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT	180
	GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AAAC TAGATA GTAAGTAAAA	240
	GTGATTTTGC TTCGCAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG	300
40	CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAAACC TCATCATCTT TGAGGGATCT	360
	TATAACCGAA GTTGGGAAAT CTCATCTTGG AGGGGGGCTT	400

45 (2) INFORMATION FOR SEQ ID NO: 3739:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3739:

55

CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA CCGACATCTT 120
 TAATTAATTG CTnTGCACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT GATGGGAATA 180
 5 TCATGTTATC TTCAATCGTT TCACCAAACA AGTCACTTTG CTGCATCAAA TAACTGATTC 240
 GTTGACGCAA TTCTTCCGGG TCATAATCAT TATAGGGTTT ACCTTTAAAA TAAAGTTCTC 300
 10 CACTAGTTGG ACTAAACAAA TTACATATnT GCTTTTGAAA TGTACTTTTA CCACTACCTG 360
 ATGGACCTAT AATGGCAATA CTCTCGCCTT TATCTACTTT 400

(2) INFORMATION FOR SEQ ID NO: 3740:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3740:

ATCGCTTGCT TCITTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG 60
 25 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT 120
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 TGCGGCTCAT CGCATCCaTT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA AnTAATTGGC 240
 30 TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT 300
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCGTTG CGCTCTTTTC TCGTTTCGTC 360
 35 AGATtCAAAC GTTTTCACTT CGCCAAGCCA tTTTTCtTTG TGTTTGCTTT TnA 413

(2) INFORMATION FOR SEQ ID NO: 3741:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3741:

CTTAGATGCT TTCAGCACTT ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC 60
 GACAACTGGT ACACCAGAGG TATGTCCATC CCGGTCCTCT CGTACTAAGG ACAGCTCCTC 120
 50 TCAAATTTC TACGCCCACG ACGGATAGGG ACCGAAGTGT CTCACGACGT TCTGAACCCA 180
 GCTCGCGTAC CGCTTTAATG GGCGAACAGC CCAACCCTTG GGACCGACTA CAGCCCCAGG 240

TAAGCTGTTA TCCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGCCCTTCC ATGCGGAACC 360
 ACCGGATCAn TAAGTCCGTC TnTCGACCCT GntGGACTTG 400

(2) INFORMATION FOR SEQ ID NO: 3742:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3742:

GTTTTGAATG TATAAATTAC ATTCATATGT CTGGTGACTA TAGCAAGGAG GTCACACCTG 60
 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT 120
 CGCTAGAGTA GAACGTTGCC AGGCAGTTTT AAATCGGAGA ATTAGCTCAG CTGGGGAGAG 180
 CATCTGCCCTT ACAAGCAGAG GGTCCGGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 240
 TACATATTGC CGGCCTAGCT CAATTGGTAG AGCAACTGGA CTTGTAATCA GTAGGTTGGG 300
 GGTTCAGTC CTCTGGCCGG CACCATGGGA AGAGCCATTA GCTCAGTTGG TAGAGCATCT 360
 GACTTTTAAA TCAGAGGGTT CAGAGGTTnC GAATCCGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3743:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3743:

TCGCAATAAC CGCATCAAAT GTATTGCCTA AAAAGGCTGG ATTTTCCAAT GTGTCATCAT 60
 TACGGATCTC GAAGTTCTCA TAACGCACAT CATGTAATAA CATATTCATG CGTGCTAAGT 120
 TGTATGTAGT ATTGTTACGT TCTTGTCCGA AATAACGATA CACTTGCGTT TCTTTACCAA 180
 CACGTAACAA CAATGAACCG GAACCACATG TTGGGTCGTA CACGTGACGT AATTTATCTT 240
 TACCGTCTGT GACAATCTTC GCCAGTATCT TAGATACTTG TTGTGGTGTA TAGAACTCGC 300
 CTGCTTTTTT ACCCGCTGTC GCCGCAAAGC GCCCGATTAG GAATTCATAT GCATCACCTA 360
 ACATATCAAT TTCCATGGTC ACTGTGAACG AATGGGTAAG 400

(2) INFORMATION FOR SEQ ID NO: 3744:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3744:

10 CTACTGATT CAAGTCAGTT GCTCTACCAA TTGAGCTAGG CCGGCAATAT GTAAGAATAA 60
 ATGGTGGAGA ATGACGGGTT CGAACC GCCG ACCCTCTGCT TGTAAGGCAG ATGCTCTCCC 120
 AGCTGAGCTA ATTCTCCGAT TTAAACTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 180
 15 GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG 240
 ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAA ACTAGATAGT 300
 AAGTAAAAGT GATTGCTTC GCAAAACATT ATTTGATTAA GTCCTCGATC GATAGTATCG 360
 20 TCAGCTCCAC ATGTCACCAT GCTTCCACT CGnACCTATT 400

(2) INFORMATION FOR SEQ ID NO: 3745:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3745:

CATAAGTAAA CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT 60
 35 AAAAAGATTT AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACACTA GCGATTATTT 120
 CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAAATCTA 180
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA 240
 40 CTGCTTTATT nTCAAAAAAT CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTC 300
 TTAATGCATT GTCTAACAAAC CGCTTGCTTT AAAAGAATA GATTGnCAAG CGCTCGCATA 360
 AGCAATATCA CTTnAACCAA AAAATA 386

45

(2) INFORMATION FOR SEQ ID NO: 3746:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 677 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AAGGTGAAAA GCACCCCGGA AGGATGTTGA AATAGAACCT GAAACCGTGT GCTTACAAGT 60
 AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG CGAGTTACGA 120
 5 TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAk AACanGGTCT GAATAGGGCG 180
 TTTAGTATTT GGTCGTACCG AnaACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG 240
 10 TAACACTGAA TGGAGGACCG AACCGACTTA CGTTGAAAAG TGAGCGGATG AACTGAGGGT 300
 AGCGGAGAAA TTCCAATCGA ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGc 360
 TAGCCTCAAG TGATGATTAT TGGAGGTAGA GCACTGTTTG GaCGAgGGGC CCCTCTCGGG 420
 15 tTACCAATTc AGACAACTC CGAATGCCAA TTAATTTAAC TTGGGgAGTC aGAACATGGG 480
 TGATAAGGTC CGTGTTTCGA AGGGAAACAG CCCAGACCAC CAGCTAAGGT CCCAAAATAT 540
 ATGTTAAGTG GAAAAGGATG TGGCGTTGCC AGACAACTGA GGATGTTGGC TTAGAAGCAG 600
 20 CCATCATTTT AAAGAGTGCG TAATAGCTCA CTAGTCGAAG TGACACTGCG CCGAAAATGT 660
 GACCGGGCnT AAACnAT 677

(2) INFORMATION FOR SEQ ID NO: 3747:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3747:

35 GTCCAATGAT TCATATGCTT TATTATCAGG GTATTGCCTT TGAATCGCAT GCACAAAATA 60
 TGATGCTCAT TCATGAAAAT GGTGGCCTA CACGTATTGC CTTAAAAGAT TTCCATGATG 120
 GTGTTGTTTT TAAGCGTGAc ATTTAAGTGA AGCTGCTTCA CACCTGACAT TAAAGCCAAT 180
 40 GCCAGAAGCA CATAAAAAAG TGAATAGTAA TTCATTTATT GAAACAGATG ACGAACGTTT 240
 AGTACGCGAC TTTTACATG ATGCAITTTT CTTTATTAAT ATCGCCGAAA TCATCTTATT 300
 45 TATTGAAAAG CAATATGGTA TCGATGAGGA GCTGCAATGG cAATGGGkTa AAGGCATCAT 360
 CGAGGCGTAT CCAGrAGcAT TTCCaGAGTT kGAATaACTA TCCAACCATT CGGTTTT 417

(2) INFORMATION FOR SEQ ID NO: 3748:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3748:

5 ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC CTGGCAACGT TCTACTCTAG 60
 CGGAACGTAA GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG 120
 AACAGGTGTG ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA 180
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAACAT TTATTTTGAT TAAGTCTTCG 240
 10 ATCGATTAGT ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT 300
 CATCATCTTT GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA 360
 15 TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 400

(2) INFORMATION FOR SEQ ID NO: 3749:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3749:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60
 30 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120
 GTTTTAGGCA TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT 180
 TGCCTGGCAA CGTCTACTC TAGCGGAAGT AAGTTGGGCT ACCATCGTCG CTAAAGACCT 240
 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATTT 300
 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 360
 35 3CCAAGCCAT TTTTCTTTG TGTTTACTTT TTAATTTTGA 400

(2) INFORMATION FOR SEQ ID NO: 3750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3750:

45 ATAAAAAAA GAGACCTTGC GGTCTCAAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC 60
 AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC 120

TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 240
 ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA GAGACCTTGC 300
 5 GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGGC AACGTTCTAC TCTAGCGGAA 360
 nTAAnTTGGG CTACCATCGA CGCTAAGAAC CTTTCTTGGA 400

(2) INFORMATION FOR SEQ ID NO: 3751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3751:

CACTCACCGC AGATnTTTAA GTCCTGTGCG TCTGCCAGTT CCGCCACCCC GGCACTATAA 60
 AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC CTTGGCAAGG TTGTATTCTA 120
 CCGCTGAACT ACTTCTGCAT ATGCGGGTGA AGGGAGTCGA ACCCCCACGC CGTAAGCTnA 180
 25 GnATTCTCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240
 GGATTCTGAAC CTCTGGACCC TCTGATTAAA AGTCAGATGC TCTACCAACT GGAGCTAATG 300
 GCTCTTTCCA TGGTGCCCGG CCAGAGGACT TGGAACCCCC AACCTACTGA TTACAAGTCA 360
 GTTGCTCTAA CCAATTGAGC TAAGCCGGGC AATATGTTAn 400

(2) INFORMATION FOR SEQ ID NO: 3752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3752:

TTAnAnAnCC GCGACATTAT AGAGCCAATC ACTAGCCTAT CTCAGAATCA CCAACGAATC 60
 CTTCAATTATT AAGGAATCTA GGCATCTTTA CGGCGTGGTT CTAATCGCAT CTTTTTCAAT 120
 CTAAGTGCGT TTGTGACAAC ACTTACTGAA CTTAGTGCCA TTGCAGCACC AGCAACCCAT 180
 50 GGCGCAAGTA AGCCCAATGC AGCTATAGGG ATACCGGCAA TATTATAGCC GAATGCCCAA 240
 AATAGATTTT GACGAATATT ACGAATGGTT GcTTTACTTG cATAAATGGC TTTAGGaATa 300
 AGCATCAAGT cGCCACCAAG AATAGTAATA TCAGCTGCTT CAATGGGCAA CTTCTGTTAC 360

(2) INFORMATION FOR SEQ ID NO: 3753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3753:

CCTTGCGGTC TCAATGGCGG CTCATCGCAT CCATTTTTTTG CCTGGCAACG TTCTACTCTA 60
 GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT 120
 TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 180
 TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT 240
 TTACTTTTTTA TTTTGACGTT TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC 300
 TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTGGCTACCA 360
 TCGACGCTAA GAACCTTTCT TGA CTGGTGA CAACGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 3754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3754:

CTGAGCTAAG CCCCCAAATA GGTATTAAAT TAATGGTGGG CCTAAGTGGA CTCGnACCAC 60
 CGACCTCACG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTAATTTGA 120
 ATGAnCAAAC ATTCAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG 180
 ATGTTCCGAA TATATCCTTA GAAAGGAnGT GATCCAGCCG CACCTTCCGA TACGGCTACC 240
 TTGTTACGAC TTCACCCCAA TCATTGTGCC CACCTTCGAC GGCTAGCTCC TAAAAGGTTA 300
 CTCCACCGGC TTCGGGTGTT ACAAACCTCTC GTGGTGTGAC GGGCGGTGTG TACAAAACCC 360
 GGGAACGTAT TCACCGTAGC A 381

(2) INFORMATION FOR SEQ ID NO: 3755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3755:

5 AGCTCCCCAA AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCAAGGCAT 60
 CCCC GTGCGC CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTAA 120
 CATGAAGTTA CGTTCCTTTA TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTCT 180
 10 TTCGAACATA GCGGATTATT TCTTATGAAT TCAAGCTTAT TTAAACTCT TTATTCATC 240
 GGTTTTGCTT GGTAAAAACn ATATTTTACT TACTTATCTA GTTTTCAATG TACAATTTCT 300
 TTTTAGTCAA GCGCTCGCAT ACTGCTTTAT TTTCCATAAG CAATAnCACT TTAACCAAAA 360
 15 AATATTTGGA ATGTTnAAAT AAACATnCAA AACTGAATAC 400

(2) INFORMATION FOR SEQ ID NO: 3756:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3756:

CTACTCACAC CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA 60
 30 CGCCCTTAGA ACGCTCTCCT ACCATTGTCC AAAGGCATGC GCACAGCTTC GGTAATATGT 120
 TTAGCCCCGG TACATTTTCG GCGCATGTCA CTCGACTAGT GAGCTATTAC GCACTCTTTA 180
 AATGGATGGC TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCCAC ATCCTTTTCC 240
 35 ACTTAACATA TATTTTGGGA CCTTAGCTGG TGGTCTGGGC TGTTTCCGGn GGGGnACACG 300
 GACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCCG ATTTGTCTGA 360
 40 ATCGGTAACC CGAGAGGGCC CnTCGTCCAA ACAGTGCTCT 400

(2) INFORMATION FOR SEQ ID NO: 3757:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3757:

50 GGCAGATGCT CTCCCAGCTG AGCTAATTCT CCGATTAAAA ACTGCCTGGC AACGTTCTAC 60

ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT 180
 TCAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAAGT 240
 5 CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT CGAACCTATT 300
 AACCTCATCA TCTTTGAGGG aTCTTATAAC CGAArTttGG GAAtCTCATC TTGAGGGGGG 360
 gCTCATGctT AGATGCTTcA GCACTTATCC CGTCCACACA TAGCTAnCCA GCTATGCCGT 420
 10 TnGCACGACA ACTGGTACAC CAGAnGTATG TCCATCCC 458

(2) INFORMATION FOR SEQ ID NO: 3758:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3758:

AGCGCTCGCA TACTGCTTTA TTTTCAAAAA ATCAAATGCT CATTTACAAA AGTAAACTCC 60
 25 GCTTTAATTT TTCTTAATGC ATTGTCTAAC AACCGCTTTC TTTAAAAAGA ATAGATTGTC 120
 AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAAATAT TTGAATGTTA AATAAACATT 180
 30 CAAAACTGAA TACAATATGT CACGTTATTC CGCATCTTCT GAAGAAGATG TTCCGAATAT 240
 ATCCTTAGAA AGGAGGTGAT CCAGCCGCAC CTTCCGATAC GGCTACCTTG TTACGACTTC 300
 ACCCCAATCA TTTGTCCAC CTTGACGGC TAGCTCCTAA AAGGTTACTC CACCGGCTTC 360
 35 GGGTGTTACA AACTCTCGTG GTGTGACGGG CGGTGTGTAC 400

(2) INFORMATION FOR SEQ ID NO: 3759:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3759:

GACTTGGGTA TTCCTCCAAA ATTATATGGA CTTGCAGGA CTCGAACCTG CGACCGAACG 60
 50 GTTATGAGCC GTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT TTTACAACCTA 120
 ATAAATAGTG GCGGTGGAGG GGATCGAACC CCCGACCTCA CGGGTATGAA CCGTACGCTC 180
 TAGCCAGCTG AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGA GACTAGCGGG 240

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC 360
 AAGTGCTCTA CCAAGCTGAA GCTACTTTCC CGTATAATTA 400

(2) INFORMATION FOR SEQ ID NO: 3760:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3760:

CACTTAATGC CCGTACCACA CATAGCTACC CAGCTATGCC GTTGGCACGA CAACTGGTAC 60
 ACCAGAGGTA TGTCCATCCC GGTCTCTCTG TACTAAGGAC AGCTCCTCTC AAATTTCTTA 120
 CGCCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTT TGAACCCAGC TCGCGTACCG 180
 CTTTAATGGG CGAACAGCAA nCCCTTGGGA CCGACTACAG CCCAGGATG CGATGAGCCG 240
 ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACCTTTG GGGGAGATAA GCCTGTTATC 300
 CCCGGGGTAG CTTTTATnCG TTGAGCGATG GnCCTTnCAT GCGGAACACC GGATCACTAA 360
 GTCCGTCTTT CGACCCCTGCT CGACTTGTAG GTCTCGCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3761:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 623 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3761:

TATGTATTTT ATAATGTACA GTCGTTGAn TcnTATTTTT CTTATATTA AGTGCCATTA 60
 ATACAAAACC TAGCTCTCGT TTAACCTTAT TTATTCCTCG AACTGACATT CGAGTGAACC 120
 CAAAATAGCC TTCATAAATC CAAAAACAGG CTCTACATCA ATTTTCTTT GACTATAGAT 180
 TTTTTTCGTT TCTGGTTCAG AAAGCTTTTG ATTAATTTGG ACTTTAAAGT ATTCCCAATT 240
 ATAATTCTTC ATGATTTTCT TATTGGATTT CGAATTTGGT TTCATGCATT GATGTCTCAA 300
 AGAACATGAT GAACAGTCAT CACATTCATA TAGTTTGAAG TCTCGTTTAA AACCATATCT 360
 ATCATTACGG TATGCATATC TTTTAAAACC TATTCTTTTG TTATTAGGAC ATATAAATTC 420
 ATCATTAAAGT TCGTCATATT TCCAATTTTA AGTGTTGAAA ATGTCACCTT TAACTTTCT 480

AATAGCCATA TAGTTTTGCT CACTACCATA ACCGGCATCA GCTACAAATA TACTCCGGTA 600
 AATAACCGAG GGATTGTTGG AAT 623

(2) INFORMATION FOR SEQ ID NO: 3762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 718 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3762:

ATTTTAAAA TAGTTCTTTA AATTATATAC CCACCACATT TGGTGGAGAA CCTAAAAAAA 60
 AGCACTTCCC AAAAATGGAA AGTGCAAGTA GTGAGCCATA GAGGATTCTGA ACCTCTGACC 120
 CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG GCTCTAATGG CTGGGCCTAG 180
 CTGGATTCTGA ACCAACGAGT GACGGAGTCA AAGTCCGTTG CCTTACCGCT TGGCTATAGC 240
 CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG GAGCGGATTT 300
 ACAGTCCGCC GCGTTTAGCC ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT 360
 CaAAATGGTG GaGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC 420
 TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTACCG 480
 CCGTGAAAGG GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT 540
 CGAACCTTAC GACCGATCGG TTTAACAGCC GATAGCTCTT ACCACTGGAG CTACTGTGGG 600
 ATTAATATTA TGCCTGGGCA ACGTTCTTAC TCTTAGCGGA ACGTTAAGTT CCGACTTACC 660
 ATCCGACGCT AAGGAGCTTT AACTTTCTnG TGTTCCGGC ATGGGGGGAA CAGGTGGT 718

(2) INFORMATION FOR SEQ ID NO: 3763:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3763:

TnCACTCACC GCAGATTTTT AAGTCCTGTG CGTCTGCCAG TTCCGCCACC CCGGCACTAT 60
 AAAAATGGAG CAGAAGACGG GATTCTGAACC CGCGACCCCA ACCTTGCAA GGTGTATTC 120
 TACCGCTGAA CTAATTCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCT 180

AGGATTTCGAA CCTCTGGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGGAGCTAAT 300
 GGCTCTTTCCA TGGTGCCGGC CAGAGGACTT GGAACCCCCA ACCTACTGGA TTTACAAGTT 360
 5 CAATTGCTCT AnCAATTTGA GCTAAGGCCG GGCAATATGT 400

(2) INFORMATION FOR SEQ ID NO: 3764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3764:

TTAAAGTATT CCCAATTATA ATTCTTCATG ATTTTCTTAT TGGATTTCGA ATTTGGTTTC 60
 20 ATGCATTGAT GTCTCAAAGA ACATGATGAA CAGTCATCAC ATTCATATAG TTTGAAGTCT 120
 CGTTTAAAAC CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA 180
 TTAGGACATA TAAATTCATT ATTAAGTTCG TCATATTTCC AATTTTGAGT GTTGAAAATG 240
 25 CCACTTTTAA ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT 300
 TTATTAAAAT CATCTATAAT AGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT 360
 ACAATATACT CTGGTAAATA ACCGAaGGaT TTTGAATCAT TGTTAAAAAT GGGATTAATG 420
 30 TTCTAGTATC TGTTGGGTTT TGAAATAGGT CATAGGATAA AACAAATTGr GAATTTGTCT 480
 CTATTTGgTA AATGGGTATC CTGGCTTAAG TTGGGCCATT TTTCCATATG GGCCTTCCTT 540
 35 CCATTCTCCA TAAAAGTTGG CATCATGGAT CCAGATCCnG TTTTAGGAAA ACCTAATTCC 600
 AACCTTTAAG 610

(2) INFORMATION FOR SEQ ID NO: 3765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3765:

CTTCTTGGTG CTGCATATCC CCTACAATAA TTAAACCTTT TTTCTTATTT AAAATGTGTC 60
 50 TTAATGCCGA TGCATCTATA CTTTTTTGAT AGTGCGGTAA AATCTTCATC TCAGAnGTTA 120
 ACAATTCTGT TGCATTCAAA TCAGGTGTTA ACGGATCTCT AAATGGCAAG TTAAAATGAA 180

CACAATGGTC TCTTTACTAT CATCCGCAAT AGGCATATCG AACTCATAnC TTACATAATT 300
 ATTAAACATA TTTACTTGAT TAATCGCTTG TGGTGC GCCT ACAnTTCTTA ATTCAGCGGA 360
 5 CGGTCACTTG TTAACCGGT TTAAGGTATT CTACTAATTh 400

(2) INFORMATION FOR SEQ ID NO: 3766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3766:

CnTTTAACCT TTTTAAGGAA TCCTGCTAAT GCGGGTTTTG GCATTTTCGA nTnTTTrGTA 60
 20 tCTCACGCAA tCTTGGTGGT CATTCAGTTC GTATATGGCA TCCATTAAAGA CGCGAAGATC 120
 AAATGGACTA TTGATGACTT CTGGAATACC ACGATCTATA TTTAGTAATT GATAAACAGC 180
 TTCCATGGCA GTACGAACCG AATATTCTGT TGTAATACA GTGTCTCGCT CTGTTTCTGC 240
 25 AAAGTTACCA ATAAATGCTA AGTTCTGAGA TTGATGCGGG ACGACTAAAG GTCTGTGCGCC 300
 GATAGCACGC GTCATGAAAT AAGATGTGAT ATATGGCATA TAAACAGGgA ATCGTATTAG 360
 30 ATGCATGTnT TGCTAAGTCT TCAATTTTGG TCAGTTGATA CACCTAAGTG GATACAGCCA 420
 TTCTTGGCAT ATTTCAATTAC CACTACATnC T 451

(2) INFORMATION FOR SEQ ID NO: 3767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3767:

ACACGTGAAC GTCTTCAAAT GGAAGTACGT GACGTTCACT ACTCTCACTA TGGCCGTATG 60
 45 TGTCCAATTG AACACCTGA GGGACCAAAC ATTGGATTGA TTAATCATT ATCAAGTTAT 120
 GCACGTGTAA ATGAATTCGG CTTTATTGAA ACACCATATC GTAAAGTTGA TTTAGATACA 180
 50 CATGCTATCA CTGATCAAAT TGACTATTTA ACAGCTGACG AAGAAGATAG CTATGTTGTA 240
 GCACAAGCAA ACTCTAAATT AGATGAAAAT GGTCGTTTCA TGGATGATGA AGTTGTATGT 300
 CGTTTCCGTG GTAACAATAC AGTTATGGCT AAAGAAAAAA TGGATTATAT GGATGTATCG 360

(2) INFORMATION FOR SEQ ID NO: 3768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3768:

CCTACGACCG ATCGGTTAAC AGCCGATAGC TCTACCACTG AGCTACTGTG GATTAATATT 60
 ATGCCTGGCA ACGTTCTACT CTAGCGGAAn TAAGTTCGTA CTACCATCGA CGCTAAGGAG 120
 CTTAACTTCT GTGTTCCGCA TGGGAACAGG TGTGACCTCC TTGCTATAGT CACCAGACAT 180
 ATGAATGTAA TTTATACATT CAAAAC TAGTAAGTAA AAGTGATTTT GCTTCGCAAA 240
 ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT CnGCTCCACA TGTCACCATG 300
 CTTCCACCTC GAACCTATTA ACCTCATCAT CTTTGAGGGA TCTTATAACC GAAGTTGGGG 360
 AAATCTCATC CTGnAGGGGG CTTCATGCTT AGATGCTTTC 400

(2) INFORMATION FOR SEQ ID NO: 3769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3769:

CTTGACCGAA GTTCTTACCT ACATCACCTA AATTAATGAC ATGTCCACCA GTCATATACT 60
 CTAATCCATG GTCGCCGATA CCTTCAACGA CAACATCTAC ACCACTATTT CTAATACAGA 120
 ATCTTTCTnC TGCACTACCG TTAATAAATG CCTTACCACT TGTCGCACCA TAGAATGAGA 180
 CGTTACCAGC AATAATTTCA TTTTGTGCGTT CTTCAAAGG TGCTTTGACA ATGACCGTAC 240
 CACCAGATAA TCCTTTACCA ACATAGTCAT TCGCATCTCC AGTATGATGA ATCATTAAGC 300
 CTTTCGGTGC ATATGCTGCA GGACTTTGGA CCAGCATGAC CATTTCGTATA AACATTAATT 360
 GTATTTTCAG GGAGGTCCTG CTTCTCCATA TTGTTTCGGA 400

(2) INFORMATION FOR SEQ ID NO: 3770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3770:

5 CATTACGTAA TTAAAAGATA GTCATTAAGA GAGGnTGATA ACCATGCAAG AAGCATACAT 60
 TGTAGCTTAT GGGCGTTCAG CGCAGCGAAA CAAAGCAAGG CGCATTATTC CACGAAAGAC 120
 CTGATGATGT CGCAGCCAAA GTATTACAAG GCGTATTGAA ACGTATTGAC GGAAAATTCA 180
 10 ATAAGAATAT GATTGAAGAT GTCATTGTTG GTACGGCTTT TCCAGAAGGA TTACAAGGCC 240
 AAAACATTGC ACGAACGATT GCATTGCGTG CGGGATTATC TGACACGGTA CCGGTCAAAC 300
 AGTGAATCG CTACTGCTCA TCCAGGnTTT ACAAACCATT CGCGATTGCA GGCCAATCAA 360
 15 ATTATGGCnG GTCCAAGGAG ATATACTTGT TAGCTGGTGG 400

(2) INFORMATION FOR SEQ ID NO: 3771:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3771:

ACTCTCTTGC AnTAAGGGCA GGAATGACC GATGGGATTA AAAGATCAAG CTGTTACCTG 60
 30 GGGAAAGGTAT TTTCATCAAT TTCCAGAACT ATCCGATAAA GAATTTAAGA CTACACAAAA 120
 AATTAAAGAT ATTTTAACAG AACATCATAT TAGAATATTA GACTTACCAC TTGCGACTGG 180
 GCTTGTTGCT GAAGTGGGAC AAGGTCTGAG TTGTATAGCT GTTCGGGCTG ACATTGATGC 240
 35 TTTACCGATT CAAGAGCTTG TTGAACAGGA TTTTAAATCT GAAAATGAAG GTGTTATGCA 300
 TCGTGTTGGT CATGATATTC ACATGGCTAG nATTTTGGCT ACAGCTGGTA AAATTTAAAG 360
 40 AGATTGAGGG CACTCTTACT GGGCGTGTTA AATCCATTG 400

(2) INFORMATION FOR SEQ ID NO: 3772:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3772:

50 TTTATTTTGA CGTTTTAGAC ATAAAAAAA GAGACCTTGC GGTCTCAATG CGGCTCATCG 60

GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG 180
 CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 240
 5 GTTTTCACCT CGCCAAGCCA TTTTCTTTG TGTGCTTTT TTATTTTGAC GTTTTAGACA 300
 TAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTT TGCCTGGGCA 360
 ACGTTCTACT CTAGCGGGAA CGGTAAGTTC GGACTTACCA 400

(2) INFORMATION FOR SEQ ID NO: 3773:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3773:

TTGATATTCC TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGGnATAGGC 60
 GACGTGCGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG TATTAGGCAA ATCCGGTACT 120
 25 CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT TCGAGTCGTT GATTTTCACAC 180
 TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCCGTAC CGCAAACCGA CACAGGTAGT 240
 CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA AGGAACTCGG CAAAATGACC 300
 30 CCGTAACTTC GGGAGAAGGG TGCTCTTTAA GGTTAACGCC CAGAAGAGCC GCATGGAATA 360
 GGCCCAACGA nGTTTATTCA AAAACACAGT CTCTGCTAAA 400

(2) INFORMATION FOR SEQ ID NO: 3774:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3774:

TACTTAGACA ATCGAAAGTG TACATTATTA AATTATCATT TCCAGTTCTA CTCTAGCGGA 60
 ACGTAAGTTG GCTACCATCC TCGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT 120
 CTTTCCTCTC CTTGCGCTCT CACTTACTCA TTTAGCTCTA CTAACTCGT TCGGTTCTTT 180
 50 TCTCGTTTCG TCAGATTCAA ACGTTTTTCAC TTCGCCAAGC CATTTTTCTT TGTGTTTGCT 240
 TTTTATTTTG ACGTTTTAGA CATAAAAAAA AGAGACCTTG CGGTCTCAAA TGCGGCTCAT 300

GACGCTAAGG AGCTTAACT TCTGTGTTTC GGCATGGGGA

400

(2) INFORMATION FOR SEQ ID NO: 3775:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3775:

CGGTTTATCA AGAATGGAAA GAGTTGTACG TGAAAGAATG TCAATTCAAG ATACTGAGTC	60
TATCACACCT CAACAATTAA TTAATATTCG ACCTGTTATT GCATCTATTA AAGAATTCTT	120
TGGTAGCTCT CAATTATCAC AATTCATGGA CCAAGCAAAC CCATTAGCTG AGTTAACGCA	180
TAAACGTCGT CTATCAGCAT TAGGACCTGG TGGTTTAACA CGTGAACGGC TCAAATGGAA	240
GTACGTGACG TTCACTACTC TCACTATGGC CGGTGTGTCC AATTGAAACA CCTGAGGGAC	300
CAACATTGG ATTGATTAA TCATTATCAG TTATGCACGT GTAAATGGAA TTCGGCTTTA	360
TTGAAACACC ATATCGTAAA AGTTGATTG GntACACAGC	400

(2) INFORMATION FOR SEQ ID NO: 3776:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3776:

AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG	60
TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA	120
GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA	180
CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT	240
AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACnTAG GCGATTATTT CTTATGGAAT	300
TCAAGCTTAT TTAAACTCT TTATTCACCT GGTTCCTTGCCT GGGTAAAATC TAnATTTTAC	360
TTACnTATCT AGGTTTTCAA TGTACAAATA ATGGTGGGGC	400

(2) INFORMATION FOR SEQ ID NO: 3777:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3777:

	AATTATAAAA TTAAATGGCG GTCTCGACGG GAATCGAACC CGCGATCTCC TGC GTGACAG	60
10	GCAGGCGTGT TAACnCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA	120
	ACCCCCGCGA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGACTTG	180
	GGTATTCCTC CAAAATTATA TGGACCTTGC AGGACTCGAA CCTGCGACCG AACGGTTATG	240
15	AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA TAATTTTACA ACTAATAAAT	300
	AGTGGCGGTG GAGGGGATCG AACCCCCGAC CTCACGGGTA TGAACCGTAC GCTCTAGCCA	360
	GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG	400

20

(2) INFORMATION FOR SEQ ID NO: 3778:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3778:

	CAAATCCTGC ACCATCAGAA AGTGGGGCAG ATGTTCTGTC AGTCATAGTG CCGTCAGCTT	60
	TAAATACTGT ACGTAATTTG GCTAATGCCT CCATCGTGGT GTCAGGGCGT ATAAATTCAT	120
35	CTTGGTCAAA GATATTTGTG TGTACTTTTG GTCCTGCGTT TGTATATTCA ACTGAGTTTA	180
	CTTGTATTGG AATAATTTCA TCTTTGAACC GACCATCACG TTGTGCGTCA TAGGCACGTT	240
	GaTGACTTCT GACAGCATAA GCATCTTGaT CTTCGCGTGA TACGTCAAAT TGGGATGCTA	300
40	CATTTTtCAG CAGTTAAACC CATAGGATAT GACGCACCTA TATCATCaA TTGTAAGGTT	360
	GGATTGTTTG TGGGCTTCGT TnGCCACnn TTGGTACGGC	400

45

(2) INFORMATION FOR SEQ ID NO: 3779:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3779:

55

CAATCTAAAT CGTTCAAATT TGGCACAACG ACAAATAAGG CTTCAACACG AATATATTCT 120
 CTCGGTTGAA ACCTTACTTA TTCATTTATT TTTTATAAAT TAGTGACATA AACTGTATT 180
 5 AGCATCTGCA CGATCGGTTG AAATATATGT TACATTTTCT TGCTGCTTAA TAAATGCATC 240
 ATAGTAATCA TATTGCGACG AATGATATGT GCCATTTCAT GTATCATTTG GGTTTAGCAA 300
 ACAGCCATAA CCTTCGTCAT ATAAATGTTT ACnGAGCATA AGGGGCGTCA TGTTTTAGAA 360
 10 CCACCTTACC TACATAAAAT TnGCCTCCAT AGGGATCATA 400

(2) INFORMATION FOR SEQ ID NO: 3780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3780:

ATGGnCGGTC TCGACGGGAA TCGCAACCCG CGATCTCCTG CGTGCACACn CAGGCGTGTT 60
 25 AACCGCTACA CTACGAGACC ATTAGTAAAA CGGAGGAAGA GGGATTTCGAA CCCCCGCGAG 120
 CCGTTAAGCC CCTGTGGTTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 180
 AAAATTATAT GGACCTTGCA GGA CTGCGACCGA ACGGTTATGA GCCGTTAGCT 240
 30 CTAACCAACT GAGCTAAAGG TCCTAAATAT AATTTTACAA CTAATAAATA GTGGCGGTGG 300
 AGGGGATCGA ACCCCCGACC TCACGGGTAT GAACCGTACG CTCTAGCCAG CTGAGCTACA 360
 35 CCGCCTTATA TAGTTTGTAATAAATATGGT GGAGACTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3781:

AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC CGCCTGATTC 60
 TCTAGCACGT TCATAAATAG TTA CTGATA TCCTAGTAGA TTAAGTTCTT CAGCAGCAGC 120
 50 TAATCCTGCT GGACCGCTTC CAACGATTGC CACTTTTTC TCTCTACGGC GACTCGGAAC 180
 TTTGCGCGCT ACCCAACCAT TTTCAAAGC TTCATCAATA ATTGTGCGTT CAATACCTTT 240

TACACGCCCT GTAAAGTCAG GAAAGTTATT TGTTCGCTT AAGCGTCATA AGCAGTTTTA 360

AAATCTTGAT GATACACCAA GTCGTCCanT CAGGATGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3782:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3782:

ACATGATGCG TGTGGTATTG GTTTTTATGC GAATATGGAT AATAAAAGGT CTCACGACAT 60

CATTGATAAA TCGCTTGAAA TGTTCGACG CTTAGATCAC AGGGGCGGGG TCGGCGCAGA 120

TGGCATCACT GGTGATGGCG CAGGTATTAT GACTGAAATA CCTTTTGCAT TTTTCAAACA 180

ACATGTAACG GACTTTGATA TCCCAGGTGA AGGTGAATAT GCCGTGGGGT TATTTTTTTC 240

CAAAGAACGC ATTTTAGGTT CTGAACATGA AGTAGTTTTT AAAAAATATT TTGGAAGGCG 300

AnGGGTTATC AATTCTTGGT TAACGTAATG TACCAGTTAA TAAAGATGC CATTGCCTAA 360

ACCATGTAGC AGATACGATG GCCAGTCATT CCACCAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3783:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3783:

AATCGGGTGA TGTGGACGA TGATACGCAG GGAACGTTGC GTTATTCGTA TATGAAATAT 60

TGGATAACTG TTTAACAAT GATGGTAGAG ATATTTTCATC ATTTGTAACA TCGTCAATTT 120

TGATATTGTG ATGATTTAAC ATAACGACAT CATCGATATT GAATTGGTAT GAAAAACCTG 180

CTGTTGCTGA ATCTGTTAAT TTGGCTCCAA TATTTAAAT TAAATCGCTG TTGTCCACAT 240

AATCTCGTAT TTTATCTTCG GCAATTTTCC CATCGTAAAT ACCCATATAA TATGGATTTT 300

CCTCATTAAG AGCACCTTTT CCTAATGAAA GTTGTGCTAC TGGGTATCTG TGTTTGanTT 360

ACAAAATCTT CnaAGTCCTG GATGGAGGTG AAAACTGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3784:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3784:

10 GGTAATAAGA TGTTTCAGTT CTCCGGGTGT GCCTTCTGAT ATGCTATGTA TTCACATATC 60
 GATAACATGA CATAACTCAT GCTGGGTTTC CCCATTCGGA AATCTCTGGA TCAAAGCTTA 120
 CTTACAGCTC CCCAAAGCAT ATCGTCGTGA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180
 15 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAA 240
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 300
 TTTAAAATAA TTTAACTCAT TGTCTGCAAA ACGTTTTCTT TTATAAAAAG AATTTAAACG 360
 20 CGTTAATGAA GCTGTGAGTG TTCCTTCGAA CACGAGnGA 400

(2) INFORMATION FOR SEQ ID NO: 3785:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3785:

TACTGGAATG ACATCAGATA CATGTGCACC ACCAATCCAT TTCTTTTCAC CATTGATAAC 60
 35 CCAAGTATCG CCTTGnCGTT CAGCGACTGT TTCAAGACCT CCGCAACGT CCGAACCGTG 120
 TTCTGGTTCA GTTAAAGCAA AGCATGTACG CAGTTCATGT GACTGTAATT TAGGTACATA 180
 TTTCGCAATT TGTTCCTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG 240
 40 AACACCGAGT AGGGTAGCTA AGGAAATATC AAATCGCGCG AGTAGGTAAG ACATGAAAAA 300
 CTGAAATAGT TGACTAGGCA TTTTGGCGTT TGGACGATCC TTGTAAAGTA ATGGATTGTT 360
 AAAATAATTT AATTCTCCCA GTCTTTAAAT AGTCCTCGGG 400

45

(2) INFORMATION FOR SEQ ID NO: 3786:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TCATTTGACG AATTTTCATTG TTATTCAAAA TTCTATCTAA TCGTGCTTTT TCAACATTTA 60
 ATATCTTACC TCGTAATGGT AAAATCGCCT GCGTTCTAGA GTCACGACCA GATTTTGTAG 120
 5 ACCCCCCGGC AGAGTCCCCT TCGACTAAGA AAATCTCACA TTCTTCAGGA CTTTACTAG 180
 AGCAATCGGC TAATTTACCT GGAAGCTTGC TACATCTAAC GCTGATTTAC GACGTGTTAC 240
 TTCACGCGCT TTTTTCGCAG CAACACGTGC ACGGCCCGCC ATAATACCTT TTTCAACCAC 300
 10 TGTACGTGCG ACTTGTGGGA TTTTCATATA AAAATCGTTC AAAGTGCTCT GAGAATAATT 360
 TATCTACAAC TTGACGCACT TCAGAATTAC CTAATTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3787:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3787:

25 TCTCTTCCCG TTTCGCTCGC CGCTACTAAG GGAATCGAAn TTTCTTTCTC TTCCTCCGGG 60
 TACTAAGATG TTTCAGTTCT CCGGGTGTGC CTCTGATAT GCTATGTATT CACATATCGA 120
 TAACATGACA TAACTCATGC TGGGTTTCCC CATTTCGAAA TCTCTGGATC AAAGCTTACT 180
 30 TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG 240
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTAT AAGTCAAACG 300
 TTAACATGAA GTTACGTTCT TTTATAAAAA GATTTAACG CGTTATTAAT CTTGTGAGTG 360
 35 TTCTTTCGGA CACTAGCGAT TATTCTnAT GATnCAAGCT 400

(2) INFORMATION FOR SEQ ID NO: 3788:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3788:

ATTCTCTGCT TTCATCTCAT TTGGTACTA ATACCCTGAT TTTGTCCAAG TAAATGCTTC 60
 50 ATAAAGTATT CTTGACCTTT TGCAGAACTT GAAATTAAGT TTGAACGCCA TATATAATGA 120
 TTTTGGATGA TTCTTTTCA AATCAGGATC TCTATTGCAA ATTGTGTTTG TnTTGATTC 180

TCTTCTGCAA ACAACAACT ATTTTATTA AATTGTGGAT ATGATGGTAA CCAACCAAGT 300
 CTAGCTGCTA AaACATTATA ATCAGCTGGA TGTTGATGCT TTAACTCCTC TGTTTTAGCT 360
 5 AATGGAGATT TTAAACGATC TACATTGAC TCTTCATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3789:

CGGTTTCTTA ATTATGAACG CAACTATGAA TGGCTTATTA ACTATCACGG GCACATTGGC 60
 AAAAGATCAG CTTGCACAAA ATGGACAAGG CATGGTGCTC GGTATACAAA CGGTTGAAAC 120
 CGGTGTTTTT GGCGGGATTA TCACAGGTAT TATGACCGCA ATACTTCACA ACAAATATCA 180
 CAAAGTGGTA TTACCACCGT ATTTAGGTTT CTTTGGTGGC TCTAGATTTG TCCCTATTGT 240
 CACAGCATTT GCCGCAATCT TTTTAGGTGT ATTGATGTTT TTCATTTGGC CAAGCATACA 300
 nGCCGGCATT TATCATGTTG GTGGGATTTG TAACGAAAAC AGGTGCCATC GGTACTnTTG 360
 TTTATGGGTT CATCTTTAGG ATTGTTAGGT CCACTCGGTT 400

(2) INFORMATION FOR SEQ ID NO: 3790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3790:

ATAATGGACT GTGCCGnGTA ATAATATnGn TCTCTAAAAG TTGTATTTTA AAAATAGTTC 60
 TTTAAATTAT ATACCCACCA CATTGGTGA kGAACCTAAA AAAAAGCACT TCCCAAAAAT 120
 GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA 180
 GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 240
 AGTGACGGAT CAAAnGTCCG TTGCCTTACC GCTTGGCTAT AGCCaATATA TAGATGGTGG 300
 AGGGGGGCAG ATTGCAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC 360
 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 420

CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGTGrTCTT 540
 AACCGtTGAC CAAGGAGCCA TGGCTCaCca GGTAgGACTC GAACCTACGA CCGATCGGTT 600
 5 TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGGATTA ATATTATGCC TGGCAACGTT 660
 CTA CTCTAGC GGA ACTAAAG TTnGAACTnA CCATCGACGC TAAAGGAGCT TAACTT 716

(2) INFORMATION FOR SEQ ID NO: 3791:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3791:

TGTCATGACG TTATTTGAAG ATATCGCGCA AGTCTTTTAA AAGGTAACAC TATCATTTAT 60
 GCAATACGGC GCATTACCAG AGTTGCATGG TCAAAATATA TTGTTGTCAT TTGAAGATGG 120
 ACGTGTACAA AAATGCGTGT TACGTGATCA TGATACTGTC AGAATTTATA AACCATGGCT 180
 25 AACAGCACAT CAGCTTTCAT TGCCGAAGTA TGTGTCAGA GAAGATACAC CTAATACGCT 240
 AATTAATGAG GATTTGGAAA CATTCCTTGC nTGATTTTCA AACATTAGCT GTGATCGGTA 300
 AATCTATATG CCATTATTGA TGCAATTCCA AGATTTATTT GGTGTGAAGT GnAGCATGAA 360
 30 CTTATGTCGT TGTTAAAACA AATTTTGAAA AAAGGAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3792:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3792:

TTTTACACA ATACATGGAC ACCATGGTTC AATGCTTCTA TAGAAAGATC AGCATGGAAT 60
 45 TTATTAGGTG TACAAATGAC CACCGCATCA ACAAGTTTAA ACAGCTCGCT AGGTGTCTCA 120
 ACTGCATGAG GTATATTAAA GCGCTTCGCA ACATCAATCA TCTGCACTGT ATTAATATCT 180
 TGTACTGCAA CTAATGAGAC TGTGTCTTTG AGTTTCAGCA ATGCTGGAAT ATGACGGTCT 240
 50 TGTGCAATAC CACCAACACC TATCACACCA ACTTTTAATT TTGTCATGAT GTGCCTCCTT 300
 ACCGTATGAT GTtATTCAAA GTAAATTGCT TTGCCTGATT TkGCAGACTG ATaAATyGCT 360

TACCA

425

(2) INFORMATION FOR SEQ ID NO: 3793:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3793:

15	GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG	60
	AGTGACGGAG nAAAGGTCCG TTGCCTTACC GCTTGGCTAT AGCCCAATAT ATAGATGGTG	120
	GAGGGGGGCA GATTGGAAC TCCGAACCCG AAGGAGCGGA TTTACAGTCC GCCGCGTTTA	180
20	GCCACTTCGC TACCCCTCCA GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG	240
	ACGGGTTCGA ACCGCCGACC CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT	300
25	CTCCAAAATA ATGACTCCTA CGGGACTCGA ACCCGTGTTA CCGCCGTGAA AGGGCGGTGT	360
	CTTAACCGCT TTGACCAAGG AGCCATGGCT CCACAGGTAG	400

(2) INFORMATION FOR SEQ ID NO: 3794:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3794:

40	ATCAGCAGGG TTGAAAGTAC CTGCTGCAAC AGTAATACCA TTATTAGTTC CAGCAATACC	60
	TGCTACAGTT GCTGCAGATG CTTCTTTCAC CCATGGACTC GTATTATTGC GACGTGTAAA	120
	TGTnTCACAA CGTTACCATT ACGTTTAATA ACTAATTTAT CAGCGTATGT CGTTACGTTA	180
45	CCGGCATGTG TATTCAGTGT TTGGTTTGCT CCAGGTGCAA TTGTAATCGC TCCTGCCGCT	240
	GTTTCAGTCA CASTTGTTTT CGCTGGTTGC ACATCTTTTA CTACAAATTT CGCTGGTAAA	300
	GATGTTGCAA AAGTATGTCC GTTATAGATG ACGTCCATAT TTTGCGTTAA CGACTTTAGC	360
50	CACATTCGGT TTATTCATAG CGGACCAGTT TGCCTCCATT	400

(2) INFORMATION FOR SEQ ID NO: 3795:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3795:

GC GCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACAA 60
10 TGGTAGGAGA GCGTTCTAAG GCGTTGAAG CATGATCGTA AGGACATGTG GAGCGCTTAG 120
AAGTGAGAAT GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT 180
AAGGTTTCCA GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCTAAGC TGAGGCCGAC 240
15 AGGCGTAGGC GATGGATAAC AGGTTGATAT TCCTGTACCA CCTATAATCG TTTAATCGAT 300
GGGGGGACGC AGTAGGATAG GCGAACGTGC CATTTGATTG CACGTCTAAA GCAGTAAAGC 360
TGAGTATTAG GCnAATCCGG TACTCGTThA AGGCTGAACT 400

20

(2) INFORMATION FOR SEQ ID NO: 3796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3796:

GCACATGTTG CCATgCTTGA GCTAAATTAC CTTGCATCAT TGCTAGCTTT TCTTGTATTA 60
ACTGATATTT ACTAATTGGT TTGCCGAATT GCTTACGCTC AGTGACATAA TCTAATGTGG 120
35 CACGTAAAGC GCCACCATAC CACCTGTAGC CATATAAGCA ACGsCTGCTC TCGTTGAATA 180
AAGAATTTTG GCAATATCTT TAAAGCTTGT TATGTTTTGT AAGCGATCCG CTTCATCTAC 240
40 TTTGACATTA GTTAATTTAA TTAGGGCGTT AGGAACAATG CGAAGTGCGA TTTTATTATC 300
AATGACTTCA ATATCGACGC CATCTTGTTT TGGTCTGACT ACAAAGCAAT GGGGTTTGCC 360
AGTTTCnGTT ATTTACTGCG AATACTGGGG GGGnGnGTT 400

45

(2) INFORMATION FOR SEQ ID NO: 3797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3797:

GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAAGTG ACGCTGATGT GCGAAACGTG 120
 GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT AAACGATGAG TGCTAAGTGT 180
 5 TAGGGGGTTT CCGCCCCCTTA GTGCTGCAGC TAACGCATTA AGCACTCCGC CTGGGGAGTA 240
 CGACCGCAAG TTGAACTCA AAGGAATTGA CGGGGACCCG CACAACGGTG GGAGCATGTG 300
 GTTTAATTCG AAGCAACGnA GAGAACCTTA CCAATCTTTG ACATCCTTTT GACTCTAG 360
 10 GAGATAGAGC CTTCCCTTCG GGGGGACnAA GTGACAGTTG 400

(2) INFORMATION FOR SEQ ID NO: 3798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3798:

CACAAAACAA GCCAAGCAAA ACAACGCAT ATAACGTAAC AACACATGGA AACGGCCAAG 60
 25 TATCATATGG CGCTCGCCCA ACACAAAACA AGCCAAGCAA AACAAATGCA TACAACGTAA 120
 CAACACATGC AAACGGTCAA GTGTCATACG GAGCTCGCCC GACATACAAG AAGCCAAGTA 180
 30 AAACAAATGC ATACAATGTA ACAACACATG CAGATGGTAC TGCGACATAT GGGCCTAGAG 240
 TAACAAAATA AGTTTGTAAC TCTATCCAAA GACATACAGT CAATACAAA CATTACGTAT 300
 CTTTACAACA GTAATCATGG CATTCTATGG ATGCTTCTAA CTGGAATTAA AGCATCGGAA 360
 35 CAATCGGGAn GCATATTTCT AAAATTATTT ATTCCATTAT 400

(2) INFORMATION FOR SEQ ID NO: 3799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3799:

CTTCGCCGAT ATGGGGGAAG CTAGGTGATA AGATCAGCCG AAAATGGATG GTGTTAAGAG 60
 50 CGTTACTTGG TTTGGCGGTA TGCTTATTTT TAATGGCATT GTGTACGACA CCATTACAGT 120
 TTGTACTTGT GAGGTTATTG CAGGGACTAT TTGGTGGTGT TGTTGATGCA TCAAGTGCCT 180
 TTGCGAGTGC AGAGGCGCCA CTGAAGGATC GTGGAAGGT ATTAGGAAGA CTGCAAAGTT 240

TTTtagTGCg TtactGATGA GTATTGCCGT TATTACTTTT ATTGTCTGTh TTTTCGGTGc 360
 CATTAAAATG ATTGAAACGA CACATATGGC CAAAnnCACA 400

(2) INFORMATION FOR SEQ ID NO: 3800:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3800:

GGAATCTATT ATATTAGATG TAAAAAATTT CGCGCAAAAT GTGTTAGGTA AAGGTGTCAT 60
 TGTCGTCAAT GATGTGCCTG GCTTTGTCGC AAATAGAGTC GGCACGCAAA CAATGAATGA 120
 TATTATGTAT CGCGCCGAGC AACACAAGAT AAGCATTGTA GATGTGGATG CTTTAACTGG 180
 GCAAGCGATT GGTCTGCCTA AAACAGGTAC ATATGCGCTA TCTGACCTAG TCGGTTTAGA 240
 TATTGCAGTG TCTGTAAATT AAAGGCATGC AACAAGTACC TGAAGAAACA CCTTATTTTC 300
 ATGATGTCAA AATGTAAATA CGTTGTTTGA CCATGGGCGC ACTCGGACGT TAAAnnCGnAA 360
 ACCAAGGGTT TTTACCAAAA AGGGTTAAAG GgnAACTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3801:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3801:

TGCAGGCGTT TCTGGTCTGC ATAGTTTACG CATACGACCT GCGCGATCCT TATCTGGTAA 60
 TAAATTGTAA AACGATAGTT CCCGTTGTTC CTAATAGTTG TATTCTATCT GACGCATAAT 120
 GTGAAAAATA ACCTGCCATC TCTAAGCCCG GTCTTGATAT ATCAGCATTT TTAATTGGCT 180
 TCGATAGTCC TTCTTCACCA GCGATTAAAT CTAACTTTAA TGTTTCAACT AGTTTTTCTG 240
 TCGTTAACAT GGGTTCACCT CAATTGTATT TACCCTACTC TTACATCTCT TCTTATCATA 300
 TCAAAAATAT AACACCAATC TACATTGAAA AGCTAAAnTA AATATTAATG TTCATTATTG 360
 TTAThATTTT ACAAGTCAAT ATCATCATAA TTTATTGCTG 400

(2) INFORMATION FOR SEQ ID NO: 3802:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3802:

10 TTTCACCTTTT GAACCATGCG GTTCAAAATG ATTATCCGGT ATTAGCTCCG GTTCCCGGAA 60
 GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC ACCCGTCCGC CGCTAACATC 120
 AGAGAAGCAA GCTTCTCGTC CGTTCGCTCG ACTTGCATGT ATTAGGCACG CCGCCAGCGT 180
 15 TCATCCTGAG CCAGGATCAA ACTCTCCATA AAAATTATGA TGTTTGATTA GCTCATAAAT 240
 ACTAAATAAT GTTTGTAAC TATAGTTACG TTTTTTGGAA TTAACGTTGA CATATTGTCA 300
 TTCAGTTTTT AATGTTTATT TTTCTTACCG ACAAGAATTA ATTATACATT TTATTAACAT 360
 20 TTAAGTCAAT AACTTTnTTT ATCCTGTCCA TTnATTTTT 400

(2) INFORMATION FOR SEQ ID NO: 3803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3803:

35 TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAC TAGATAGTAA GTAAAAGTGA 60
 TTTTGCTTCG CAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 120
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 180
 40 AACCGAAGTT GGGAAATCTC ATCTTGAGGG GGGCTTCATG CTTAGATGCT TTCAGCACTT 240
 ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC GACAACTGGT ACACCAGAGG 300
 TATGTCCATC CCGTCTCT CTACTAAGG ACAGCTCCTn TCAAATTTCC TACGnCCAnG 360
 45 ACGGATAGGG ACCGAACTGT TTTCACGACG GTnCTGAACC 400

(2) INFORMATION FOR SEQ ID NO: 3804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AGTnCACTCA CnCCAGATGT TTAAGTCCTG TGCCTCTGCC AGTTCCGCCA CCCCGGCACT 60
 ATAAAAATGG AGCAGAAGAC GGGATTTCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 120
 5 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 180
 TTAGwATCCT AAGTCTAGTG CGTCTGCCAA TTCCGCCACA CCCGCAAATG GTGAGCCATA 240
 GAGGATTCTGA ACCTCTGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG 300
 10 GCTCTTCCAT GGTGCCGGCC AGAGGACTTG AACCCCAAC CTACTGATTA CAAGTCAGTT 360
 GCTCTtACCA ATTGaGCTAG GCCGGCAATA TGTaAGAATA AATGGTGGAG AATGACGGGT 420
 15 TTCGAAACCG CCGnACCTC TGGCTTGTTA AGGGCAG 457

(2) INFORMATION FOR SEQ ID NO: 3805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3805:

ACTTTTTTATT TTGACGTTTT AGACATAAAA AAAGCTCAG GTCTCAACTT GCCTGGCAAC 60
 GTTCTACTCT AGCGGAACGT AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120
 30 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT 240
 TTCTTTGTGT TTACTTTTAA TnTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300
 35 TCAATGCGGC TCATCGCATC CATnTTTTGC CGGGCAACGT TCTACTCTTA GCGGAACGTA 360
 AGTTGGCTAC CATCGTCGCT AAAGACCTTT TTGACTGTG 400

(2) INFORMATION FOR SEQ ID NO: 3806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3806:

GTTATGAAAG TCGCGCTTAA AATGCGTTAA TGTGACAAGG ATAATTCAAC ATCGTTTCAT 60
 TTTACTGAGT CATTGCACTT ATCATAACACA TTATATTTAG CATGAGTTAT ATTACTAAAA 120

TCATTGGCTT AATATTTACA GCGCTTGGTA TTGCAGGTGC CGTATTACCT TTA CTGCCAA 240
 CGACCCCTTT TTTACTCGTA GCAGTTTTTT GCTTTGCTCG AAGTTCAGAT CGCTTTTACA 300
 5 ATTGGGCnnA TTAATCAAAA AATTTATAAA GAATATGTAG AAAACCTTTn TTTGACATCG 360
 AGGCTACACG CTACAACAGA AAATTGAAAA TTTAATTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3807:

20 AGGAGAACAT GCTGTTACAT TTGGAGAGCC TGCTATTGCA GTGACCGTTT AACGCAGGTA 60
 AAATCAAAGT TTTAATAGAA GCCTTAGAGA GCGGGA ACTA TTCGTC TATT AAAAGCGATG 120
 TTTACGATGG TATGTTATAT GATGCGCCTG ACCATCTTAA GTCTTTGGTG AACCGTTTTG 180
 25 TAGAATTAAA TAATATTACA GAGCCGCTAG CAGTGAACGA TCCAAACGAA TTTACCACCA 240
 TCACGTGGAT TAGGATCGAG TGCCAGCTGT CGCGGTGCT TTTGTTCTGT CAAGTTATGG 300
 ATTTTTTAGG GnAAATCATT AACGAAAGnA AGAACTCATT GGAAAAGGCT nATTGGGCCA 360
 30 GAAGCAAATT GCCACATGGT AAAACCAA 388

(2) INFORMATION FOR SEQ ID NO: 3808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3808:

45 ATGCGCAGAG TATATGGAGG AACACCAGTG TCGAAGCGCA CTTTCTGGTC TGTA ACTGAC 60
 GCTGATGTGC GAAACGTGkG GGATCAAACA GGATTAGATA CCCTGGTAGT CCACGCCGTA 120
 AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG TGCTGCAGCT AACGCATTAA 180
 GCACTCCGCC TGGGGAGTAC GACCGCAAGT TgAAA ACTCA AAGGrATTGA CGGGGACCCG 240
 50 CAcAAGCGTG GGAGCATGTG GtTTAATTCG AaGCAACGnn GAGGAACCTT ACCAAATCTT 300
 GACATCCTTT GACAACTCTA GAGATAGAGC CTTCCCTTC nGGGAACAAA TGACAGGTGG 360

ACCCTTAAGC TTATTGCCA TCATTAA

447

(2) INFORMATION FOR SEQ ID NO: 3809:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3809:

CCAAGTGAAG TACTGAACCA TAATAAAAT GTAATGACTG GCGGTCTCGA CGGGAATCGA 60
 ACCCGCGATC TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACACTACGA GACCTATAAA 120
 ATATTGCGGG AGGCGGATTT GAACCACCGA CCTTCGGGTT ATGAGCCCGA CGAGCTACCG 180
 AACTGCTCCA TCCCAGGATA ATAAAAAATA ATGGCGGAGG AAGAGGGATT CGAACCCCCG 240
 CGGCCCGTTA AGGCCTGTC GGTTTTCAAG ACCGATCCCT TCAGCCGGAC TTGGGTATTC 300
 CTCCATTATT ATAGGTAAAT CGCTATTAAT TATAAAATTA AATGGCGGTC TCGACGGGAA 360
 TCGAACCCGC GATCTCCTGC GTGACAGGCA GGCGTGTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3810:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3810:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA ATAATGGTGG 60
 GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCCTCTT AACCAGCTGA 120
 GCTATAGGCC CATTTTTTTG AATGTTAAAT AACATTCAA AACTGAATAC AATATGTCAC 180
 GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG AGGTGATCCA 240
 GCCGCACCTT CCGATACGGC TACCTTGTTA CGACTTCACC CCAATCATTT GTCCACCTT 300
 CGACGGCTAG CTCCTAAAAG GTTACTCCAC CGGCTTCGGG TGTTACAAAC TCTCGTGGTG 360
 TGACGGGCGG TGTGTACAAG ACCCGGGAAC GATTTCACCG 400

(2) INFORMATION FOR SEQ ID NO: 3811:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3811:

GCTTCATGCT TAGATGCTTT CAGCACTTAT CCCGTCCACA CATAGCTACC CAGCTATGCC 60
10 GTTGGCACGA CAACTGGTAC ACCAGAGGTA TGTCCATCCC GGTCTCTCTG TACTAAGGAC 120
AGCTCCTCTC AAATTTCTTA CGCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTC 180
TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTGGG ACCGACTACA 240
15 GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGGAATCTT 300
TGGGGGAGAT AAGCCTGTTA TnCCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGnnCTTCC 360
ATGCGGGAAC CACCGGGATT 380

20

(2) INFORMATION FOR SEQ ID NO: 3812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3812:

30

GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA TGCTTAGATG 60
CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTAGC ACGACAACTG 120
35 GTACACCAGA GGTATGTCCA TCCCGGTCCT CTCGTACTAA GGACAGCTCC TCTCAAATTT 180
CCTACGCCCA CGACGGATAG GGACCGAACT GTCTCACGAC GTTCTGAACC CAGCTCGCGT 240
ACCGCTTTAA TGGGCGAACA GCAACCCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 300
40 GCCGACATCG AGGTGCCAAA CCTCCCGTC GntGTGAACT CTTGGGGGAG ATAAGCTGTT 360
ATCCCCGGGT GAGnTTTnTC CGTTGA 386

45

(2) INFORMATION FOR SEQ ID NO: 3813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3813:

55

CTTGGTACTT CTGGTGTGG TGGCGTTGGT GTTCCGGCT CACTGGGTAC TTCTGGTGTC 120
 GGTGGCGTTG GTGGCACGAT TGGAGGTGTT GTATCTTCTT CAATCGTTTG TTGACCTTCA 180
 5 TTTTGGCCGC TTACTTTTGG AAGTGTATCT TCTTCAAAGT CAACACTATT GTGTCCACCG 240
 AATTGATAAC TTGGTTTATC TTTATTTGTA TCTTCTTCAA TAATTTTCACT GTGCTTATTG 300
 AATCCGTGAA TATGTGGCAC nTGGTCGAAG TCGATATCAA TGATGTTACC GCCATGTTCA 360
 10 TACTTAGGTT TGTCTTTTTC TGTAnCTTCC TCGAATGACT 400

(2) INFORMATION FOR SEQ ID NO: 3814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3814:

TAATTGGGCT ACCATCGTCG CTAAAGACCT TTCTTGACTT GTGACAATCG CTGCTTCTT 60
 25 TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCnACTA AACTCGTTGC GChCTTTTCT 120
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTCTTTTGT GTTTACTTTT 180
 TATTTTGACG TTTTAGGCAT AAAAAAAGA GACCTTGCGG TCTCAATGCG GTCATCGCA 240
 30 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGGCT ACCATCGTCG 300
 CTAAAGACCT TTCTTGACTT GTGACAATCG CTGCTTCTT TCCTCTCCTT CGGCTCTCGC 360
 35 TTACTCATTT AGCTCTACTA AACTCGGTGC GCTCTTTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3815:

45

TTCTTTCATA TGATTTTTTA GATTTTAGTA AGTCAATAAA GCCAATTTTC TCCAACGATT 60
 GAATGTAACG TTGATTGATA AATGTATTTT TTGGTAAATC ACCACCCGCT AAAATTGTGG 120
 CGATATTTAA GGCAATATGA TAATCATGGT CGCTAATAAA ATGACCCCGT CTTTGCGCAT 180
 CTAATTGTCC TTGGATCAAT GCTTTGAAGT CTTACCTAA AGCGATATAT TGATGTCTAG 240

50

55

GTTGTGCTGT ATTGAAAATA ATCGTATCTG GTATCACGTA AATnACCATA ACGACGTGCC 360
 TCCAAAGGCA TTTGGTANGA GCCTTCGGCA ATGCCGATAA 400

(2) INFORMATION FOR SEQ ID NO: 3816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3816:

CCAATATTTA TATTAATGAA AATAAGATGT TATATTCATT GTTAATTTAA CACATAGTAA 60
 GAAAAACAGT CATAAATTGA TTTCTAATTG AAATCATCTT ATGACTGCTT TTTATTATAC 120
 TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TCTTTCTTTG 180
 TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT CTCAATGCGG 240
 CTCATCGCAT CCACTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA GTCGGACTAC 300
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG GAACAGGTGT GACCTCCTTG 360
 GCTATAGTCA CCAGACATAT GAATGTAAAT TCATACATTC 400

(2) INFORMATION FOR SEQ ID NO: 3817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3817:

TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGGG GGGnATTATG AAGCGATGCA 60
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180
 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240
 TACCGAACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300
 TCATGATAAT TTCTTTGAAT TAGGTGGCCA TTCATTAAAA GCAACGTTAT GGnTGGAATC 360
 GGATAGAGGC ATCTACTGGG GAAACGATTA CCAATTGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3818:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3818:

10 TCGGAATCTG GGAGGACCAT CTCCTAAGGC TAAATACTCT CTAGTGACCG ATAGTGAACC 60
 AGTACCGTGA GGAGAAGGTG AAAAGCACCC CGGAAGGAAG TTGAAATAGA ACCTGAAACC 120
 GTGTGCTTAC AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA 180
 15 CCGGCGAGTT ACGATTGAT GCAAGGTTAA GCAGTAAATG TGGAGCCGTA GCAnAACATG 240
 TTCTGAATAG GGCCTTTAGT ATTTGGTCGT AGCCGnAAAC CAGGTGATCT ACCCTTGGTC 300
 CAGGTTGAAG TTCAGTAAC ACTGGAATGG AGGACCGAAC CGACTTACGT TTGAAAAGTG 360
 20 AGCGGATGAA CTGAAGGTAG CGGAGAAATT CCCAATCGAA 400

(2) INFORMATION FOR SEQ ID NO: 3819:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3819:

CAACGAGAGA CTCGGTGAAG TCATAGTACC TGTGAAGATG CAGGTTACCC GCGACAGGAC 60
 35 GGAAAGACCC CGTGGAGCTT TACTGTAGCC TGATATTGAA ATTCGGCACA GCTTGTACAG 120
 GATAGGTAGG AGCCTTTGAA ACGTGAGCGC TAnTTACGTG GAGGCGCTGG TGGGATACTA 180
 CCCTAGCTGT GTTGGCTTTC TAACCCGCAC CACTTATCGT GGTGGGAGAC AGTTTCAGGC 240
 40 GGGCAGTTTG ACTGGGGCGG TCGCCTCCTA AAAGGTAACG GAGGCGCTCA AAGGTTCCCT 300
 CAGAATGGTT GGAAATCATT CATAGAGTGT AAAGGCATAA GGGACTTGAC TGCGAGACCT 360
 45 ACAAGTCGAG CAGGTCCAAA AACGGACnTA GTGATnCGGT 400

(2) INFORMATION FOR SEQ ID NO: 3820:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

TGGCTCGAAC CACCGACCTC ACGCTTATCA GCGTCGCTC TAACCAGCTG AGCTATAGGC 60
 CATTAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT ATTCCGCATC 120
 5 TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC GCACCTTCCG 180
 ATACGGCTAC CTTGTTACGA CTTACCCCA ATCATTGTG CACCTTCGA CGGCTAGCTC 240
 10 CTAAGAGTT ACTCCACCGG CTTGGGTGT TACAACTCT CGTGGTGTGA CGGGCGGTGT 300
 GTACAAGACC CGGAACGTT ATTCACCGTA GCATGCTGAT CTACGATTAC TAnCGATTCC 360
 AGCTTCATGT AGTCGAGTTT GCAGACTACA ATnCGAACTG 400

(2) INFORMATION FOR SEQ ID NO: 3821:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3821:

25 TATTAAATTA ATGGTGGGCC TAAnTGGACT CGAACCACCG ACCTCAGCT TATCAGGCGT 60
 GCGCTCTAAC CAGCTGAGCT ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA 120
 30 ATACAATATG TCACGTTATT CCGCATCTT TGAAGAAGAT GTTCCGAATA TATCCTTAGA 180
 AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC 240
 ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT CGGGTGTTAC 300
 35 AAATCTCTGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC ACCGTAGCAT 360
 GCTGATCTAC GATTACTnAG CnTTCCAGC TTCCATGnTA 400

(2) INFORMATION FOR SEQ ID NO: 3822:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3822:

50 TCTACCAACT GAGCTAATGG CTCTAATGGC TGGGCTAGCT GGATTCTGAAC CAACGAGTGA 60
 CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAA TATATAGATG GnGGAGGGGG 120
 GCAGATTCTGA ACTGCCGAAC CCGAAGAGCG GATTACAGT CCGCCGCGTT TACCACTTCG 180

GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCA GCTGAGCTAA TTCTCCAAAA 300
 TAATGACTCC TACGGACTCG AACCCGTGTT ACCGCCGTGA AAGGGCGGTG TCTTAACCGC 360
 5 TTGACCAAGG AGCCATGCTC CACAGTAGGA TTCGAACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3823:

AACTTGCCCTC TTTAGGTACA GCATGAGGCC CTAGGAAAGT ATGTTTCATG TCTAAATCAT 60
 20 ATTTCTCAGC TAAACGATTA GACACTTTCA ATTGCTTCAG TTCATTTTCT CTATCTAATC 120
 CATAACCACT CTTACTTTCA ACTGCAnGCA CGCCGTGTTT AATCATAGTA AGCAAATCAT 180
 GCTCTGCTTT TTAAACAAG TCATCTTCGG ATGTTTCTCT AGTAGCATT ACGGTAGATA 240
 25 ATATGCCACC ACCCATTTCT AATATTTCAA GGTAAGACTT ACCTGGACGT TTTAATGACA 300
 TCTCATGTTC TCGAGATCCA CCAAATGTnA AATGGGGTAT GTGGCATCTA CTAAGCCGGG 360
 GGACACTAnC TTTCCCACTA GGCATCAATC G 391

(2) INFORMATION FOR SEQ ID NO: 3824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3824:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60
 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120
 45 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA 180
 ACGCGTTATT AATCTTGTGG AGTGTTCCTT CGAACACTGA GCGATTATTT CTTATGAATT 240
 CAAGCTTATT TAAACTCTT TATTCACGCG GTTTTGCTTG GTAAATCTA TATTTTACTT 300
 50 ACnTATCTAG TTTTCAATGT ACAATTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC 360
 TTTGAACCAA AAAAGATTGG AAGGTGAAAT AAACATTCAA 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3825:

ATCGATAACA TGACATAACT CATGCTGGGT TTCCCCATTC GGAAATCTCT GGATCAAAGC 60
 TTACTTACAG CTCCCCAAG CATATCGTCG TTAGTAACGT CCTTCATCGG CTTCTAGTGC 120
 CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT TTCCATCCTA CAGGAAACGC 180
 GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTCTTATG AATTCAAGCT 240
 TATTTAAAC TCTTTATTCA CTCGGTTTTG CTGGGTAAA TCTATATnTT ACTTACTTAT 300
 CTAGTTTTCA ATGTACAATT TCTTTTTAGT CAAGCGCTCG CATAAGCAAT ATCACTTTAA 360
 CCAAAAAATA TTTGAATGTn AAATAACAT TCAAACTGA 400

(2) INFORMATION FOR SEQ ID NO: 3826:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3826:

TCACTCACCG CAGATTTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA 60
 AAAATGGAGC AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT 120
 ACCGCTGAAC TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGnCT 180
 TAGATCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240
 GGATTCGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT CTACCAACTG AGCTAATGGC 300
 TCTTCCATGG TGCCGGCCAG AGGATTTGAA CCCCCAACCT TATTGGTTAC AAGTCAGTTG 360
 CTCTTACCAA TTGAGCTAGG nCGGCAATAT GTTAAGATTA 400

(2) INFORMATION FOR SEQ ID NO: 3827:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3827:

5 AGTGGTGGAA TGGTCTTAAA AGTTGGTGGT CTAACCTTTAG AGAAGACCAA AAGAAGAAAA 60
 GTGATAAATA CGCTAAAGAA CAAGAAGAAA CAGCTCGTAG AACAGAGAA AATATAAAGA 120
 AATGGTTTGG AAATGCTTGG GACGGCGTAA AACTAAAAC TGGTGAAGCC TTTAGTAAAA 180
 10 TGGGCAGAAA TGCTAATCAT TTGGCGGCG AAATGAAAAA AATGTGGAGT GGAATCAAAG 240
 GAATTCCAAG CAAATTAAGT TCAAGTTGGA GCTCAGCCAA AAGTTCTGTA GGATATCACA 300
 CTAAGGCTAT AGCTAATTAG TACTGGTAAA ATGGTTTGA AAAGCTTGGC CAATCTGTTA 360
 15 AATTCGACTA CAGGAAGTAT TTACATTCAA ACTAGGCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3828:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3828:

25 TCTCAGTTCC AGTGTGGCCG ATCACCCTCT CAGGTCGGCT ATGCATCGTT GCCTTGGTAA 60
 GCCGTTACCT TACCAACTAG CTAATGCAGC GCGGATCCAT CTATAAGTGA CAGCAAGACC 120
 30 GTCTTTCACT TTTGAACCAT GCGGTTCAAA ATATTATCCG GTATTAGCTA CGGTTTCCCG 180
 AAGTTATCCC AGTCTTATAG GTAGGTTATC CACGTGTTAC TCACCCGTCC GCCGCTAACA 240
 35 TCAGAGAAGC AAGCTTCTCG TCCGTTGCT CGACTTGCAT GTATTAGGCA CGCCGCCAGC 300
 GTTCATCCTG AGCCAGGATC AACTCTCCA TAAAAATTAT GATGTTGANT AGCTCATAAA 360
 TACTAAATAA TGTTGTAAC TATAGTACGT TTTTnGAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3829:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3829:

50 CAAGCGCCAT GACATCATAA CTTTCTTGCA CAAGATATGT GAACGGCGGT GTTGATCCTA 60
 GATTCGTGGC ATGCATACGC AAACCATTTT CTTCATTAC TTCACCAAGG CGTTTAAAT 120

55

ATTGATAAAA CCTTGATGTG TTTCGTGTCA ATGACATACC ATATCGACTA GGTACCTTTT 240
 TAGAATGTTG ATTAATCACA ACAAATATCA TGGCAAGGTC ATCTTCAAAA TGATTGATT 300
 5 CAAGTGGGA_r sGGCATATGA CGTCTCATCA CtATACCCTt TnTnCCCATT CTGCAAATnC 360
 ACCCATAAAT ACTACGGGAC GGAGAACCCG TACCCATTTC 400

(2) INFORMATION FOR SEQ ID NO: 3830:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3830:

20 GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT 120
 ACTTACAGCT CCCCAAAGCA TATCnCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180
 25 GGATCCACCG TCGGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTTA TAAGTCAAAC 240
 GCTCACATAC GGCTTCGTTT TCATTATTTT AAATGCTCAT TTACATAAGT AAATCTGCT 300
 TTAAAATAAT TTAATCATT GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG 360
 30 TTATTAATCT TGTGAGTGGT CCTTCGAACA CTAGCGATnA 400

(2) INFORMATION FOR SEQ ID NO: 3831:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3831:

AAATGCGGCT CATCGCATCC ATTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 60
 45 TTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT 120
 CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTAATAAACT CGTTGCGCTC TTTTCTCGTT 180
 TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240
 50 TTGACGTTTT AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA 300
 TTTTTTGCCT GGGCAACGTT CTACTCTAGC GGAACGTAAT TGGGCTACCA TCGACGCTAA 360

(2) INFORMATION FOR SEQ ID NO: 3832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3832:

AGCTTATTTT AAAACGTCGT TTATTCACCTC TGGTTTTGCT TGGTAAAATC TATATTTTAC 60
 TTACTTATCT AGTTTTCAAT GTACAATTTT TTTTAGTCA AGCGCTCGCA TAAGCAATAT 120
 CACTTTAACC AAAAAATATT TGAATGTAA ATAAACATTC AAAACTGAAT ACAATATGTC 180
 ACATTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 240
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCATCAT TTGTCCCACC 300
 TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 360
 TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTTCA 400

(2) INFORMATION FOR SEQ ID NO: 3833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3833:

TTTTCTTCTG GTAAAATATC TGCAATAACA GTATCTATGC CTAATTGTTT TGCAATGGCT 60
 TGAGCAGTGT TTTTATTATC GCCAGTTAAC ATGGCAACTT CAATGCCCAT ATCATGCAAT 120
 TGTATTATAG CATCTTTGGC ATGATCTTTG ACAGTATCTG CCACTGCnAT GATACCAGTT 180
 AATGAATAAT TAACAGCAAT GAGCATAGCA GTTTTACCAT CTCGTTcATA ATGTGTTAAA 240
 TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG CCATTAATnT ACGGGTTACC 300
 AACCAATATA TGGTGATGAT CAATCCGTGG CTTCAATACC ATGGCCAGGT ACCGCTTnAA 360
 AGTTGTTGTC TCAGTTAATA TTAATTGCTT TCCTTTTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3834:

5 NAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTTATGAG CCGTTAGCTC 60
 TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TnGCGGnnGA 120
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 180
 10 CGCCTTATAT AGTTTGTAAG TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC 240
 TGCGTGCAAA GCAGGCGCTC TCCCAGCTGA GCTAAGCCCC CATAATAATT ACAGTATATC 300
 GGGAGACAG GATTCTGAACC TGCGACCCCT TGGTCCCAAA CCAAGTGCTC TACCAAGCTG 360
 15 AGCTACTTCC CGTATAATTA ACGCGCCCGA TAGGAGTCGA 400

(2) INFORMATION FOR SEQ ID NO: 3835:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3835:

AATAACAATT GCGCCACTAA AACTCAAAAT TTCCACCACC AACATCCAAA TTATCAACAT 60
 30 CGCAACATAA CCAAATGTTA TAATAAATCT ATTACACAAA GAGATAAATT ACTTATGCAA 120
 AGGCGGAGGA ATCACATGTC TATTACTGAA AAACAACGTC AGCAACAAGC TGAATTACAT 180
 AAAAAATTAT GGTCGATTGC GAATGATTTA AGAGGGAACA TGGATGCGAG TGAATTCCGT 240
 35 AATTACATTT TAGGCTTGAT TTTCTATCGC TTCTTATCTG AAAAAGCCGA ACAAGnATAT 300
 GCAGATGCCT TGTCAGGTGA AGACATCACC TATCnAGAAG CGTGGGCAGA TGAAGAATAT 360
 40 CGTGAAGACT TnAAAAGCAG GAATTAATTG GTTCAAGTCG 400

(2) INFORMATION FOR SEQ ID NO: 3836:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3836:

CTAATCGCAT CTTTTTCAAT CTAAGTGCCT TTGTGACAAA CTTACTGAAC TTAGTGCCAT 60

ATTATAGCCG AATGCCCAAA ATAGATTTTG ACGAATATTA CGAATGGTTG CTTTACTTGC 180
 ATAAATGGCT TTAGGAATAA GCATCAAGTC GCCACCAAGA ATAGTAATAT CAGCTGCTTC 240
 5 AATGGCAACT TCTGTACCTG TACCAATGGC GATACCGATA TCAGCTTTAA CTAAATGCAG 300
 GTGCATCATT TACACCGTCA CCAACCATCG CAACCTTCTT ACCTGTTGGC TGTAGTTTCG 360
 10 CAATTGTGGC AGCTTTTTnC TTCCGGnGAA AATATChGGC 400

(2) INFORMATION FOR SEQ ID NO: 3837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3837:

AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC CCCTCCAGCT TATTCATATA 60
 ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG 120
 25 GCAGATGCTC TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC 180
 CGTGTTACCG CCGTGAAAGG GCGTGTCTTA ACCGCTTGGA CCAAGGAGCC ATGGCTCAAC 240
 30 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 300
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTA CTCTAGC GGAAGTAAn TCGGACTACC 360
 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3838:

AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC TACTAAACTC 60
 GTTGCCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTC 120
 50 TTTGTGTTTA TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG AAGTAATTGG 240
 GCTACCATCG ACGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 300

TCAGATCCAA ACGTTTTTCAn TCGnCCAAGC CAATTTGCCT

400

(2) INFORMATION FOR SEQ ID NO: 3839:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3839:

15	TTACGGCCGC CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGTAGAcrc GACTCCTCTT	60
	AACCTTCCAG CACCGGGCAG GCGTCACCCT gATAcATCAC CTTACGGTTT AGCAGAGACC	120
	TGTGTTTTTG ATAAACAGTC GCTTGGGCCT ATTCAGTGGC GCTCTTCTGG GCGTTAACCC	180
20	TAAAGAGCAC CCCTTCTCCC GAAGTTACGG GGTCATTTTG CCGAGTTCCT TAACGAGAGT	240
	TCGCTCGCTC ACCTTAGAAT TCTCATCTTG ACTACCTGTG TCGGTTTGCG GTAGGGcACC	300
	TATTTTCTAT CTAGAGGCTT TTCTCGGCAG TGTGAAATCA ACGACTcGAg GACACAATGT	360
25	CTTCTCCCCA TCACAGtTCA GCCTTgAACG rGTaCCGGAT TTGnCTAATG ATTCAG	416

(2) INFORMATION FOR SEQ ID NO: 3840:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3840:

	AAGTTAGGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT	60
40	TCCTCTCCTT CGGCTCTCGC TTAATCATT AGCTCTACTA AACTCGTTGC GCTCTTTTCT	120
	CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT	180
45	TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT CTCAAACCTG CCTGGCAACG	240
	TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT	300
	GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA	360
50	CTCGTTGGnG CTCTTTTTTCT CGGTTTnGTC AGAnTTCAAA	400

(2) INFORMATION FOR SEQ ID NO: 3841:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3841:

CGCGACTGAn GAATACAATG nCTACGATAA CTAAACCCAA TCAATCTTTT CATTCTATCA 60
10 ATTCCTTTCA AAATCTTCAC TATATATCAT TAATGTCTAC GTATGAATCT AGCTAGAACA 120
TTCCCTAGCG TTTGAATCAC TTGGACAATA ATGACTAATA CAATAACGGT AATAATAATG 180
ACCGTCGTAT CAAATCTTTG ATAACCATAC ACTAAAGCTA AGTCTCCTAT ACCACCACCG 240
15 CCAACAGCTC CTGCCATCGC CGTACTTCCA ATAAGTCCAA TAATCGCAGT GGTAAATTGCT 300
AATACTAACG AACCTAAAGC TTCAGGAATT AAAAAATATC TAATGATTG TAGTGGTGAA 360
GCGCCCATCG CTTTCGCCGC TTCAATAATC CCCTCGTCTA 400
20
(2) INFORMATION FOR SEQ ID NO: 3842:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3842:

TCGCGATTCTG CGTGTTTCAGA AATCATCGGC ATCGCGTCAT TCAATGATTG ATATGCATCT 60
AAAGCAATAG AAGATAATGT GTCTGGCACA TATACCCATG CCAACGTATC AGTAGACGTA 120
35 TGATGTTCTG CTACCGCAAA AACAGTTGTC TCTGGAATAT ACACACCTGA TTGTTTTAAT 180
CCTTGCTCTGA CATTGGGACG ATTACATATC ATCGCTAATA ACTTAGCATT AAAACCGCTT 240
GATGCGCCAC CACAAGCCCC ACATTCAAGT GATGCATGAT GTGGATTATT GTGAGAATGA 300
40 CTAGCATGAC CTGCTAACAC AACGAACGGC GCAAATGCTT CGGkTAAATC CATCAATTTT 360
AACGCTgTAA CGCGAATCAA TTGCTCTGCT CAGTAAATCC 400

45 (2) INFORMATION FOR SEQ ID NO: 3843:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3843:

55

GCCAACATCC TAGTTGTCTG GGCAACGCCA CATCCTTTTC CACTTAACAT ATATTTTGGG 120
 ACCTTAGCTG GTGGTCTGGG CTGTTTCCCh GTCGAACACG GACCTTATCA CCCATGTTCT 180
 5 GACTCCCAAG TTAAATTAAT TGGACATTCG GAGTTTGTCT GAATTCGGTA ACCCGAGAGG 240
 GGCCCCCTCGT CCAAACAGTG CTCTACCTCC AATAATCATC ACTTGAGGCT AGCCCTAAAG 300
 10 CTATTTTCGGA GAGAACCAGC TATTTCCAGG TTCGATTGGG AATTCTCCGC TAACCTCAGT 360
 TCATCCGnTC ACTTTCAACG TAAntCGGGT CGGGTCTCCA 400

(2) INFORMATION FOR SEQ ID NO: 3844:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3844:

25 ACTTTTACTT GCTGCGCCTC CAGCCAAACC TGCTGTTCCA GCACCGATCG CTGCACCTTT 60
 TTTGCCATTA TGATGATCTT TAGACTTATC TTGAGACGCT TTATCCTCAG TCGAGTTATT 120
 CGCCTTGCCA GAATTACTTT TGTTTTGAGC GTCATTTGAA TGTTTCTTAG CTTTAGAAGC 180
 30 AGCCATTGCA CCAGCTGCAC CTGCAACACC TGCTGTTCCA GCACCAATAG CTGCTGCTTT 240
 TTTACCATTA TGATGTTCTT TAGGTTTCATC TTGATCTTGT TTTACAGAAT CATTATCATG 300
 TTCATTTTTT GATGTTTCTG ATTGGTTAGC ACCTGTTGTA AAATATGGTT TAGGTTGCTG 360
 35 AGATTGTTCA GCTTCACTCT TATCAGAAAC TGTTGAATGC TCAGTGTTAT TTTCTGCATT 420
 TTTAATAGTA TCGTGTTTAn CCATTGTCCT CGAATGGGTT CnGGATGTG 469

(2) INFORMATION FOR SEQ ID NO: 3845:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3845:

50 GCTTCACTAC CAAGTGAAGA AGTTGCTGAA ACTCCTGCAG CACCTGCAnC AGTAACATTA 60
 GAAGGCGACT TCCCAGAAAC AACTGAAAAA ATCCCTGCTA TGCGTAGAGC AATTGCGnAA 120
 CATGGnTTTA ACTCTAAGCA TACTGCACCT CATGTAACAT TAATGGATGA AATTGATGTT 180

TTAACATTCT TACCTTATGT TGTAAAGCA CTTGTTTCTG CATTGAAAAA ATACCCAGCA 300
 CTTAACACTT CATTCAATGA AGAAGCTGGT GAAATCGTTC ATAAACATTA CTGGGAATAT 360
 5 CGGTATTGCA GCAGACACTG ATAGAGGATT ATTAGTACCT 400

(2) INFORMATION FOR SEQ ID NO: 3846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3846:

TTAAGCTACC ATCCTCGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 60
 20 TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT 120
 TTCGTCAGAT TCAAACGTTT TCACTTCGCC AAGCCATTTT TCTTTGTGTT TACTTTTTAT 180
 TTTGACGTTT TAGACATAAA AAAAGAGACC TCACGGTCTC AACTTGCCTG GCAACGTTCT 240
 25 ACTCTAGCGG AACGTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT GACTTGTGAC 300
 AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTACT CATTAGCTC TACTAAACTC 360
 30 GTTGGCGCTC TTTTCTCGGT TCGTCAGATT CAAACGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 3847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3847:

ATCGTCAACT TATTATTAGA CGATGTACAA GTTACATTAG ACAAAAAGG TATTACGATG 60
 GACGTTTCTC AAGATGCGAA AGATTGGTTA ATTGAAGAAG GCTATGATGA AGAATTAGGT 120
 45 GCACGTCCAT TAAGACGTAT TGTTGAACAG CAAGTACGTG ACAAATTAC AGATTACTAT 180
 TTAGATCATA CAGACGTAA ACATGTGGAT ATAGATGTTG AGGGATAACC AATTAGTCGT 240
 50 AAAAGGTAAA TAACGACACT TTAACATATC GCGCATCAAA AATGAGCATC AGGTCGCCCT 300
 TGCCTGTGGC TCATTTTTTT GAATTATTC CCTGGGAAAA TGATTCGCTG TGTGCTGTTC 360
 TGTThCCACA ACAATCACGA TTGAATGTGC ACATGTGACC 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3848:

TTTAAAACTC TTTATTCACT CGGTTTTGCT TGGTAAAATC TATATTTTAC TTACTTATCT	60
AGTTTTCAAT GTACAAATAA TGGTGGGCCT AAGTGGACTC GAACCACCGA CCTCAGCCTT	120
ATCAGGCGTG CGCTCTAACC AGCTGAGCTA TAGGCCCATTT TTTTGAATG TTAAATAAAC	180
ATTCAAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA	240
TATATCCTTA GAAAGGAGGT GATCCAGCCG CACCTTTCCG ATACGGCTAC CTTGGTnACG	300
ACTTCACCCC AAATCATTTG TCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTCCACC	360
GGCTTCGGGn GTTACAAACT CTCGTGGGTG TGACnGGCGG	400

(2) INFORMATION FOR SEQ ID NO: 3849:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3849:

GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC	60
TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT	120
TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCCTTTCTC GTTTCGTCAG ATTCAAACGT	180
TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA	240
AAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT CCATTTTTTG CCTGGCAACG	300
TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT	360
GACAATCGCT TGCTTCTTTC CTnTCCTTCG GCTCTCGCTT	400

(2) INFORMATION FOR SEQ ID NO: 3850:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3850:

5 GTCTACTAAT GTTACAACCA CACCTGATTa ATTGCTTTTT TAGCAGTAAT TGCCACATCT 60
 GTGTGACGAT AATGATATGC GACAGTTAAT AATTTGTGAT TTTTATTAGC CGCTTCAATC 120
 ATGCGATCAC ACTCTTCCGT CGTCATCGCC ATTGGCTTTT CACACAATAC ATGGACACCA 180
 10 TGGTTCAATG CTTCTATAGA AAGATCAGCA TGAATTTAT TAGGTGTACA AATGACCACC 240
 GCATCAACAA GTTTAAACAG CTCGCTAGGT GTCTCAACTG CATGAGGTAT ATTAAAGCGC 300
 TTCGCAACAT CAATCATCTG CACTGTATTA ATATCTTGTA CTGCAACTAA TGAGACTGTG 360
 15 TCTTTGAGTT TCAGCAATGC TGAATATGA CGGTCTTGTC CAATACCACC AACAACTATG 420
 CACACCAACT TTAAaTTTG TnCATGATGT GCCnGCTThA CCG 463

(2) INFORMATION FOR SEQ ID NO: 3851:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 628 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3851:

30 TATGCTCTAA TGCTGGGCTT AGTGGATTTC ACCAACGAGT GACGnAGTCA AAGTCnGTTG 60
 CTTTACGCTT GGCTATAGCC CCAATATATA GATGTTGGAG GGGGCAGATT CGAACTGCCG 120
 AACCCGAAGG AGCGGATTTA CAGTCCGCCc CGTTTAGCCA CTTCGCTACC CCTCCAGCTT 180
 35 ATTCATATAA TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT 240
 GCTTGTAAGG CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG 300
 ACTCGAACCC GTGTTACCGC CGTGAAAGGG CGtGTcTTAA CCGCTTGACC AAGGAGCCAT 360
 40 GGCTCaCAGG TAGGACTCGA ACCTACGACC GATCGGTAA CAGCCGATAG CTCTACCACT 420
 GAGCTACTGT GGaTTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTtCG 480
 GACTrACCAT CGACGCTgAA GGAGCTTAAa CTTCTGTGTT CgGCATGGGa ACAGGTGTGA 540
 45 CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTGAATTT GATGACATTG CAAAAnTAGn 600
 TTAGTAAGTA AAAGTGGATT TTGGnTTh 628

(2) INFORMATION FOR SEQ ID NO: 3852:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3852:

5 TAAAGATTTA AAAGTAGCTG TTATTGGnAC AGGTCGAATT GGCCGTGTAG TAGCCGATAT 60
 ATTTGCCAAT GGTtATCAAA GTGATGTGGT CGCATACGAC CGTTTCCTAA TGCTAAAATT 120
 GCAACGTATG TCGATTACAA AGATACGATT GAGGAAGCGG TTGAAGGTGC TGATATCGTG 180
 10 ACATTACATG TACCTGCAAC GAAATATAAT CATTATCTAT TTAATGCTGA ATTATTTAAA 240
 CATTTTAAAA AGGGCGCnTA TTTGTCAATT GTGCGAGAGG TTCTTTAGTA GGATACTAAG 300
 GCGTTATTAG ACGCATTAGA CAATGGTGTG ATTAAAGGTG CAGCACTTgn TTACGTATGG 360
 15 ATTTGGAACG GCAAACTTTT TCCCAAGTGG TCCAAAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3853:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3853:

25 TCTTAAACAT TAGCCACAGC TAATTGTGAC TTA AAAATAG GAATACATGA GTAAACTCA 60
 30 TCATAAGAAA TACTAATTTT TATAGAAAAA GTATTACTTT ATCGTTGTCC CACCCCAACT 120
 TGCACATTAT TGTAAGCTGA CTTTCCGCCA GCTTCTGTGT TGGGGCCCCG CCAACTTGCA 180
 CATTATTGTA AGCTGACTTT TCGTCACTTG CTGTGTTGGG GCCCCGCCAA CTTGCACATT 240
 35 ATTGTAAGCT GACTTTTCGT CACTTnCTGT GTTGGGGCCC CGCCAACTTG CATTGTCTGT 300
 AGAAATTGGG AATCCAATTT CTGCTATGTT GGGGCCCA CA CCAACTnC GCATTGCCTG 360
 TAGAATTTCT TTTCGAAATT CTCTGTGTTG GGGGCCCA 400

(2) INFORMATION FOR SEQ ID NO: 3854:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3854:

50 GTGCAATCTG CGTTAACAAA TGTAATCGT GTCAATGAGC GATTAACGCA AGCAATTAAT 60

55

GAAATCAATA nATCAGTAAC TACTGATGGT ATGACACAAT CATCAATCCA AGCATATGAA 180
 AATGCTAAAC GTGCGGGTCA AACAGAATCA ACAAATGCAC AAAATGTTAT TAACAATGGT 240
 5 GATGCGACTG ACCAACAAAT TGCCGCAGAA AAAACAAAAG TAGAAGAAAA ATATAATAGC 300
 TTAAAACAAG CAATTGCTGG ATTAnCTCCA GACTTGGCAC CATTACAAAC TGCAAAAnCT 360
 CAGTTGCAAA TGnTATTGTC AGCCACGAGT ACGGCTGGTA 400

10 (2) INFORMATION FOR SEQ ID NO: 3855:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3855:

TGTGTGAAAA ACCAATGGCT GAAAACGACA GCAGAAGCTC AAAAAATGAT AGATACAGCT 60
 AAATCAACAG GTAAAAAATT AACAATAGGT TATCAAAATC GTTCCGAGC AGATAGTCAA 120
 25 TTTTACATC AAGCAGCGCA ACGTGGCGAC TTAGGAGACA TTTACTTCGG AAAGGCACAT 180
 GCCATTCGTC GTCGAGCAGT ACCAACATGG GGTGCTTTC TAGACGTAGT AAGCTCAAGG 240
 TGGAGGACCA TTAATCGATA TCGGTACACA CGCTTTAGAT TTAACGTTAT GGATGATGGA 300
 30 TAnTTATGGA ACCAGAATCA GTGATGGGTT TCAACATTCC ATAAATTnAA TAAACAGCCT 360
 CATGCGGGCA AACGCTTGGG GTTTCAGGnG TTCCAGATGG 400

35 (2) INFORMATION FOR SEQ ID NO: 3856:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3856:

CGTTCTCAAT AGAATGATTT AAATCTTCGA TTTCTTTATC TAAATGACTA CCAATTAAAT 60
 CTATTTCTTC TATTGTTAAA TCGCTATCTC CATCTTCTTT TATCTCTGGT ATTATTTTTT 120
 CTTCAACTAA GTCACGATAT AATGTTTTTG AATTTTCGTT CAATTTGAT TCGTGATTTT 180
 50 GAATACTTTT CTTCACACA AATGTATATC TATTGGCATT AGCTTCTACT TTTGTACCAT 240
 CAATAAAAAT TGAATTATTA TCAATAAGAT TTTGCTTTAA ACATTGACTA TGGAAGTGAA 300

TATAAGAAGG nGGTTGGAnC nTGAGCGAAC CACAnCATCC

400

(2) INFORMATION FOR SEQ ID NO: 3857:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3857:

15	GGCATACCAT GGTCAAACGC GTGATGATCA AGTAACATCA CATGTTCAAC ATATTTTTGA	60
	AGTTGTGAAT GCACATGGTA AACATTTTTG TGCATTACCA CGTGAAGATG AAGATATTGC	120
	AAAATGGCAG GCACAAGGTG TACAAACATT TATTTTAGGT GATGATCGCG GAAAAATATA	180
20	TCGCCATTTA AGTGCATCTC TAGCGACGTC TAAACAGAAA GGGGATGAAG GCTAATGCGT	240
	AAAGTTCAAC CTGTTATTGA ACAATTAAAA GCACAATCTC ATCCAGTTTG TCATTAnATC	300
	TATGATTTAG TCGGACTGGG ACATCATTTG CAnCATATTA CATCGnCCTT GCCGAGTAAT	360
25	TGTCAAATGT ACTATGCAAT G	381

(2) INFORMATION FOR SEQ ID NO: 3858:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3858:

	GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG	60
40	ATGAGGTTAA TAGGTTTCGAG GTGGAAGCAT GGTGACATGT GGAAGCTGAC GAATACTAAT	120
	CGATCGAAGA CTTAATCAAA ATAAATGTTT TGCGACAATT CACTTTTACT TACTATCTAG	180
	TTTGAATGT ATAAATTACA TTCATATGTC TGGTGAATAT AGCAAGGAGG TCACACCTGT	240
45	TCCCATGCCG AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC	300
	GCTAGAGTAG AACGTTGCCA GGCAAAAAAT GGATGCCGAT GGAGCCGCAT TGAGACCGCA	360
50	GGnCTnTTTG TTTTTTATGT CTAAAACGTC CAAATTAAnA	400

(2) INFORMATION FOR SEQ ID NO: 3859:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3859:

	GTTTATTAAT CGTGTCATTA GCATCTTTAT AATTGCTTCT AATCGTATTC AAATCACCTA	60
10	ATGTTAAATC TGTTTAAACA TTATTTTGAA TTTTCATTCAT GCATCTGAAT CTGAATCGCT	120
	ATCTGAATCT GAGTCGTTGT CTGAGTCCGA nTCGCTATCT GAnTCTGAGT CGCTGTCTGA	180
	ATCTGAATCG CTATCCGAGT CTGAGTCGCT ATCTGAGTCT GAGTCGCTAT CTGAATCTGA	240
15	ATCGCTGTCT GAGTCTGAAT CGCTATCTGA GTCTGAATCG CTGTCCGAAT CTGAGTCGCT	300
	ATCTGAATCT GAATCGCTAT CTGAATCTGA GTCGTTGTCT GAGTCCGAAT CGCTATCTGA	360
	ATCTGAGTCG CTATCTGAGT CTGAGTCGCT ATCTGAATCT GAGTCGCTGT CTGAATCTGA	420
20	ATCACTGTCT GAGTCTGAGT CGCTGTCTGA AGTCTGAATC GCTGTCAGAA TCTGAGTCGC	480
	CAACTGAGTC TGAATCTGAA TCACTGGTCT GAGTCCGAAT CGCnATCTGA ATCnGAATCG	540
25	CnAACCGAGT CCGAAGCCGC nAATCCGAAT CTG	573

(2) INFORMATION FOR SEQ ID NO: 3860:

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3860:

	GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GATCGAACCG	60
40	CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA	120
	CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT	180
	ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT	240
45	CTTGATCCGT AGTCAAACGC TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGnA	300
	AAATGGTGCC GAGGnACCGG GAATCGGAAC CGGTACGGTT GATnCACTCA CCGGCAGGAT	360
	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGnGC	400

50

(2) INFORMATION FOR SEQ ID NO: 3861:

(i) SEQUENCE CHARACTERISTICS:

55	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3861:

5 TGTTCGACT AAACCATTAC CTATCGCACA TATGACGAAA CCAATGATAA CTGCAATGAC 60
 ATATTGTGAT GCCAATAATT GAGTCATGCT AATAATAGTG ATGCCGATGA CAGGGAACAA 120
 CGGACCAATG ATGAGCATCA ATTTGCCACC GAAACGTAAT GTTGCTTTTT CACCTAAACG 180
 10 AATCATCGCA ACTGCCACAA TGGCATATGG CAATGTAACA nGTCCAGATT GCGCACTGAT 240
 AAACCAAGGT GTGTTTGAGC ATATATGAAA AAGACCACTG TTACGCCTAG ACCGCTATTT 300
 AAAACAAAGT TATTTAAAAA TGCACCAATG GAACGGACGG TTGCGTAATA CTGGAGAAnt 360
 15 CAATAAAAGG TACTTCCATG TCCGACGTTT CGATGGATGG 400

(2) INFORMATION FOR SEQ ID NO: 3862:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3862:

GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGA ATTAGGGATC 60
 30 GGTACTTTAT ATGAAGACGT GCTGCTTCCA TTAAATGAGT GATGCGATTT TGGCATGAAG 120
 GTCACCTTAA ATGTACATTG TTGTAATAAA ATTGCCTATA AATTTTTAGC ACATAAAATA 180
 AGAGGAGCCA ACCATTGTGA GACTATAACA ACGGTTGGCT CTTTAATTGT AAAAAGAAAA 240
 35 CCATACGCTA TCGGTATGGT TCAGAAAAGG TCTACCATTG TCACCAAAAA TGCATCTCTA 300
 CGTGCTAGAA TAAATATTGG TCAGCCAACC AAAATAATCC ACACGGGGAG ATGCTATTTA 360
 ATGTCCTCCT GACACCAACA GTTAGCACCA TACAAAATGG 400

(2) INFORMATION FOR SEQ ID NO: 3863:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3863:

TCGGCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 60

CTAGCGGAAC GTAAGTTGGC TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC 180
 GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG 240
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 300
 TGTTCGCTTT TTATTTTGAC GTTTTAGACA TAAAAAAAG AGACCTTGC GTCCTCAAATG 360
 10 CGGCTCATCG CATnCATnT TGCCGGCAAC GTTCTACTCT 400

(2) INFORMATION FOR SEQ ID NO: 3864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3864:

GTAATATAGA ATTAAAGAAT TATAAAAATA TAATCCTGAT TAGCTTGTTG TCAAGTCATC 60
 GTTCATAATG AAGATATCAC GTTCAATTGT ATTGTTTGTT TATGGGAAAT GAATTAATGT 120
 25 AATAGTATAT GTATGCGGTT ACATAAAAAG CGAACATCTA ACCTGATATT TAAATGAACC 180
 TGACGCTCAA TCAACTAATT TACAACCGTA TTTTATAAT CAACCATAAA GGAGGAGATA 240
 30 GAAAATGAAT AGTGCAAAAT TGATTGATCA CACTTTATTG AAGCCTGAGT CAACACGTAC 300
 GCAAATCGAT CCAAATCATC GATGAAGCGA AGCATACCAT TTAAATCTG TATGTGTGAA 360
 TCCAACGCAT GTTAAAnGTG CCAGCAGAGC GACTAGCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3865:

GCAGCACGTC TTCATATAAA GTACCGATCC CTAATTCAAC GCATGTAGTA CCACATCTTC 60
 AAAGCTTGAT AGTTCCCATG CGCACACCAC GTTTCATACT AGCTATGCGA GCTCAACTTG 120
 50 GTTCATAAAC TCTTTAATAT AAGTCAATGT TTCAACCATC GCTGGTGGTC TTGGCACATG 180
 TCCTTCTGCC ATTTGATAAA ATGTTTCATG CGTGGCACCT TTAACTCTA GTTGGTCCGC 240
 TAAATAATAC GCATGATGAA TACCAACTTG CTGGTCTTTC CCTCCATGTA CAATTAATAT 300

TTTTTTCGGA TGACCAATCA TTCTTCGTAG CATGCCTCTT

400

(2) INFORMATION FOR SEQ ID NO: 3866:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3866:

15	AAGTCAATAA CTTTTTTTAT CTTGTCCATT TTATTTTITA ACCAAAATTT GATTAAAAAA	60
	CTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTCGA nCTACCATCG ACGCTAAGGA	120
	GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA	180
20	TATGAATGTA ATTTATACAT TCAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA	240
	AACATTATTT TTGATTAAGT CTTGCATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT	300
	GCTTCCACCT CGGAACCTAT TAACCTCATC ATCTTTGGAG GGGATCTTAT AACCGGAGGT	360
25	TGGGGnAAAT CTCATCTTGA GGGGGGGCTT CCAGGCTTAG	400

(2) INFORMATION FOR SEQ ID NO: 3867:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3867:

	CACCTATAAT CGTTTAAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT GnCGATTGGA	60
40	TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC	120
	TGTGATGGGG AGAAGACATT GTGTCTTCGA GGTGTTGAT TTCACACTGC CGAGAAAAGC	180
	CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC AGGTAGTCAA GATGAGAATT	240
45	CTAAGGTGAG CGAGCGAACT CTCGTTAAGG AACTCGGCAA AATGACCCCG TAACTTCGGG	300
	AAGAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC ATGAATAGGC CCAAGCGACT	360
50	GTTTAnTCAA AACACAGTCT CTGCTAAACC TAAGGATGTA	400

(2) INFORMATION FOR SEQ ID NO: 3868:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3868:

TTCTTTGGAA ATAGTAACGT TGAAGTTGTA CTCACTGGTG ATACATTTGA TCACTGTTTA 60
10 GCTGAAGCTT TAACTTATAC AAGTGAACAT CAAATGAnCT TTATAGATCC ATTCAATAAT 120
GTTCATACAA TTTCTGGACA AGGTACGCTT GCTAAAGAAA TGCTAGAACA AGCAAAGTCT 180
GACAATGTTA ACTTTGATTA TCTATTTGCC GCAATTGGTG GTGGCGGTTT AATTTCAAGT 240
15 ATTAGTACTT ACTTTAAAC CTATTCACCT ACCACGnAAA TTATAGGTGT TGAACCTTCA 300
GGTGCCAAGT AGTATGTGAT GGAATCTGTT GTGAAATATT CAGGTAGTCA CATTGCCCTA 360
AnTCGATAAA TTTGTGGACG GTG 383

20

(2) INFORMATION FOR SEQ ID NO: 3869:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3869:

CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA CTTAACCCAA CATCTCACGA CACGAGCTGA 60
CGACAACCAC CACCTGTCAC TTTGTCCCC GAAGAAGnGC TCTATCTCTA GATTGTCAAA 120
35 GGATGTCAAG ATTTGGTAAG GTTCTTCGCG TTGCTTCGAA TTAAACCACA TGCTCCACCG 180
nTTGTGCGGT TCCCCGTCAA TTCCTTTGAG TTTCAACCTT GCGGTCGTAC TCCCCAGGCG 240
GAGTGCTTAA TGC GTTAnTG CCAGCACTAA GGGGCGGAAA CCCCCTAACA CTTAGCACTC 300
40 ATCGTTTACG GCGTGGACTA CCAGGGTATC TAATCCTGTT TGATCCCCAC GGTTTCGCAC 360
ATCAGCGTCA TTTACAGACC AGAAAGTCGn CTTCGGCAAT 400

45

(2) INFORMATION FOR SEQ ID NO: 3870:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3870:

GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC TCATGCTGGG 120
 TTTCCCCATT CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 180
 5 GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGC GC CCTTAATAAC 240
 TTAATCTATG TTTCCATCCT ACAGGAAACG CGTTATTAAT CTTGTGAGTG TTCTTTGAA 300
 CATGAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 360
 10 GCTTGGTAAA AGCnnGn 377

(2) INFORMATION FOR SEQ ID NO: 3871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3871:

ATAACGTTGC CCCTCCCATG TATATCCTAC CCAAACATGA CCATCTTGTA ACATCACTTC 60
 25 TGTATAATCA CAATACCCAC CAGGTTGGAA CTGATAACCC ACTGGACAAG ATAAGAATGG 120
 CCCCACTTTT CTTACTGTGA TTGGTTGATT GCCGTTTGTG AATCTAGCAC TTTCTTCCAT 180
 GTAGTAAGTA CCATATTTAT TACGTTTCCA TGCACTTGCA ACTGGTTTAA CTGTATTACT 240
 30 TGAAGCGCTT GACTCATTAG AGACAGTGGC AACCGGTATT TTACCATCCA TGTACGCCCT 300
 AAATCTGCTT GATAAAGTAG TCTTTTAAGT TGCAACCGCT TGTCTTCTGG GCAATAGACC 360
 35 GCGAGTTACn GGGGTCCAAA CCCnTGGTGT AAAAnCGAAC 400

(2) INFORMATION FOR SEQ ID NO: 3872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3872:

CGCTACACTA CGAGACCATT AGTAAACGC AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 60
 TTAAGCCCCT GTCGGTTTTT AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120
 50 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG TTATGAGCCG TTAGCTCTAA 180
 CCAACTGAGC TAAAGGTCCT AAATATAATT TTACAACTAA TAAATAGTGG CGGTGGAGGG 240

GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GGATCGAACC GCTGTACCTC 360
 CTGCGTGCAA ACGGGCGCTC TTCCCAGCTG nAGCTAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3873:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 584 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3873:

ACAGCTCAG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 60
 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCTTCG 120
 GTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGTT TCGTCAGATT 180
 CAAnnGTTTT CAATCGCCAA GCCATTTTTC TTTGTGTTTA CTTTTATTT TGACGTTTTA 240
 GGCATAAAAA AAAGAGACCT TGCGGTCTCA AnTGCGGCTC ATCGCATCCA TTTTTGCCT 300
 GGCAACGTTT TACTCTAGCG GAANTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 360
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 420
 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 480
 GCCATTTTTC TTTGTGTTTA CTnTnATTT TGACGTTTTA GACATAAAAA AAAGAGACCT 540
 TGCGGTCCAA ATGCGGGCTC ATCGCATCCA TTTTTGCCT GGGC 584

(2) INFORMATION FOR SEQ ID NO: 3874:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3874:

TTTGCTGGC AACGTTCTAC TCTAGCGGAA CGTAAnTTGG CTACCATCGT CGCTAAAGAC 60
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 120
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180
 TCGCCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 240
 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCTGGCA ACGTTCTACT 300

GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT

400

(2) INFORMATION FOR SEQ ID NO: 3875:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3875:

TCTGCTAATT TAAAAATGAT ATTTTCTATC TTTTCTTTAT TATTAACGTC TAATGCACTG 60
 GTCGATTCAT CTAATAAAG AATATCCGGT GTATACATCA GTTGGCGCGC TATAGCAATT 120
 CTTTGCCGCT CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA 180
 CCGACATCTT TAATTAATTG CTTTGACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT 240
 GATGGGAATA TCATGTTATC TTCAATCGGT CACCAAACAA GTCACTTTGC TGCATCAAAT 300
 AACTGATTGC TTGACGCCAA TTCTTCCGGG GCATAATnCA TATAGGGGTT ACCTTAAAAA 360
 TAAAGGTCCT CCACTAGTTG GCCTAnACnA ATTACATAAn 400

(2) INFORMATION FOR SEQ ID NO: 3876:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3876:

AGATAGACTT TCTGGTGAAG ATACACGTGA AGGTATGACA GCAATTATAT CTATCAAACA 60
 TGGTGATCCT CAATTCGAAG GTCAAACGAA GACAAAATTA GGTAATTCTG AAGTGCCTCA 120
 AGTTGTAGAT AAATTATTCT CAGAGCACTT TGAACGATTT TTATATGAAA ATCCACAAGT 180
 CGCACGTACA GTGGTTGAAA AAGGTATTAT GCGGGCACTG CACGTnTTGC TGCGAAAAAA 240
 GCGCGTGAAG TAACACGTCC GTAAATCAGC GTTAGATGTA GCAAGCCTTC CAGGTAAATT 300
 AGCCGATTGC TCTAGTAAAA GTCCTGAAGA ATGTGAGATT TCTTAGTCGA AGGGGCTCTG 360
 CCGGGGGGTC TACAAAATCT GGTCTGACT CTAGACCGCA 400

(2) INFORMATION FOR SEQ ID NO: 3877:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3877:

ACCAATTTCT CCTTTGTATC CGCCATCTTT AAATAATTTT ACTGCTCTAG CATGAGCCAC 60
10 CATCATGTTA TGTGATTGGA ATACTTTTTC AAAATCATAT TTAATACCTG GAGGGAATTT 120
ACCTACTAAA TATTGACCAT CACCAATAGG TCCAATTTCA TTGAATGTAG TCCAATATTT 180
TACTTCTGGG AATTCTTTAA AACAATATTC AGCATAATCT ACAAAGTAGT CAATCGTTTT 240
15 ACGnTTTAGA AAATCGCCAT CTTTGGTGGT ACACCTTCTGG GnGTATCAAA ATGnTGCAAT 300
GTTACAAATG GTTCAACATG ACGGTTTATG GnCACTCTGC AAATAACCTT ATGGTAATAC 360
TCAACACCTT AGGGGTAAAC TTCGGCCATA TCCCTTTTGG 400

20

(2) INFORMATION FOR SEQ ID NO: 3878:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3878:

ATTAAAGCAG TTTCTGGATC TGGTAAAAAT GGTCGTATTA CAAAAGAAGA TG TAGATGCA 60
TACTTAAATG GTGGTGCACC AACAGCTTCA AATGAATCAG CTGCTTCACT AACAAGTGAA 120
35 GAAGTTGCTG AAACCTCTGC AGCACCTGCh GCAGTTAACA TTAGAAGGCG ACTTCCCAGA 180
AACAACCTGA AAAAATCCCT GGCTATGCGT AGAGCAATTG CGAnAACATG GGTTTAACTC 240
TAAGCATACT GCACCTCATG TAACATTAAT GGATGAAATT GGATGTTCAA GCATTATGGG 300
40 GATCACCGTA AGAAATTTAA AGAAATCGCG GCTGAACAAG GTACTAAGTT AACATTCTTA 360
CCTTATGTTG TTAAnGCACT GTTTTCGGCA TGGnAAAAAT 400

45

(2) INFORMATION FOR SEQ ID NO: 3879:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3879:

55

TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 120
 TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 180
 5 GCTACCATCG ACGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 240
 CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT TCTCGTTTCG 300
 TCAGATTCAA ACGTTTCACT TCGCAAGCCA TTTTCTTTG TGTGCTTTT ATTTGACGTT 360
 10 TAGACATAAA AnAAGAnCCT TGCGGnCTCA ATGCGGCCAT 400

(2) INFORMATION FOR SEQ ID NO: 3880:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3880:

TAGGTGTAAA TCCTGCGATT CGATCTGGAC CATATTTTTT TATTGTATAC AGTAATTGTG 60
 25 CTGCGATTAT CTCTGTAACG TCTTTCCAAT TTGAACGCAC GTGCCCTCCC ATACCTCGGG 120
 CTTGCTTATA TTGTTTGGCT TTGTCTTCAT TTTCAACAAT AGACGCCCAT GCAGCAACGC 180
 GATTACCATT GTTTTCTTCT AATGCTTCAG TCCATAAATC CCAGAGTTTT CCACGAATAT 240
 30 ATGGATATTG ATTCTGAACG GACTGTATCA TACCAAGAGA ATGACGCACT CGTGGACATC 300
 CTCTCGGTCA TATTCAGGCA TATCCGGACA CAACTTGGAT AGCAGTTGTG ATTTCCCAGG 360
 35 AATCACACCA TTTCACAAAC TTCCAGACAT GGCTGACAGT 400

(2) INFORMATION FOR SEQ ID NO: 3881:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3881:

TGAGTAGCGA AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAGGTTT CCAGAGGAAG 60
 50 GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA AGCTGAGGCC GACAGnGTAG GCGATGGATA 120
 ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCAGTAGGA 180
 TAGGCGAACG TGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC 240

TCACACTGCC GAGAAAAGCC TCTAAGATAA GAAAATTAGG TGCCCGTACC GCAAACCGAC 360
 ACAGGTAGTC CAAGATGGAG AnTCTnAAGG TGGAGCGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3882:

CATCCCCAAC TTGCACATTA TTGTAAGCTG ACTTTTCGTC ACTTCTGTGT TGGGGCCCTC 60
 ACCCCCAATC GCATTGCCTG TAGAATTTCT TTTGCGAAAT CTCTGTGTG GGGCCCCTGA 120
 CTAGAATTGA AAAAAGCTTG TTACAAGCGC ATTTTCGTTT AGTCAACTAC TGCCAATATA 180
 ACTTCGTAGA GCATAGAATA TTGATTTATG TCCCAGCCTG AGTTAATTTT CTATAAAAGT 240
 ATATTTAATT TGCCTTTATA CCGTCAAAC TCACTTTAGC TTTGTCAAAC CCCTTTCTAT 300
 TAAGTTTTC GAAATAAACC TATCTTAAAA TATAAAAAA TCGAGAATTC GTAGTTTAAT 360
 AACGAAATTC TCGTTCTTAT CCTTTTGaAT aTACTCAATT TTCCACAAAA ACAAACAAGT 420
 AGTATATCTG TTCTAGCTAC TAGAATGACA TACTACTTGT TATTAAAATA CTTAACTAAA 480
 CTTTATTAGT TATCTTTnTT CTCTATATTT CTACGTGGAC TGACGCTTTT CAnGAATGTC 540
 AGATTCTATA TCTTCTTGGT TGGACTCCTG GATATATTCT TGGTAAGCGG ATGGTTTATT 600
 CGGAGTCAA 609

(2) INFORMATION FOR SEQ ID NO: 3883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3883:

ATATATTGGC GGACATAACG ATGTACTAGC AGGTGTCGTA ACCGTCAAAG ATGAATCACT 60
 CGCGCAACAG TTGTTTGATT TTCACAACAT GACTGGCGCA ACACTTTCAC CAATAGATAG 120
 TTATTTGTTG TTACGTGGAC TTAACACTTT GCATTTACGC ATTGAGCGTG CGCAATCAAA 180
 CGCTAGAAAA CTTGCTAAAA AATGTCAGTC ACTTCAAGCA ATTGACGAAt ACTaTATAGC 240

GAAAATTTAG ACATTTGcAT TTTTGCAGAA AGTTTAGGag GTACKGAAAC ATTAGTGACC 360
 TTCCCTTACA CCCAAACACT GTTGATATGC CAGT 394

(2) INFORMATION FOR SEQ ID NO: 3884:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3884:

CGATTATGA ATTAACAGAA TACGGACCAG AAACGATAAC ACCAGGTCAT CGAGACGAAT 60
 TTGATCCGAA GTTACCAACA GGAGAGAAAG AGGAAGTTCC AGGTAAACCA GGAATTAAGA 120
 ATCCAGAAAC AGGAGACGTG TTAGACCACC GGTGCGATTAG CGTAACAAAA TATGGACCTG 180
 TAAAAGGAGA CTCGATTGTA GAAAAAGAAG AAATTCCATT CAAGAAAGAA CGTAAATTTA 240
 ATCCTGATTT AGCACCAGGG ACAGAAAAAG TAACAAGAGA AGGACAAAAA GGTGAGAAGA 300
 CAATAACGAC GCCAACACTA AAAANTCCAT TAACTGGAGA ATTATTAGTA AAGGTGATCG 360
 AAAGAGGAAT CACAAAAGTT CcTTTTATGA TTAACAGATA 400

(2) INFORMATION FOR SEQ ID NO: 3885:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3885:

TGAGCGGATT ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120
 CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG TCGCTCTAA CCAGCTGAGC 180
 TATAGGCCCA TTTTTTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTCACG 240
 TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG 300
 CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 360
 GACGGCTAGC TCCCAAAGG GTACTnCCAn CGGGnTTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3886:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3886:

10 TACGGTAGGT GGCAAGCAGT TATCCnGGAA TTATTGGGCG TAAAGCGCGC GTAGGGGTTT 60
 TTTTAAGTCT GATGTGAAAG CCCACGGCTC AACCGTGGAG GGTCATTGGA AACTGGAATn 120
 CTTGAGTGCA GAAGAGGAAA GTGGAATTCC ATGTGTAGCG GTGAAATGCG CAGAGATATG 180
 15 GAGGAACACC AGTGGCGAAG GCGACTTTCT GGTCTGTAAC TGACGCTGAT GTGCGAAACG 240
 TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300
 20 GTTAGGGGGT TTCCGCCCCCT TTAGTGCTGC AGCTAACGCA TTAAAGCACT CCGCCTGGGG 360
 GAGTTACGAC CGCAAAGTTT GGAAACTCAA AGGGAATTGG 400

(2) INFORMATION FOR SEQ ID NO: 3887:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3887:

35 ATTTTTTAAT TTTCATGCAA ATTTTTAAGC ACCATATAAT GCCTACCAA TTTCAATAAT 60
 CTTTGTTGCC GTTTAAATAA TGTGAATGTC AATAAATTCT CCAAAGTAGT CGAAAATAAA 120
 GGGAGTnGGA CATAAATCCC TAAAAAACA GCAGTAAGAT AATTTTCAAT TAGAAAATAT 180
 40 CTTACTGCTG TTCTCTATTT ATACAATACT TCGTATTGAA TGGCTTCGCT TTCCnAGGGT 240
 GCCGTCTCAG CCTCGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 300
 ACGTATTAAAC ATGGAATTTT ACTTTTACAT ACTTTAAAAA ATAAGnCACT TTGGCCAACT 360
 45 TACTACTACCA TAGGAACCCT GGTAGGAATC CCCCAAATGn 400

(2) INFORMATION FOR SEQ ID NO: 3888:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

ATACGACAAT CACAGCAATA ATAATTGCTT TAGAAAGTCG TGCCGAACTG GAACTTACAA 60
 GTCTAGTTCG AACACACACT GATGTGAGTG GTTTTATTTA TTTTAAACAT GAACAATCAG 120
 5 ATAAGTTACT AGCATTAGCA AATATTATTA AATCAAAGGG CTCGATTCA TAAAATTAAA 180
 ACAATGATTA AAATTAGACG TGTAATGTT AAATTCTAAA ACGGAAATAA CCACCATCCC 240
 10 ATTAAACCAC TTTnATnGTT CAATCACTAT ATTTACACACA GCTTCATTAA TAAAACGACT 300
 TGCTTCAACC CGCTTCAACT TCAACTGGCT TCAACTTCAG CCTACTTCAT TCAATnACAA 360
 AACGAATCCG CTTTCATCCAA AATCAnCCAT TCTAACGCAC 400

(2) INFORMATION FOR SEQ ID NO: 3889:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3889:

CCATGCnAGA CGCATACATT GTaGCTTATG GgCGTTCAGC gCAGCGAAmG aAAGCAAGGC 60
 GCATTATTCC ACGAAAGACC TGATGATGTC GCAGCCAAAG TATTACAAGG CGTATTGAAA 120
 30 CGTATTGACG GAAAATTCAA TAAGAATATG ATTGAAGATG TCATTGTTGG TACGGCTTTT 180
 CCAGAAGGAT TACAAGGCCA AAACATTGCA CGAACGATTG CATTGCGTGC GGGATTATCT 240
 GACACGGTAC CGGGTCAAAC AGTGAATCGC TACTGCTCAT CAGGATTACA AACCATCGCG 300
 35 ATTGCAGCCA ATCAAATTAT GGCTGGTCAA GGAGATATAC TTGTAgCTGG TGGCGTTGAA 360
 TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA ACAATCCaAC CTTwACAATA 420
 tGaTGATATA GGTGCGTCCA TATnCTATG GGTtTnAAnT GCTGGAAAAT GTTAGCCTnC 480
 40 CCAAT 485

(2) INFORMATION FOR SEQ ID NO: 3890:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3890:

AGGCAGATGC TCTCCAGCT GAGCTAATTC TCCAAAATAA TGACTCCTAC GGGACTCGAA 60

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 180
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTA CTCTAGC GGAATGAAT TCGGACTACC 240
 5 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT 300
 ATAGTCACCA GACATATGAA TGTAAATTTAT ACATTCAAAA CTAGATAGTG AAGTAAAAGT 360
 10 GGTTTTGCnT CGCAAAACAT TTATTTTGn 389

(2) INFORMATION FOR SEQ ID NO: 3891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3891:

CAGATGTTTA AGTCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA AAAATGGAGC 60
 AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT ACCGCTGAAC 120
 25 TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGCTn AGATCCTAAG 180
 TCTAGTGCCT CTGCCAATTC CGCCACACCC GCAAAATGGTG AGCCATAGAG GATTGGAACC 240
 30 TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGG AGCTAATGGC TCTCCATGG 300
 TGCCGGCCAG AGGACTTGAA CCCCCAACCT ACTGGATTTA CAAGTCAGTT TGCTCTACCA 360
 ATTGGAGCTA GGGCCGGGCA ATATGGTAAG AATAAATTGG 400

(2) INFORMATION FOR SEQ ID NO: 3892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3892:

CTCTCGGTGG TCGTGCTACA ACTGGTAAAA ATGTACATGT AGGGGCTGGC GCAGTATTAG 60
 CAGGTGTGAT TGAACCCCTT AGTGCTTCAC CGGTTATAAT CGAGGATGAT GTATTAATCG 120
 50 GTGCAAATGC AGTTATTTTA GAAGGTGTAC GTGTTGGTAA AGGTGCTATT GTTGCAGCTG 180
 GCGCGATTGT GACACAAGAT GTACCAGCTG GTGCAGTTGT TGCTGGTACA CCTGCAAAAG 240
 TGATTAAGCA AGCTTCTGAA GTACAAGATA CTA AAAAAGA GATTGTAGCA GCATTAAGAA 300

CCACCnTAAT GGTnTAGCAT TGAATAAACT TATGnnCCCC

400

(2) INFORMATION FOR SEQ ID NO: 3893:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3893:

GAATGTAGTT GTGGTAAATA CAAACGTGTT CGCTACAAAG GCATGGTCTG TGACAGATGT	60
GGAGTTGAAG TAACTAAATC TAAAGTACGT CGTGAAAGAA TGGGTCACAT TGAACCTGCT	120
GCTCCAGTTT CTCACATTTG GTATTTCAAA GGTATACCAA GTCGTATGGG TATTATTACT	180
TGACATGTCA CCAAGAGCAT TAGAAGAAGT TATTTACTTT GCTTCTTATG TGTGTAGAT	240
CCAGGTCCAA CTGGTTTAGA AAAGAAACT TTATTATCTG AAGCTGAATT CAGAGATTAT	300
TATGATGAAA TACCCAGGTC AATTCGTTGC CAAAAATGGG TGCCAGAAGG TCATTAAAAG	360
ATTTACTTGA AGnnGATTGA TnCTTGACGA GGGAACTTnA	400

(2) INFORMATION FOR SEQ ID NO: 3894:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3894:

CACGTGAAGT TAGAGATACT TCATTACGTG TACCTCACGG CGCTGGCGGT ATCGTTCTTG	60
ATGTAAAAGT ATTCAATCGT GAAGAAGGCG ACGATACATT ATCACCTGGT GTAAACCAAT	120
TAGTACGTGT ATATATCGTT CAAAAACGTA AAATTCATGT TGGTGATAAG ATGTGTGGTC	180
GACATGGTAA CAAAGGTGTC ATTTCTAAGA TTGTTCTGA AGAAGATATG CCTTACTTAC	240
CAGATGGACG TCCGATCGAT ATCATGTTAA ATCCTCTTGG TGTACCATCT CGTATGAACA	300
TCGGACAAGT ATTAGAGCTA CACTTAGGTA TGGCTGCTaA AAATCTTGGT ATTCACGTTG	360
cATCACCAGT ATTTGaCGGT GCaAACGrTG aCGATGTATG GTCAnCAATT GAAGAAGCTG	420
GTATGGCTCG TGATGGTAAA ACTGTACTTT ATCGATGGAC GTACCAGGTG ACCCnTCCGA	480
TAACC	485

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3895:

GAACAACATA CCTTTGTTTG TTGATTCTTC TCCACCTGTT TCAAGTAGTT CAGATTTCTT 60
 AGATTGTGGT TTTTATAGTT GTGCCACTGc TTAAACCTTT TCATTGATTT CAATAACAGG 120
 TGTTACTACT TTACCTTGTT CCACTGGTTT AGAAGGCTTT TTAGGTTCTT CTTTGGCAGG 180
 TGGTACTGGT TTACCAAGTT CAGCTGGTAC CTCTGGTGTG GCGGGTGTG GAGTTTCTGG 240
 CTCCTCGGC ACTTCTGGTG TCGGTGGTGT TGGTGTTC GGTCACTTG GTACTTCTGG 300
 TGTTGGTGGc GTTGGTGTTC CCGGCTCACT TGGTACTTCT GGTGTCGGTG GCGTTGGtGG 360
 CACGATTGGA gGTGTTGTAT CTTCTTCAAT CGTTTGTGA CCTTCATTTT GGGCCGCTTA 420
 CTTTGGGAA GTGTATCTTC TTCAAAGTCA AACTAATGT GGTCCACCGG AATTGATAAC 480
 TGGGGTTAAC CTTAAATTGG AACCTCC 507

(2) INFORMATION FOR SEQ ID NO: 3896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3896:

CTAGCGGAAG TAATTGGCTA CCATCGTCGC TAAAGACCTT nGGnGACTTG TGACAATCGC 60
 TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 120
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTCACTTCG CCAAGCCATT TTTCTTTGTG 180
 TTTACTTTTT ATTTTGACGT TTTAGGCATA AAAAAAGAG ACCTTGCGGT CTCAATGCGG 240
 CTCATCGCAT CCATTTTTTG CCGGCAACG TTCTACTCTA GCGGAAnGTA ATTGGGCTAC 300
 CATCGTCGCT AAAGACCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 360
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 400

(2) INFORMATION FOR SEQ ID NO: 3897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3897:

	TTGAAGAAGA TCGCGATGAC TATACAATCA ATATCGAGTA TAATACCGAT TTATATCACT	60
10	CAGAAACAGT TCGTCACATG GGTAATCAAT GTATGATTAT GATTGATTAT ATTTTGAAGC	120
	ATCAAGATAC ACTACAAATT TGTGATATAC CAAACGGCAC GAGGAACTTC TAAATTGGGT	180
	CAATACGCAT GTTAACGATC GAATGCTTAA TGTCCCGGGA AATAAATCTA TCATAAGTTA	240
15	CTTTAATGAA GTTGTCTCAC GACAAGGTAA TCATGTTGCG CTAGTCATGA ATGAnTTGAC	300
	AATGACGTAT GAAACATTAC GCAACTATGT GGGATGCCAT TCGGCACATG CTCCTATCAA	360
20	ATGGTGTGGG CAATGGTCAA CGGGTTGCCT TGGTGTACAG	400

(2) INFORMATION FOR SEQ ID NO: 3898:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3898:

	GAAATCAGTA TTAAAGCAGT TAATCCACAA GGGAAAGTGG TTAATACAGT TGGCTCTGGT	60
	GATAGTACAG TTGCAGGCAT GGTGGCTGGA ATTGCTTCAG GTTTAACGAT TGAAAAAGCA	120
35	TTCCAACAAG CAGTCGCATG CCGTACTGCC ACGGCATTG ATGAGGACTT AGCAACACGG	180
	GACGCTATAG AAAAAATAAA ATCACAAGTT ACGATTAGCG TACTTGATGG GGAGTGAAAA	240
	TAATGAGAGT AACAGAGTTA TTAACAAAAG ATACAATAGC AATGGATTTA ATGGCAAATG	300
40	ACAAAAATGG TGTTATTGAT GAGTTAGTAA ATCAATTAGA CCAAGCAGGT AAATTAAGTG	360
	ATGTCGCGTC ATTTAAngGA AGCGATTAC CATCGnGATC	400

(2) INFORMATION FOR SEQ ID NO: 3899:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3899:

55

CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 120
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGCTTG 180
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 240
 TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA nACCTCACGG TCTCAACTTG 300
 CCTGGCAACG TTCTACTTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC TnAAAGACCT 360
 10 TTCTTGGACT TGTGGACAAT CGGCTTGGCA nTCTTTnCTC 400

(2) INFORMATION FOR SEQ ID NO: 3900:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3900:

TGCACGCGTA TCTGATGGTT GCTCAGTTGC ATCTACCCAA GGTAACCATT CCCTAAGTGA 60
 25 ATTTCTTGAA CGATTGACTA AATTGAAAAG CGCTTCTGTG TCATGAGCTT CTAAAATTTT 120
 TAATGTTATT TGTTCAITCA CTTTCATTCC AAACATACCA TCACATCCTC ATTCATTTTT 180
 CATATAATTC TGTAATATAT CATTATAATA ACATATTAAT GTTACGCATT GTATCTTAAA 240
 30 TTTGTTGTCC TTCCCCAACT TGCATTGCTT GTAGAATTTT TTTTCGAAAT TCTCTATGTT 300
 GGGGCCCCGCh AACTTGCAAT GTCTGTAGAA ATTACGGACC CAATTCTCT AGGTGGGGCC 360
 CATCCCCAAC TTGCACATTA ATnGCAAGCh GACTTTCCGT 400

(2) INFORMATION FOR SEQ ID NO: 3901:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3901:

TACTGCTGTT CACTTTTTAT AATACTTCTG AATGTCTTCA CTTATACITC TAGTCACAGA 60
 TTTAAATAAT CAAAGTGCA CATTATTAAA ATATCAATTT CACACTCAAT GCGGCTCATC 120
 50 GCATTCATTT CTTGTCTCAA CGTTCTACTC TAGCGGAAGT AAGTTAGCTA CCATCCTCGC 180
 TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 240

TTTCACTTCG CCAAGCCATT TTCCTTGGT GGTTTACCTT TTAATTGGA CGGTTTAGAC 360
 ATnAAAAAAG GGGACCTCAC GGGCCCAACT TGGCCTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3902:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3902:

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120
 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTAG CTCTACTAAA 180
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT 240
 TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300
 TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGGCAACG TTCTACTCTA GCGGGAACGT 360
 AAGTTGGGCT ACCAnCGGCG GCTAAAGACC TTTCCTGGAC 400

(2) INFORMATION FOR SEQ ID NO: 3903:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3903:

TTGTTATAAC GAAAACCATT AATAGATTTT TATTTGGTGA TTTCAAATCA TGAGACTGGG 60
 ACAGAAATGA TGTTTTTATA AAAATTATTT CGTTGTTCCA CTCTCATGAT TTTTTTGATG 120
 AAACATAATT ACATGATTGA TTGCATCATT TTGTTAAACA AGTGATTGCA AACCTGCCAT 180
 TTCACACTGA AAATTTACAT AATAAGTGAC GATATTTTAC AAGTCATATA CAAATAACAT 240
 ATATTGTAA ATAATTTTAC CTAATCTTAA CATTAAATTT ACAATTATAA GCGATAATCT 300
 AAATATAAAG CTTATTTGAG GTGAAATAAT GGAAATGTCG GTTACAGAAG TCATTTTCTC 360
 CTTTTTAGGT GGGTTTAGGG AATTTCCnTT ACGGCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3904:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3904:

10 CATAAGACAT AATCGCTAGT GTTCGAAAGA GCACTCACAA GATTAATAAC GCGTTTCCTG 60
 TAGGATGGAA ACATAGATTA AGTTATTAAG GGCGCACGGT GGATGCCTTG GCACTAGAAG 120
 CCGATGAAGG ACGTTACTAA CGACGATATG CTTTGGGGAG CTGTAAGTAA GCTTTGATCC 180
 15 AGAGATTTCC GAATGGGGAA ACCCAGCATG AGTTATGTCA TGTTATCGAT ATGTGAATAC 240
 ATAGCATATC AGAAGGCACA CCCGGAGAnC TGAAACATCT TAGTACCCGG AGGAAGAGAA 300
 AGAAAATTCG ATTCCCTTAG TAGCGGCGAG CGAAACGGGA AGAGCCCAA CCAACAAGCT 360
 20 TGCTTGTTGG GGTGTAGGG CACTCTATAC GGAGTTACAA 400

(2) INFORMATION FOR SEQ ID NO: 3905:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3905:

AACTAACATT ACAACATGCA TGTGAACAAT TAAAAACATA TTTTAAGTAG GTGAATGAAA 60
 35 TGgTAAATGA ACAAATCATT GATATTTTCA GTCCGTAAA GGGCGAAATA GAAGTGCCGG 120
 GCGATAAGTC AATGACACAC CGTGCAATCA TGTGGCGTC GCTAGCTGAA GGTGTATCTA 180
 CTATATATAA GCCACTACTT GGCGAAttCG TCGTACgATG GaCATTTTCC gACTGTTAGG 240
 40 TGTAGAAATC AAAGAAGATG ATGAAAAATT AGTTGTGACT TCCCCAGGAT ATCAATCTTT 300
 TAACACGCCA CATCAAGTnT TGnTACAGG TAATTCCGGG TACGACAACA CGATTGATAG 360
 TTTGGTTAAT GGGTTAAGTA TTGAAAGTGT TTTGTCCGG 399

45

(2) INFORMATION FOR SEQ ID NO: 3906:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TTCTTTAAAA ATAAACGCCT ATnCGTTATC GGTGGTGGTG ATTcAGCAGT AGAAGAGGGA 60
 ACATTCTAAA CTAAATTTGC TGACAAAGTA ACAATCGTTC ACCGTCGTGA TGAGTTACGT 120
 5 GCACAGCGTA TTTTACAAGA TAGAGCATTc AAAAATGATA AAATCGACTT TATTTGGAGT 180
 CATACTTTGA AATCAATTAA TGAAAAAGAC GGCAAGTGG GTTCTGTGAC ATTAACGTCT 240
 10 ACAAAGATG GTTCAGAAGA AACACACGAG GCTGATGGTG TATTCATCTA TATTGGTATG 300
 AACCATTAAc AGCGCCATTT AAnGCTTAGG TATTACnAAT GATGTTGGTT ATATTGTGAC 360
 AAAGGTGGAT TGGCCAC 377

(2) INFORMATION FOR SEQ ID NO: 3907:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3907:

25 AATTAGGTAA TTCAAATAA TATTAGCGCG GGATGGAGCA GTTCGGTAGC TCGTCGGGCT 60
 CATAACCCGA AGTCGGtGGT TCAAATCCGC CTCCCGCAAT ACATAGTTTT TAATTTAATA 120
 GGTCTCGTAG TGTAGCGrTT AACACGCCTG CCTGTCACGC AGAGATCGCG GGTTCGATTc 180
 30 CCGTCGAGAC CGCCATTATT ATTACCATTa CGGTTcAGTA GCTCAGTTGG TAGAGCAATG 240
 GATTGAAGCT CCATGTGTcG GCAgTTCGAC TCTGTcCTGa ACCATTCTTA ATTCATGGCG 300
 GTTGTGGTGA AGTGGTTAAC ACATCGGATT GTGGTTCCGA CATTcGAGGG TTCGATCCCC 360
 35 TTCAGCCGCC CCATAATCGT TTACATTAGC GGGTGTAGTT TAATGGcAAA ACCTCAGCCT 420
 TCCAAGCTGA TGTTGTGGGk TtCGrTTCCC AtCAmCCnGy TCCaTaATTT CnAAnAATTC 480
 40 CAACAGTAGC CGCAAGTnGG TA 502

(2) INFORMATION FOR SEQ ID NO: 3908:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - 45 (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3908:

AAAAAATGCA TCTCTACGTG CTAGAATAAA TATTGGTCAG CCAACCAAAA TAATCAACAC 60

TAAGTATCAT ATTGTCTTTG CACCTAAATA CAGAAGACAA GTGATATATG GAAAAATAAA 180
 AAAAGATATA GGGATTATAT TCGTCAATT ATGTGAAAGA AAAGGTGTAG AGATAATTGA 240
 5 AGCAGAGGCA TGTAAGATC ATATCCATAT GTTAGTTAGT ATACCACCCA AACTTGGGGG 300
 TATCATCATT TGTTGGGCTA TTTAAAAGGG AAAAAGTAGT TTAATGGATA TTTGGATAGA 360
 CATGGCTAAC TTAAAGTATA GATATGGGAA ATAGGAAAGT 400

(2) INFORMATION FOR SEQ ID NO: 3909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3909:

GGTTTAACTA TTGAAGAAAA TGTGCCGACA ATTAACAAGA TAAAAAATGC GGTATATTCA 60
 GCAGATAAAG CTTTACCTAA GATTAATGAC TTTGCGAATA AAATTGTATA TTTGAATAAC 120
 25 CACCAAGCGG ATTTAGATAA ATATGCCAAT GATTTTAGAA AACTAGGAAA TTATAAAGGT 180
 GATATTTTAG ATGCTCAGAA AAAATTAAAC GAGTCAATGG TGCTATTCCG CAACTTAATG 240
 AAAAGGCTAA GTTGGATATT AGCTTTTAAA TAATTATATG CCGGAAAATT GGAAAAAGCG 300
 30 TTAAATTTT GCAGCTGGAT GACGTGCCAC GCGTTCCCT AAAATTAATC CAGGGCTTAA 360
 CATTGCGAGT CCAGGTATTG GntCCAAGCT AATGGGGCCG 400

(2) INFORMATION FOR SEQ ID NO: 3910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3910:

TTACCCGATA TCGGAAGGT ATCCACGAAG GTGAAATTGT AAAATGGTTT GTTAAAGCTG 60
 GAGATACTAT TGAAGAAGAC GATGTTTTAG CTGAGGTACA AAACGATAAA TCAGTAGTAG 120
 AAATCCCATC ACCAGCATCT GGTACTGTAG AAGAAGTTAT GGTAGAAGAA GGTACAGTAG 180
 50 CTGTAGTTGG TGACGTTATT GTTAAATCG ATGCACCTGA TGCAGAAGAT ATGCAATTTA 240
 AAGGTCATGA TGATGATTCA TCATCTAAAG AAGAACCTGC GAAAGAGGGA AGCGCCACAG 300

GCCATGCCTT CCAGTTACGT TAAATACGCA CGTGGAAG

400

(2) INFORMATION FOR SEQ ID NO: 3911:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3911:

CGTGTA_nCTC AAGTTATGGG TCCTGTAATT GATGTTCGAT TTGAACATAA CGAATTCCTA 60
 AAATTAATAA CGCCTTGGTT ATTGATGTGC CTAAAGAAGA AGGTACAATA CAACTAACAT 120
 TAGAAGTTGC GCTGCAATTA GGTGACGACG TTGTTCTGAC AATTGCGATG GATTCAACTG 180
 ATGGTGTCCA AAGAGGCATG GATGTAAAG ATACAGGCAA AGAAATTAGT GTACCTGTTG 240
 GTGACGAAAC ATTAGGTCGT GTATTTAATG TACTAGGTGA AACAATTGAC CTTAAAGAAG 300
 AAATTAGTGA TTCTGTTCTG CGCGATCCTA TCCATCGTTC AAGCACCAGC ATTCCGATGG 360
 AACTTTTCAA CAGAAGTCC AAATTTT_nTAG G_nACAGGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3912:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3912:

TTGTACAAGT TGAAGAAAA TCAACACAAC CAAAAGGTAG AAAATTCAAA GATTTCACTA 60
 GTAAATT_nTAA TATAGCATCA GAAGCTAAAG AAAATGAACC TATATCAGTC ATTGGTTATC 120
 CAAATCCTAA TGGAAATAAA CTACAAATGT ATGAATCAAC TGGTAAAGTA TTATCAGTGA 180
 ATGGGAATAT AGTGTCTCG GATGCAATTA TTCAGCCTGG TAGCTCTGGT TCACCTATAT 240
 TAAATAGTAA ACACGA_nGCT ATTGGTGTA TCTATGCCG TAATAAGCCA TCAGGTGAAA 300
 GCACCAGAGG GATTTGCTGT TTATTTCTCT CCTGAAATTA AGAAATTCCA TTGCAGATAA 360
 TTTAGATAAA T_nATTAAGAC CT_nGACATT CACCCAATCC 400

(2) INFORMATION FOR SEQ ID NO: 3913:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3913:

	ACTCATTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT	60
10	TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA	120
	AAAAAAGAGA CCTTGCGGTC TCAATGnGGC TCATCGCATC CATTTTTTGC CTGGCAACGT	180
	TCTACTCTAG CGGAAGTAAG TTGGCTACCA TCGACGCTAA GAACCTTTCT TGACTTGTGA	240
15	CAATCGCTTG CTCTTTTCCT CTTCCTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT	300
	CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTT CACTTCGCCA AGCCATTTT	360
	CTTTGGGGTT TGCnnTTTGA ATTTGGACGT TTTAGACATA	400

20

(2) INFORMATION FOR SEQ ID NO: 3914:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3914:

30

	TGGAATGAGC GGATATAAGC ATCTTTAGAT AATGCACCAT CAACTAATGG ATATTTATGT	60
	CCAGTTGGAC GCCAGAAATC ATAAACGTCT TCAGTGTAAG CAACAGCATC TTCATTTAAT	120
35	GCCAAAATGC TTGGATTATG TGCAATAACC ATCGCAACTG nGCCACACCT TGTGTTGGCT	180
	CGCCGCCTGA ATTCAATCCA TAACGTGCTG TATCTGTAGC AATAACTAAT ACTTTTTCAT	240
	TCGGTCTAGT TGCTAAATAA TCTTTAGCTA ATTGAATTGC TGGTGTGCA GCATAACAAG	300
40	CTTCTTTCAT TTCAAAGCAG CGTGCAAAAG GTTGGnATAC CTAATAAGTT GTGGAATTTG	360
	nACAGCGGCT GCTTTACGAA TTCCAACGTC TGATTCCAGT	400

(2) INFORMATION FOR SEQ ID NO: 3915:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3915:

55

TCTTTATTTA TCCAGTTTCA TAGTCAATGT TTAAAGCAAA ATCTTATTGA TGGTACAAAA 120
 GTAGAAGCTA ATGCCAATAG GTATACATTT GTGTGGAAGA AAAGTATTCA AAATCACGAA 180
 5 TCGAAATTGA ACGAnAATTC AAAAACATTA TATCGTGA CT TAGTTGAAGA AAAAATAATA 240
 CCAGAGATAA AAGAAGATGG AGATAGCGAT TTAACAATAG AnGAAATAGA TTTAATTGGT 300
 10 AGTCATTTAG ATAAAGAAAT CGAGGTTTAA ATCATTCTAT TGAGACGnGA TAGTACTCAA 360
 ATTAGAAACA G 371

(2) INFORMATION FOR SEQ ID NO: 3916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3916:

ACCATGGACG ACGGTTAGGT TTATGAATGT TATCCAAAT AGGTTTCTCT ATAAAATAGC 60
 25 TTTAGTTGGA AAAGATGAGA AAAAATATAA AGATGGACCT TACGATAATA TCGATGTATT 120
 TATCGTTTTA GAAGACAATA AATATCAATT GAAAAAATAT TCTGTCGGTG GCATCACGAA 180
 GACTAATAGT AAAAAAGTTA ATCACAAGT AGAATTAAGC ATTACTAAAA AAGATAATCA 240
 30 AGGTATGATT TCACGCGATG TTTCAGAATA CATGATTACT AAGGAAGAGA TTTCCTTGAA 300
 AGAGCTTGAT TTAAATTGA GAAACAAC TATTGAAAAA CAGATCTTTA CGGTAACATG 360
 GGTTCAGGAC AATCGTATTA AATGAAAACG GGGGAATATA 400

(2) INFORMATION FOR SEQ ID NO: 3917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3917:

GAGGAAATTA TTAACCTTnC GCATCGTATG GGCCnTGAAG GAATAACAaC CTTTAGACCT 60
 GGAGATTGAG CTAAAATACC TTCTAAGTTA TCTGCGTGTA ATTCTGGTGT GTGTACGCCA 120
 50 CCACCAAATG GGCTACGAAT TGTTACAGGT GCAGTTTTAG TACCGCCTGA ACGGAAACGA 180
 GTACGTGCAA TTIGTCCAGC AATCGCATCA AATACTTCGA ATACGAAACC TAAGAATTGT 240

GATTCAGCTA AAGGTGTATC GAATACTCTA TCTTCACCAA ATTCTTTTGT TAGTCCTTCA 360
 GTAACACGGA AAACACCGCC GTTAACACCA ACGTCTTCAC CAnAATnAAA AC 412

(2) INFORMATION FOR SEQ ID NO: 3918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3918:

ATAGATTGCT GAGTGACAAT ACTTCAGGAN TCGCATATGC AGGCCCAATA CCCATAATTT 60
 TCGGGTCAAC GCCTACTGCC TTAAAACCAA CGAATCGTGC AATAGGTGTC ACGCCGAGTT 120
 CTTTCACTTT ATCTCCAGAC ATTAAAACTA CAAATCCTGC ACCATCAGAA AGTGGGGCAG 180
 ATGTTCTGTC AGTCATAGTG CCGTCAGCTT TAAATACTGT ACGTAATTTG GCTAATGCCT 240
 CCATCGTGGT GTCAGGGCGT ATnAAATTCA TCTTGGTCAA AGATATTTGT GTGTACTTTT 300
 GGTCCTGCGT TTGTATATTC AACTGAGTTT ACTTGTATTG GGATnATTTC ATCTTTGGAA 360
 CCGACCATCA CGGTGTGCGT TCATAGGCAC GTTGATGnAC 400

(2) INFORMATION FOR SEQ ID NO: 3919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3919:

CAAGGGCAAC AAGGTGGCAA CGGCAATTAT TTAGAACAAA TTGGTCGTAA CCTTACnAAG 60
 AAGCACGTGA CGGTTTATTA GATCCAGTCA TTGGTCGTGA TAAAGAAATT CAAGAACTG 120
 CTGAAGTTTT AAGTAGACGA ACTAAAAACA ATCCTATATT AGTTGGAGAA GCTGGTGTG 180
 GTAAAACGTC GATTGTTGAA GGTTTAGCAC AGGCAATCGT TGAAGGAAAT GTACCAGCAG 240
 CAATCAAAGA CAAAGAAATT ATTTCTGTAG ACATTTTCATC ATTAGAAGCT GGAACGCAAT 300
 ATCGTGGTGC TTTTGAGGAA AATATTCCAA AATTAATCGA GGTGTTAAnc TTCACAAATG 360
 CCGTACTATC TTTGATGAAn CCATCAATTA TCGGTTTCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3920:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3920:

10 CTTATCCCGT CCACACATAG CTACCCAGCT ATGCCGTTGG CACGACAAC TGTACACCAG 60
 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACAGCTC CTCTCAAATT TCCTACGCCC 120
 ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 180
 15 ATGGGCGAAC AGCCAAGnCC TTGGGACCGA CTACAGCCCC AGGATGCGAT GAGCCGACAT 240
 CGAGGTGCCA AACCTCCCCG TCGATGTGAA CTCTTGGGGG AGATAAGCCT GTTATCCCCG 300
 GGGTAGCTTT TATCCGTTGA GCGATGGCCC TTCCATGCGG GAAnCAACGG ATTCACTAAA 360
 20 GTCCGTCTTT TCGAACCTGG CTCGGACTTG TAGGTCTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3921:

CGGGTTGGGC AGGTATGTTG TATTACCGTT CACAGCAGCA TCACMTTGAA CAACATTTGT 60
 35 TAACGGATTA TTTGGCAATT CGGTTAGTTG TCGAACAAATT GCTAGTTGGT GATGAGTTTA 120
 AGTCAGTCGC TAAAGATTGT GAAAGTAGAT CGGAAAATTG GTTTAAGCAA ACTGTTCAT 180
 CATGGTGTTA CTACAGTGGA TATGCCTAGC GATGTATTAC TACAACATGA CGTCAATGAA 240
 40 ATTCAAACGT TTATTCATTT TGGCAGCAAC TATGGAATAA AAATGTATTT AAAATTTATG 300
 GCTnAATTGC CnGGGGAAAT GACATACGGG ATCTCAGTTT AAAACAAAAA TTAAAGCAGG 360
 45 TCATGGAAAG TGTGGCGGGC GCCTTAGGTG TnAACCCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTTTTTTGA ATGTTAAATA AACATTCAAA 60
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 120
 5 TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC 180
 CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTIONACC GGCTTCGGGT 240
 GTTACAAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT 300
 10 AGCATGCTGT ATCTACGTTT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC 360
 AATnCGAACT GAGGAACAAC TTTTATGGGG TTTGnTTTn 400

(2) INFORMATION FOR SEQ ID NO: 3923:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3923:

AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA ATAAAGAGTT TTAAATAAGC 60
 TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAGAACTC CACAAGATTA ATAACGCGTT 120
 30 TCCTGTAGGA TGGAAACATA GATTAAGTTA TTAAGGGCGC ACGGTGGATG CCTTGGCACT 180
 AGAAGCCGAT GAAGGACGTT ACTAACGACG ATATGCTTTG GGGAGCTGTA AGTAAGCTTT 240
 GATCCAGAGA TTTCCGAATG GGGAAACCCA GCATGAGTTA TGTCATGTTA TCGATATGTG 300
 35 AATACATAGC ATATCAGAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGAGAAG 360
 AGAAAGAAAT TCGnTCCCTA GTACCGCGAn CGAAACGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3924:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3924:

ATGCGATACG TAGCACAGCT GCAACAATCC ATGCTAGTAA AATCGGAGAC ATCTCTGTAC 60
 50 CTTCAAACATA GCAATTGTAT TTCCGACACC GCCGTCAATT AATACTTGTT TAATGTACCG 120
 CCACCGCCAA TAATCAATAA CATCATTCGG ATTGGATAAA TCGCATTTCG CACTGATTCC 180

GCTATTAGCA TGGCTGTCCC TGCTGTTCCCT ATCATATAAA TGATAGATTC AAATAGATTT 300
 GTAGGGTTGT CATGCCCAGT TACAAGTTGC GTTGATCGTn GACACTAACA TTAATATGAC 360
 5 TGGTAATGTT GCTGTTAATA AACTCATACC AAnTCCGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3925:

GGCTGGGCTA GCTGGATTCG AACCAACGAG TGACGGAnAn AGGTCCGTTG CCTTACCGCT 60
 20 TGGCTATAGC CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG 120
 AGCCGGATTT ACAGTCCGCC GCGTTTACCA CTTGCTACC CCTCCAGCTT ATTCATATAA 180
 TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG 240
 25 CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG ACTCGAACCC 300
 GTGTTACCGC CGTGaAAGGG CGTGtGCTTA ACCcTTGGAC CAAGGAGCCA TGGCTCaCAG 360
 GTAGGACTCG AACCTACGAC CGATCGGTTA AcAGCCGATA GCTCTACCAC TGGAGCTGAC 420
 30 TGTGGATTAA TATTATGCCT GGCAACGTTT TGAnnCTAGC GGAAnTGAAT TCGGACTGAC 480
 CATCGACGCh AAGGAGCTGA ACTTCTGTGT TCGGGCATGG GGAAC 525

(2) INFORMATION FOR SEQ ID NO: 3926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3926:

TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGTT GCTTATTATG AAGCGATGCA 60
 45 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180
 50 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240
 TACCGnACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300

TCCGGATAGA GGCATCCACT GGGGAACGGT TACCAATTGG

400

(2) INFORMATION FOR SEQ ID NO: 3927:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3927:

TATCGATCAA TTTCTATCGA GTTGGACAAT GCCGAACGTG ACAAAGTTTT TACCATGCAT 60
 GGTTGCATTT AGCGCAACAT GACCATAGTT TTAATAAGC ACAGCGCGCA AGTGATTAAA 120
 GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT TAACTCATTT TTCAATAGAT 180
 CAGGAAGACT ACCAAGCTTA TGTTGAAGGA CATCTTTTGG CGTTACCGGG TTGGGCAGGT 240
 ATGTTGTATT ACCGTTTACA ACAGCATCAC TTTGGAACAA CATTGTGTTAA CGGATTATTT 300
 GGCAATTCGG TTAGTTGTCG AACAATTGCT AGTTGGTGGA TGAGTTTAAG TCCATCGCTA 360
 AAGATGTGGA AATAGnCCGG AAAATGGTTT TAAGCAAAC 400

(2) INFORMATION FOR SEQ ID NO: 3928:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3928:

GTGCACCTAA CGCTGAAATA TCGCCTTCTC GTGTATAGCA GACGGAATCA TTTTTTGTGC 60
 AnTTTTGTAA ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATACA 120
 GTAATACATC TCCAACATTT GCCTTTAATT CTTTTCGAT GACTACCGGT CCTGGATGTG 180
 GTGGTAAAAA GCCATGTGTC ACTGATAAAG CTGTTACCAT AGGTAGTCCT AGTTTAAACA 240
 CTGAAACATT TGCGCGTTTT GCTACTGTAA ATAATAATGG AATCAGTAAG ACTAAACCTA 300
 CTTCAAAGAA CAATGCAATA CCGACGATAA ATGCTGGCAA CAAGCATTGC CCCATTGGTA 360
 CATGGTTTTT GGACCAAATT TTTGGAATCA ACGTGTCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3929:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3929:

	CTCAAGGTGT TGCCTATACA GCTAAAAAAC TTAATTATAA CGCTGTTATC TTTATGCCAG	60
10	TCACTACACC TTTACAAAAG GTAAATCAAG TAAAGTCTT TGGAAATAGT AACGTTGAAG	120
	TTGTACTCAC TGGTGATACA TTTGATCACT GTTTAGCTGA AGCTTTAACT TATACAAGTG	180
	AACATCAAAT GAACTTTATA GATCCATTCA ATAATGTTCA TACAATTTCT GGACAAGGTA	240
15	CGCTTGCTAA AGAAATGCTA GAACAAGCAA nGTCTGACAA TGTTAACTTT GCATTATCTA	300
	TTTGCCGCAA TTGGTGGTGG CGGTTTAATT TCAGGTATTT CGTACTTACT nTTAAACCT	360
	ATTCACCTAC CACGnAAATT ATAGGTGTTG AACCCnAGT	400

20

(2) INFORMATION FOR SEQ ID NO: 3930:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3930:

30	ATATGATCCT ATGAAGCAAT TTTATGTAGT AAGTGGTTCT AAACATGACG CCCTTATGCT	60
	CTGTGAACAT TTATATGACG AGGTTATGGC TGTTTGCTAA nCCCAAATGA TACATCGAAT	120
35	GGCACATATC ATTCGTCGCA ATATGATTAC TATGATGCAT TTATTAAGCA GCAAGAAAAT	180
	GTAACATATA TTTCAACCGA TCGTGACAGT GCTAATACAG TGTTATGTCA CTAATTTATA	240
	AAAAATAAAT GAATAAGTAA GGTTTCAACC GAGAGAATAT ATTCGTGTTG AAGCCTTATT	300
40	TGTCGTTGTG CCAAATTGA ACGnTTTGA TGGCAATAAG CATGACCATA CAGATTGTGT	360
	ATTATTTCCA TGnA	374

(2) INFORMATION FOR SEQ ID NO: 3931:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3931:

55

TGCTTCTTTC GCTAGCCTCG TATGGGCATC TTTATCAATA ATATACTCGC CATGACTATC 120
 TTTCGCTTTT AAGTCAATTT CATCAAATC TTTCCACCT GTTAACGGTG CACCACTATG 180
 5 TCGTTTCCGA CCAAATGTAG CCTCTTGTTT TTCCAGCGCA GTACGATCCC ACGTTTCAAT 240
 GTGTATTGTA ATACGTCTGA CAACGCAATA AGTTCCATGT TTCGCCCATC CGTCATCAAT 300
 AAACACATAA TCTTTAAGTT GATTATTCTT CCTAGGATTA ATTGTTCCAC TTAAAAATGC 360
 10 CATTTAAATT CTAGGTGTTT CCnTAnC 387

(2) INFORMATION FOR SEQ ID NO: 3932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3932:

AAGGTAATAA TCCTGTAGTC GAAATGTG TCTCTCTGA GTGGATCCTG AGTACGACGG 60
 25 AGCACGTGAA ATTCCGTCGG AATCTGGGAG GACCATCTCC TAAGGCTAAA TACTCTCTAG 120
 TGACCGATAG TGAACCGTA CCGTGAGGAG AAGTGAAAA GCACCCCGGA AGGTAGnTGA 180
 AATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG 240
 30 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA 300
 GCCGTAGCnG AAGnAnGTTT TGAATAGGCG GTTTAGTATT TGGTCGTAGC CGATAACCAG 360
 GTGATTCTAC CCTTTGGTCA GGTGAAGTT CAAGTAACAT 400

(2) INFORMATION FOR SEQ ID NO: 3933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3933:

GCGATGGTTG AAACATTGAC TTATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120
 50 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180
 CGATTTTGGC ATGAAGGTCA CCTTAAATGT ACATTGTTGT AATAAAATTG CCTATAAATT 240

AATTGTAAAA AGAAAACCAT ACGCTATGTG nTGCCAAGGA AAAGGTTCTA CCATTGTCAC 360
 nAAAAATGCA TCTCTACGTG CTAGGAATAA ATATTGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 3934:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3934:

TTTGACGTTT TAGACATAAA AAAAGAGACC TTGCGGTCCA GATGGGGCTC ATCGCATCCA 60
 CTMTTTCCTT GGCAACGTTT TACTCTAGCG GAAnTAATCG AACTACCATC GACGCTAAGG 120
 AGCTTAACCTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC 180
 ATATGAATGT AAATTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA 240
 AACATTTAFT TTGATTAACT CTTCGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300
 GGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAnG GATCTTATAA CCGAATTGGG 360
 AAnCTCATCT GAAGGGGGCT CAGCTAGATG CTTCAnACTT 400

(2) INFORMATION FOR SEQ ID NO: 3935:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3935:

TGTTCTTTTT GGGCAGTGGG ACACAAATGG ATATTTTCGG CAAAATTTAT TTCGTTCGnT 60
 CCCACCCCAA CTTGGCACAC TATTGTAAGC TGACTTTTCG CCAGCTTCTG TGTGGGGGCC 120
 CCGCCAACCTT GCCATTGTCT GTAGAAATTG AGGAGCTAAT TTCTCTGTGT CGGGGCTCCA 180
 CCCCACCTTG CACACTATTG TAAGCTGACT TTCCGCCAGC CTCTGTGTTG GGGCCCCGCC 240
 AACTTGACACA CTATTGTAAG CTGACTTTCC ACCAGCCTCT GTGTTGGGCC CCGACTATTT 300
 TTGAAAAGAG CGTGTTACAC GGGCATTGTT TTACAGTCAA CTACTGCTAA AATAAAATTA 360
 ACGAGCTTAA GGCTTTGGnT TCTGTCCCAA GCC 393

(2) INFORMATION FOR SEQ ID NO: 3936:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3936:

10	AAAAAGAAGA CAACCAAGCC CAATAATGGA CTGGCCGCGT AATAATnGTG GCTCTAAAAG	60
	TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTTGGTGG AGAACCTAAA	120
	AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT	180
15	GACCCTCTGA TTAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC	240
	TAGCTGGATT CGAACCAACG AGTGACGGAn TCAAAAGTCC GTTGCCTTAC CGCTTGGCTA	300
	TAGCCCAATA TATAGATGGT GGAAGGGGGC AGATCGAACT GCCGAACCCG AGGAGCGGAT	360
20	TTACAGTCCG CCGCGTTTAG CACTTCGCTA CCCTCCAGCT	400

(2) INFORMATION FOR SEQ ID NO: 3937:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 609 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3937:

	GGTTTAACAC GCCTGCCTGT CACGCAGGAG ATCGCGGGTT CGATTCCCTG TCGAGACCGC	60
35	CATTATTATT ACCATTACGG TTCAGTAGCT CAGTTGGTAG AGCAATGGAT TGAAGCTCCA	120
	TGTGTCGGCA GTTCGACTCT GTCCTGAACC ATTCTTAATT CATGGCGGTT GTGGTGAAGT	180
40	GGTTAACACA TCGGATTGTG GTTCCGACAT TCGAGGGTTC GATCCCCTTC AGCCGCCCCA	240
	TAATCGTTTA CATTAGCGGG TGTAGTTTAA TGGCAAACC TCAGCCTTCC AAGCTGATGT	300
	TGTGGGTTTCG ATTCCCATCA CCCGCTCCAT TATTTTCTAT TATTCCACAG TAGCTCAGTG	360
45	GTAGAGCTAT CGGCTGTTAA CCGATCGGTC GTAGGTTCGA GTCCTACCTG TGGAGCCATG	420
	GCTCyTTGGt CAAGCGGTTA AGACACCGCC CTTTCACGGC GGTAACACGG GTTCGAGTCC	480
	CGTAGaGTyC ATACAAGCAG AAGTGnAAAT ATCGCTTCTG TTTTTTTaTT ACATAwTTAA	540
50	TkGTTGgAGG aAGtTGtCCG AgCyGGGCCG AAGGaGCACG CCTGGAAATG TGTAAGCGTT	600
	CACAAGCTT	609

55

(2) INFORMATION FOR SEQ ID NO: 3938:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3938:

10	TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC TACATGAAGC TGAATCGCT	60
	AGTAATCGTA GTCAGCATGC TACGGTGAAT ACGTTCCCGG GTCTTGTACA CACCGCCCGT	120
	CACACCACGA GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAGG AGCTAGCCGT	180
15	CGAAGTGGGA CAAATGATTG GGGTGAAGTC GTAACAAGGT AGCCGTATCG GAAGGTGCGG	240
	CTGGATCACC TCCTTTCTAA GGATATATTC GGAACATCTT CTTCAGAAGA GCGGAATAAC	300
20	GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA ATTAATGGGC CTATAGCTCA	360
	GnGGTTAnAG CGCACCTGA TnAACGTGAA GTCGGTGATT	400

(2) INFORMATION FOR SEQ ID NO: 3939:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3939:

	AGTTTTGAAT GTATAAATTA CATTCAATG TCTGGTGAAT ATAGCAAGGA GGTCCACCTG	60
35	TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC	120
	CGCTAGAGTA GAACGTTGCC AGGCATAATA TTAATCCACA GTAGCTCAGT GGTAGAGCTA	180
40	TGGGCTGTTA ACCGATCGGT CGTAGGTTTC AGTCCTACCT GTGGAGCCAT GGCTCTTGGT	240
	CAAGCGGTTA AGGACACCGC CCTTTCACGG CGGTAACACG GGTTTCGAGTC CCGTAGAGTT	300
	CATTATTTTG GAGAATTAGC TCAGTAGGGA GAGCATCTGC CTTACAAGCA GAGGGTCGGC	360
45	GGTTTCGAAC CCTnCATTTT CCACCATTTC GTTATTAAAn	400

(2) INFORMATION FOR SEQ ID NO: 3940:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

ACACAACAGC TGTTCACAAA ATGATTGGTA CAACTGCTGG TTATGTTGGT TATGATGACA 60
 ATTCAAATAC GTTAACTGAA AAAGTACGCC GTAATCCATA CTCAGTCATT CTATTTGATG 120
 5 AAATCGAAAA AGCAAATCCA CAAATTTTAA CATTGTTATT ACAAGTAATG GATGATGGTA 180
 ATTTGACTGA TGGTCAAGGT AATGTCATCA ACTTTAAAAA TACAATTATT ATTTGTACAT 240
 CAAATGCTGG CTTTGGCAAT GGCAATGACG CTGAAGAAAA AGATATTATG CACGAAATGA 300
 10 AAAAAATTCTT CCGCCCTGAA TTCCTTAACC GCTTCAACGG CATCGTGAAT TnCTTACATT 360
 TAGATAAGGT GCCnTGCAGG TATCGTCCAA CTATTATTAG 400

(2) INFORMATION FOR SEQ ID NO: 3941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3941:

ATACAATTTT AAATCTGTAT GTGTGAATCC AACACATGTT AAATATGCAG CAGAGCGnCT 60
 AGCTGATTCA GAGGTGCTCG TTTGTACGGT AATAGGATTC CCATTAGGTG CGTCGACAAC 120
 30 TGCAACGAAA GCATTGAAA CAGAAGATGC AATTCAAAAT GGTGCAGATG AAATTGACAT 180
 GGTCAACAAC ATCGGCGCAT TAAAAGATGG ACGTTTTGAT GATGTACAAC AAGACATTGA 240
 AGCAGTGGTT AAAGTCGCGA AAGGTCACAC AGTAAAAGTG ATTATTGAGA CGGTATTGTT 300
 35 GGACCATGAC GAAATTGTAA AAGCGAGTGA TTAACAAAAG CGGCTGGTGC GGA CTTCGTT 360
 AAAAACTTCA GCAGGTTTTG CCAGTGGCnG TCGCACTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3942:

CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 60
 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 120
 CATTTTATA AGTCAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG ATTTAAACGC 180

TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTGGGTAAAA TCTATATTTT ACTTACTnAT 300
 CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA TCCGAACCCG CTGACCCnAC 360
 CnGCGTGCAA AGCAGGCGCT CTACCCAGCT TGAGCTAAGG 400

(2) INFORMATION FOR SEQ ID NO: 3943:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3943:

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCTGAACCC CCGCGAGCCG 60
 TTAAGCCCCT GTCGGTTTTT AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120
 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG GTTATGGAGC CGTTAGCTCT 180
 GAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA 240
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 300
 CGCCTTATAT AGTTTGTAAT TnAnnATGGT GGGAGACTAG CGGGGTTCGA ACCGCTGGAC 360
 CTCCTGCGTG CCAAAGCAGG CGGCTTCTAC CCAGCTGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3944:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

CCAAAATTGC ACCTTGTCGT TTATTCGGAA AATCAATATn GnTAGGGGGT ATAAGATGCA 60
 CCTACTTTAA CTGTCGCCAA CATCGCCGCA ATCATTTCAA AACTACGTTC TGTAACAAG 120
 GCAACCCGTT GACCATTGCC CACACCATTG GATAGGAGCA TGTGCGCAAT GGCATCCACA 180
 TAGTTGCGTA ATGTTTCATA CGTCATTGTC AAATCATTCA TGA TAGCGC AACATGATTA 240
 CCTTGTCGTG AGAAACTTCA TTAAAGTAAC TTATGATAGA TTTATTTCCC GGGACATTAA 300
 GCATTCGATC GTTAACATGC GTATTGACCC AATTTAGAAG TTCCTCCGTG CCGTTTGGTA 360
 TATCACAAAT TTGTAGTGTA wCtTGaTGCT TCmAAATaTc AATCAn 406

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3945:

CAATGACAAC AGCAACTGAG ACAGTGTCAA ACGCTTAATA ATAATGATGT AGTGTGCAAT	60
AATACCGCAT TAAATGTACC AACTAAAACA AATGAAAATG GTTCAGGAGG ACATCTAACT	120
TTAAAGGAAA TTCAAGAAGA TGTTTCGTCAT TCTTCAAATA AACCAGAGCT AGTTGCAATT	180
GCTGGAACCA GCATCTGAAT AGACCGAAAA AGAGAAGTTA GACGTGCGGC ACCGGCAGAT	240
CCTGAATGCC AACTCCAGCA GATCCAGCGG CTGCAGCGGT TAGGAAACGG TGGTGCACCA	300
GTTGCAATTA CAGCGCCATA TACGCCAACA ACTGATCCTA ATGCCATGAN GCCAGGACAA	360
ATGGCACCTA ACGAnGCTTG TTCATTTGAT GGACAnGGTA	400

(2) INFORMATION FOR SEQ ID NO: 3946:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3946:

CTCGCTGCGA TAAAGTACCA GTTCATAGCA ACGTTTGThT TAATAGGnTC TGAAACGATA	60
CGTGTGCGCG GTTCTGTAAA TGAATAGACC AAAGCATCTT GCATACCAAC AACTATATTT	120
GCTGCAAATC CTCCAACAGC GGAAnATATG CCATCGTTAG TCCAGCGATA GGGTGATAGC	180
CAATTTTAAT AAAAAGCATT GCTGCAACGG CCGGCAAGAT AATTGTCGCA GCATCGCCGG	240
CTGTACTACC TAAAATACCA ATTAATATAA TAGTCGGTAA AATTAAGAAA CGTGGTGC GC	300
GATTACAAC AGAAATCATT AACTTATCGA AGTATCCTGT TTTCTCTGCA ACACCAATAC	360
CAATCATCAC TGCTAGGTAC TAAGCCTAAT GCTGGGnACT	400

(2) INFORMATION FOR SEQ ID NO: 3947:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3947:

5 GCGGCCGAG GGAAGTGGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT 60
 GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC 120
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 180
 10 GGCAACGTTT TACTCTAGCG GAATTAATTC GAACTACCAT CGACGCTAAG GAGCTTAACT 240
 TCTGTGTTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 300
 TAATTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCG CAAAACATTT 360
 15 A 361

(2) INFORMATION FOR SEQ ID NO: 3948:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3948:

25 TTCCGTCAGA CCCTGACATG GTTCATGGGT TCATATTGCA TAGGACCGAA ATCTTCAAAC 60
 30 ACTACGTGCT TTGGGCAGAC TTCGCAAAA TACGGCCTCA ACAAAGGAAT TAAGCCTCGC 120
 ATAAAGCGGA TTTGAGTAC AGGGAACCGC TACCTCCCCA CCTAGCACGG CAAGATATAT 180
 ATTACTATAT TTTAATAGTT AATTGCAAGT ATAAATCATT TATATCATTG TTTACTTTAT 240
 35 ACGACGTCTT GAGAAGTCAT TAATTTAAAT TCATTGCAA GATGTTTTGA AATATTATAT 300
 TGAAACGGCA TTGTATTTTC TAAATACACA nTACTTCGAA CTGTTGCnGA ATAGGCCACC 360
 GATACATCAC CAACAATTGG nA 382

(2) INFORMATION FOR SEQ ID NO: 3949:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3949:

50 GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA 60
 GACCTTGCGG TCTCAATGCG GTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT 120

TTGCTTCTTT CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 240
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATT TTTCTTTGTG 300
 5 TTTGCTTTTT AnTTTGACGT TTTAGACATA AAAAAAAGAG ACCTTGCGGn CTCAATGnGG 360
 GCTCATCGCA TCCAATTTTT GGCCTGGCAA CGGTTCTACT 400

(2) INFORMATION FOR SEQ ID NO: 3950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3950:

20 ACTCGGTTTT GCTTGGAAAA TCTATATTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 60
 CTTTTTAGTC AAGCGCTCGC ATACTGCTTT ATTTTCATAA GCAATATCAC TTTAACCAAA 120
 AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATCCGCA 180
 25 TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC 240
 CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC 300
 TCCTAAAAGG nTACnCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGCGGT 360
 30 GTGTACAAGA CCCGGGAACG nATTCACCG 389

(2) INFORMATION FOR SEQ ID NO: 3951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3951:

45 AAAGCTCGAC TTGTTTACGA TGTTGAAAAA CAAGATTATG TACCTGTATC GCAACCACAA 60
 TTACCAATTT TAAATGAATT TAATAAAGAC TTAGTGATA ACCTTGATAC CATATTCAAT 120
 GCGCAAGACG AnCGGGACTA TTTTATGGG AGACATTACG TAATAATTC TATTACTCTG 180
 50 CTATCAATGT ACCTAAAGCT ACCGATGATT TCCGAGACAT AGACCGTGCG CTTGTCTGGG 240
 GGTTCAACTG GAAACTTGGT CCATTCCAAT TATGGGATGC AATGGGATAC GAACGTGTTA 300
 AAACAnTGAT GGGAAGACGA ACTTGGGAGA CTTACCACAA TGGGATTAGT GAnTTAGATG 360

(2) INFORMATION FOR SEQ ID NO: 3952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3952:

CAAAGGGCAG CGAAACCGCG AGTCCAGAGC AAATCCCATA AAGTTGTTCT CAGTTCGGAT 60
 TGTAGTCTGC AACTCGACTA CATGAAGCTG GAATCGCTAG TAATCGTAGA TCAGCATGCT 120
 ACGGTGAATA CGTTCCCGGG TCTTGACAC ACCGCCCGTC ACACCACGAG AGTTTGTAAC 180
 ACCCGAAGCC GGTGGAGTAA CCTTTTAGGA GCTAGCCGTC GAAGTGGGAC AAATGATTGG 240
 GGTGAAGTCG TAACAAGGTA GCCGTATCGG AAGGTGCGGC TGGGATCACC TCCTTTCTGA 300
 AGGATATATT CGGGAACATC TTCTTCAGAA GAGCGGGAAT AACGTGACAT ATTGTATTCA 360
 GnTTTGAAT GTTTnnTTAA CATTnCAAAA AAATGGGGCC 400

(2) INFORMATION FOR SEQ ID NO: 3953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3953:

TGATTTTGAC GTTTTAGACA TAAAAAAG AGACCTTGCG GTCTCAAATG CGGCTCATCG 60
 CATCCATTTT TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAATTGGCT ACCATCGACG 120
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTTCTT CGGCTCTCGC 180
 TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 240
 TTTTCACTTC GCCAAGCCAT TTTTCTTGT GTTTGCTTTT TATTTTGACG TTTTAGACAT 300
 AAAAAAAGA GACCTTGCGG TCTCAATGCG GGCTCATCGC ATCCATTTT TGCCTGGCAA 360
 CGTTCTACTC nAGCGGGAAG TGAAGnCGGA CTGACCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3954:

AAACTACATA ATGAAAATGC CGTTTTAATC GGTAATTAAT ATATGGATGA GTTTGCAATG 60
 5 GGTGGTTCAA CAGAAACATC TTATTTCAAA AAAACAGTTA ACCCATTTGA CCATAAAGCA 120
 GTGCCAGGTG GTTCATCAGG TGGATCTGCA GCAGCAGTTG CAGCTGGCTT AGTACCAITTT 180
 AGCTTAGGTT CAGACACAGG TGGTTCAATT AGACAACCGG CTGCATATTG TGGCGTTGTC 240
 10 GGTATGAAAC CAACATACGG TCGTGTATCT CGATTTGGAT TAGTGCTTTG CATCTTCATA 300
 GACCAAATTG GGCCATGACT CGAATGTAAA GTAATGCCAT CGTATTAGAA GCTATTCTGG 360
 15 TGCAGATGnT AATGACTCTA CCAGTGCACC AGTGATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 3955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3955:

TCGATTGGCA TTTCTCCGCT ACCCTCAGTT CATCCGCTCA CTTTTCAACG TAATCGGTTC 60
 GGTCCCTCCAT TCAGTGTTAC CTGAACTTCA ACCTGACCAA GGGTAGATCA CCTGGTTTCG 120
 30 GGTCTACGAC AAATACTAAA CGCCCTATTC AGACTCGCTT TCGCTACGGC TCCACATTTA 180
 CTGCTTAACC TTGCATCAAA TCGTAACTCG CCGGTTCAAT CTACAAAAGG CACGCCATCA 240
 CCCATTAAAG GGCTCTGACT ACTTGTAAGC ACACGGTTTC AGGTTCTATT TCACTCCCCT 300
 35 TCCGGGGGTG CTTTTCACCT TTCTCTTCAA GGTATGGGTT CACTATCGGT nACTAGAGAG 360
 TAATTAGCTT AGGnGATGGT CCTCCAGAT TCGGAAGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3956:

GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG AACCGGTAGT 60

ATAAAATGG AGCAGAAGAC GGGATTTCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 180
 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 240
 5 CTTAGGATCC TAAGTCTAGT GCGTCTGCCA ATTCGCCAC ACCCGCAAAT GGTGAGCCAT 300
 AGAGGATTCG AACCTCTGGA CCCTCTGGAT TAAAAGTCAG ATGCTCTACC AACTGGAGCT 360
 10 AATGGCTCTT TCCATGGTGC CGGGCCAGAG GACTTTGAAn 400

(2) INFORMATION FOR SEQ ID NO: 3957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3957:

CAGACATGTG TTATACGGGA AATTGGGCGA ACCGCAACTA TTATACATTG ATTTACACCT 60
 TATACATGAA GTTACTTCTC CTCAAGCATT TGAAGGACTT AGGCTTCAAA ACAGAAAATT 120
 25 AAGACGCCCA GATTTAACAT TTGCAACACT CGATCACAAT GTTCCTACTA TTGATATATT 180
 CAATATTAAA GATGAAATTG CAAACAAACA AATCACAACA TTACAAAAAA ACGCCATAGA 240
 TTTTGGGGTG CATATTTTGT ATATGGGTTC TGATGAACAA GGTATTGTTC ACATGGTAGG 300
 30 ACCTGAGACA GGACTTACAC AGCCTGGCnA GACCATCCGT nTGTTGGGTGA CTCTCACACA 360
 GCCACACATG GnGCCTTTT 379

(2) INFORMATION FOR SEQ ID NO: 3958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3958:

TGTTAAAATA CGGTACATCT AAATTAATGT TAAGTATTT TCAAAAAGAG AATTAAATAA 60
 ATATATTCAA GGTCAGAnAC AACGCGTGAT ATTTGAAAAT GGCCATTTTG TCTAATTGAT 120
 AGTGAATATA ATTAGAGTAA GAGGCTGGGA CATAAATCCC TAAAAACAG CAGTAAGATA 180
 50 ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT CGTATTGAAT 240
 GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT GCTCCCTCAG 300

AATAAGACAT TTGnCCAACT TGACACTACC ATTAAAACT

400

(2) INFORMATION FOR SEQ ID NO: 3959:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3959:

GAGCCGCAGT GGAATGAGGC CCAAGCGACT GTTTATCAAA AACACAGGTC TCTGCTAAAC 60
 CGTAAGGATG TGTTATAGGG GCTGACGGCT GCCCGGTGCT GGAAGGTTAA GAGGAGTGGT 120
 TAGCTTCTGC GACGTACrGA ATCGAAGCCC CAGTAAACGG CGGCCGTAAC TATAACGGTC 180
 CTAAGGTAGC GAAATTCCTT GTCGGGTAAG TTCCGACCCG CACGAAAGGC GTAACGATTT 240
 GGGCACTGTC TCAACGAGAG ACTCGGTGAA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 300
 CCGCGTACAG GACGGAAAGn CCCCTGGAGC TTTACTGTAG CCTGATATTG AAATnCGGCA 360
 CAGTTTGTAC AGGATAGGTT AGGAGCCTTG GAAACGTGTG 400

(2) INFORMATION FOR SEQ ID NO: 3960:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3960:

TGGTCCCCAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA 60
 TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120
 GCGGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTGAnTnC 180
 ACTCACCGCA GATTTTAAGT CCTGTGCGTC TGCCAGTTCC GCCACCCCGG CACTATAAAA 240
 ATGGAGCAGA AGACGGGATT CGAACCCGCG ACCCCAACCT TGGCAAGTTG TTATTCTTAC 300
 CGCTGGAACT ACTTCTGGCA TATGCGGGTT GAAGGGGAGT CGAACCCCCA CGCCGTAGGC 360
 TTAAGATTCC TGAAGTCTAG TGCCTCTGGC CAATTTCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3961:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3961:

	TTTTGATACA TAATCTAAAT TTCTCAAAGC GCCAATAACA GAGGACCATC TCCTAAGGCT	60
10	AAATACTCTC TAGTGACCGA TAGTGAACCA GTACCGTGAG GGAAAGGTGA AAAGCACCCC	120
	GGAAGGGAGT GAAATAGAAC CTGAAACCGT GTGCTTACAA GTAGTCAGAG CCCGTTAATG	180
	GGTGATGGCG TGCCTTTTGT AGAATGAACC GGCGAGTTAC GATTTGATGC AAGGTTAAGC	240
15	AGTAAATGTG GAGCCGTAGC GAAAGCGAnG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA	300
	GACCGGAAAC CAGGTGATCT ACCCTTGGTC AGGTTGAAGT TCAGGTAACA CTGAATGGAG	360
20	GACCGAACCG ACTTACGTTG AAAAGTGAGC GGATGAACTG	400

(2) INFORMATION FOR SEQ ID NO: 3962:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3962:

	TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTn CGACCCCTTG GTCCCAAACC	60
	AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAnTTAAC GCGCCCGATA GGAGTCGAAC	120
35	CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTG	180
	TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
40	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAnAAAT GGATCAGAAG	300
	ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACACTT	360
	C	361

45

(2) INFORMATION FOR SEQ ID NO: 3963:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3963:

AAGTGTCTTA TTTTTTTAAA GTATTTCAAA GTAAAATTAC ATGTTAATAC GTAGATTAAT 120
 GGCAGACTC CTGAGGGAGC AGTGCCAGTC GAAGCCGTAG GCTGAGACGG CACCCTAGGA 180
 5 AAGCGAACCA TTCAATACGA AGATnThATn AAATAGAGAA CAGCAGTAAG ATATTTTCTA 240
 ATTGAAAATT ATCTTACTGC TGTTTTTTAG GGATTTATGT CCCAGCCTCT TACTCTAATT 300
 10 ATATTCACCTA TCAATTAGAC AAAATGGCCA TTTTCAAATA TCACGCGTTG GTTTCTGACC 360
 TTGGAATATA TTTAT 375

(2) INFORMATION FOR SEQ ID NO: 3964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

AAAATGGCCT TGATAGACTT GCTCAATGCA GGGTTGCCAC AAACCAATGA TGCACTTACA 60
 25 ATTTTAAATA GATTTTAAAG ACCTTGTTGG TTTTGTACAA TTAATGTGAC ATGACTAGGT 120
 CTGACAGTT TATATGCATC TTCATTACTG AGTTTTTTGT TGATTTTCGT ATGATTTAAT 180
 30 ACGCCTAATT CTTTCATTTG TTGAACCATT TTTATGAAAA TGTAAGCTGT TGCTTCTGTA 240
 TCATAAATGG CACGGTGATG TTGCGTTAAT TCTACGCCAT ATTTTTTAGC CAAGAAATTC 300
 AAACCATGTT TACCATATTC AGTATTAATC GTACGAGGAT AATTCTAAAG TATCGATAAC 360
 35 ACCATTGCTT GGATGGTCCA AACCCAAGAC GTTCATATCC 400

(2) INFORMATION FOR SEQ ID NO: 3965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3965:

ACTTTTAATT TTGTCATGAT GTGCCTCCTT ACCGTATGAT GTTATTCAAA GTAAATTGCT 60
 50 TTGCCTGATT TTGCAGACTG ATAAATCGCT TCAAGAATTT TTGTAACCTAC CATTGCTTGT 120
 TCCGGTTTCA CAACTGGTTC AGTATCATTT ACAACTGCAT CAATCCAAGC TTTTGCTTCT 180
 TCTTCAGCTT CATCCACTTC ATTACCTTCA TAAAAGTCGA CGCCTTTGTT TTCCAATTCA 240

TCAGCACCTG CTTTAGGTTT CTGATAATGA ACATTTTGGC CTCATCCACT TCTAAAnGAA 360

TTAATCGCCC AAGnGGGATT CCAAAAAGGA n 391

(2) INFORMATION FOR SEQ ID NO: 3966:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3966:

CGCTATCAGG TATTGTTTCA ACAATTTTCAT TAACATATCG TGAAATATCA TTTTGAGGGA 60

TTCTAACAGA AGTTTCTATT GGTAGTGTAG TTGGGGCATG TTATAATTTT TATACATAAG 120

GCACCTCGTT AATTTAGTTT AGTGGTATTT ATTAAATTAT AAGAAGGGAC CCAACACAGA 180

AAATTCATTT TATTGAATTT TACATTTATG TGCAAGTTGG GCAAAGTGTC TTATTTTTTTA 240

AAAGTATTTT AAAGTAAAAT TACATGTTAA TACGTATAta ATGGcGAGAC TCCTGAGGGA 300

GCASTGCCAG TCGAAGcCAA GGCTGAGACG GCACCCtAGG AAAGCGAcnC ATTcAATACG 360

AAGATTGTAT AAATAGAGAA CAGCAGTAAG ATATTTTC 398

(2) INFORMATION FOR SEQ ID NO: 3967:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3967:

GCTATAGAAA AAATAAAATC ACAAGTTACG ATTAGCGTAC TTGATGGGGA GTGAAAATAA 60

TGAGAGTAAC AGAGTTATTA ACAAAGATA CAATAGCAAT GGATTTAATG GCAAATGACA 120

AAAATGGTGT TATTGATGAG TTAGTAAATC AATTAGACAA AGCAGGTAAA TTAAGTGATG 180

TCGCGTCATT TAAGGAAGCG ATTCACAATC GAGAATCACA AAGTACAAC TGTATCGGCG 240

AGGTATTGCC ATTCCACATG CCAAAGTGGC CGCAGTTGAA GTCACCAGCT ATTGCGTTTG 300

GTAAATCTAA AGCAGGCGTG GATTATCAAn TTTGGnTATG CAACCAGCAC ACTThTTCTT 360

TGTGGTTGGC AGCG 374

(2) INFORMATION FOR SEQ ID NO: 3968:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3968:

10 ACCCCGGCAC TATAAAATG GAGCAGAAGA CGGGATTCTGA ACCCGCGACC CCAACCTTGG 60
 CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC 120
 CACGCCGTAA nCTGAGGATC CTAAGTCTAG TGCCTCTGCC AATTCCGCCA CACCCGCAA 180
 15 TGGTGAGCCA TAGAGGATTC GAACCTCTGG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC 240
 AACTGAGCTG AATGGCTCTT CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTGACT 300
 GGATTACAAG TCAGTTGCTC TACCAATTGA GCTAAGGCCG GGCAATATGT AAGAATAAAT 360
 20 GGTGGAGAAT GACGGGTTTC GAAnCGCCGA CCCTCTGCTT 400

(2) INFORMATION FOR SEQ ID NO: 3969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3969:

GCGAGTTGGG GTGTGGGCCC CAACATAGAG AAATTGGATT CCCAATTTCT ACAGACAATG 60
 35 CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC ATTAnCAATA ATGTGCAAGT 120
 TGGCGGGGCC CCAACACAGA AGCTGACGAA AAGTCATTAn CAATAATGTG CAAGTTGGCG 180
 40 GGGCCCCAAC ACAGAAGCTG GCGGAAAGTC AGCTTACAAT AATGTGCAAG TTGGGGTGGG 240
 ACAACGATAA AGTAATACTT TTTCTATAGA AATTAGTATT TCTTATGCAT GAGTTTTACT 300
 CATGTATTCC TATTTTTAAG TACACATTAG CTGTGGCTAA TGTTTAAGAC CCACTACATA 360
 45 ATAAATCATT AGTGGCTCTn TATCATTTCT GTCCCACTCC 400

(2) INFORMATION FOR SEQ ID NO: 3970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

GATAAGATCA GCCGAAAATG GATGGTGTTA AGAGCGTTAC TTGGTTTGGC GGTATGCTTA 60
 TTTTAAATGG CATTGTGTAC GACACCATT A CAGTTTGTAC TTGTGAGGTT ATTGCAGGGA 120
 5 CTATTTGGTG GTGTTGTTGA TGCATCAAGT GCGTTTGCGA GTGCAGAGGC GCCACTGAKA 180
 GATCGTGGAA AGtATTAGGA gACTGCAAAT TCAGTCAGCG CAGGtCTCTT GTGGGGCCAT 240
 10 TAATTGGCGG TGTTACAGCT TCGATATTAG GTTTTAGTGC GTTACTGATG AGTATTGCCG 300
 TTATTACTTT TATTGTCTGT ATTTTCGGTG CATTAAAATg ATTGAAACGA CACATATGCC 360
 AaaATCACAA ACACCAAATA TTAATAAAGG TnTTCGCCGT TCCAnTTnCA ATGTCTAAT 419

(2) INFORMATION FOR SEQ ID NO: 3971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3971:

AAACTTGGGA GACTTCAATA ACAGATTTAG GTTTATCTAA AAATCAGGCA TATAATTTCT 60
 TAATTACATC TAGTCAAAGA TGGGGCCTTA ATCAAGGGAT AAATGCAAAT GGCTGGATGA 120
 30 GAACTGACTT GAAAGTTTCA GAGTTTACTT TTACACCAGA AGCGCCAAAA ACAATAACAG 180
 AATTAGAAAA AAAAGTTGAA GAGATTCCAT TCAAGAAAGA ACGTAAATTT AATCCGGATT 240
 TAGCACCAGG GACAGAAAAA GTAACAAGAG AAGGACAAAA AGGTGAGAAG ACAATAACGA 300
 35 CACCAACACT AAAAAATCCA TTAAGTGGAG TAATTATTAG TAAAGGTGAA CCnnAAGGAG 360
 GGGTTTCCAn AGTCCGTTAT G 381

(2) INFORMATION FOR SEQ ID NO: 3972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3972:

GGGTTCAGAA CGTCGTGAGA CAGTTCGGTC CCTATCCGTC GTGGGCGTAG GAAATTTGAG 60
 AGGAGCTGTC CTTAGTACGA GAGGACCGGG ATGGACATAC CTCTGGTGTA CCAGTTGTCTG 120
 55 TGCCAACGGC ATAGCTGGGT AGCTATGTGT GGACGGGATA AGTGCTGAAA GCATCTAAGC 180

GAnGTTAATA GGTTCGAGGT GGAAGCATGG TGACATGTGG AGCTGACGAA TACTAATCGn 300
 TCGAnGACTT AATCAAATA AATGTTTTGC GACCAAATCA CTTTACTTAC TATCTAGTTT 360
 5 GAATGATAAA TACATCATAT GCTGGnGCCA TACCAAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3973:

TCTTTTAATT ACGTAATGGC TTACCAGTTT TTAACATATG TGCAATTCTT TCATATGATT 60
 20 TTTTAGATT TAGTAAGTCA ATAAAGCCAA TTTTCTCCAA CGATTGAATG TAACGTTGAT 120
 TGATAAATGT ATTTCTTGGT AAATCACCAC CCGCTAAAT TGTGGCGATA TTTAAGGCAA 180
 TATGATAATC ATGGTCGCTA ATAAAATGAC CCCGTCTTTG CGCATCTAAT TGTCTTGGA 240
 25 TCAATGCTTT GAAGTCTTCA CCTAAAGCGA TATATTGATG TCTAGGATTC GGAATATAGT 300
 TTGTTTCTGC TTCATATTC GCACGTGTGA GCGCAACTTC GACACGnTGG TGCCTGGATT 360
 30 nGAAAATAAA CCGGAnCCnG GGATCCACGG GAAATAACCC 400

(2) INFORMATION FOR SEQ ID NO: 3974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3974:

TGCCATGTT ACCTTGTTTA AAATCAAGGT TTGTAATGTT TCCTTGTGTC ACGATAATAG 60
 45 GCGTAATATC ACTCTTTGCA TGATTGCGGA TGTAAGTCTAA ATCAAAGTTG ATTAATAAAT 120
 CACCTTGTTT AACTTCTTGA CCTTCCTCAA CATGTAAAGT AAAGCCTTCT CCGTTTAATT 180
 TAACAGTGTC TAAACCGATG TGGATTAATA GTTCTAAACC ACTATCTGAA TACAAGACCA 240
 50 ATTGCATGTT TTGTTGGGAA AATCATTTGT TACTTTACCG TTGAAATGGT GCACGAAACT 300
 TCACCTTGTC AnGTTTTTGG ATAGCGATAC CGTCACCCCA TCCATTTTTT TTCGCTGAAA 360
 55 CACTTGGATC AnGGCACTTC TGAATAAATG GTGGTTAACT 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3975:

CCTTTGCAGC GCCTCCGTTA CCTTTTAGGA GCGGACCGCC CCAGTCAAAC TGCCCGCCTG	60
ACACTGTCTC CCACCACGAT AAGnGCGGGn GTTTAGAAAG CCAACACAGC TAGGGTAGTA	120
TCCCACCAGC GCCTCCACGT AAGCTAGCGC TCACGTTTCA AAGGCTCCTA CCTATCCTGT	180
ACAAGCTGTG CCGAATTTCa ATATCAGGCT ACAGTAAAGC TCCACGGGGT CTTTCCGTCC	240
TGTCGCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC ACCGAGTCTC TCGTTGAGAC	300
AGTGCCCAAA TCGTTAACGC CTTTCGTGCG GGTGCGAACT TACCCGACAA GGAnTTTCGC	360
TAACTTAGGA CC	372

(2) INFORMATION FOR SEQ ID NO: 3976:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3976:

AGGGAATCGA ATTTTCTTTC TCTTCCTnCG GGTACTAAGA TGTTCAGTT CTCCGGGTGT	60
GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC	120
CCCATTCCGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA	180
GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AAATAACTTA	240
ATCTATGTTT CCACCATTTT TATAAGTCAA ACGCTCACAT ACGGCTTCGT TTTCATTATT	300
TTAAAGCTCA TTTACATAAG TAAACTCTGC TTAAATGAT TTAATCATT GTCTGCTAAA	360
ACGGTTTnTT TTATGAAAAG GTTTGAAACG GGTTh	395

(2) INFORMATION FOR SEQ ID NO: 3977:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3977:

5 TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCG 60
 ATAGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120
 GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTnnTTCA 180
 10 CTCACGCAGA TTTTAAGTCC TGTGCGTCTG CCAGTTCGCG CACCCCGGCA CTATAAAAAT 240
 GGAGCAGAAG ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGTTGTT ATTCTACCGC 300
 TGAACTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA GGCTTAGATC 360
 15 CTTAAGTCTA AGTGCGTCTG GCCAATTTCC GCCAnACCCG 400

(2) INFORMATION FOR SEQ ID NO: 3978:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3978:

AAGTGTTAA ATATTATAGA AAACATCAAA GGATGTTAAG AAATACAATT TATTACCCAG 60
 30 CATTTAATAA TGGTGCTATA GAAGGAATTA ATAATAAGAT AAAATTAATC AAGTGAATTT 120
 CTTTGGTTA CAGAAATTTT AACCACTTTA AAGCACGTAT AATGATGATT TTCAGCTTGT 180
 ACAAGGAGA AAAAAAGAAG ACAACCAAGC CCAATAATGG ACTGGCCGCC TAATAATAAA 240
 35 AGCTCTAAAA GTTGATTTTT AAAAATAGTT CTTTAAATTA TATACCCACC ACATTTGGTG 300
 GAGGAACCTA AAAAAAGCA CTCCCAAAA ATGGGAAAGT GCAGTnAGTG GAGCCATAGA 360
 GGATTCCGAA CCTCGGACCC TCnGAnT 387

(2) INFORMATION FOR SEQ ID NO: 3979:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3979:

50 TGGAGCAGAA GACGGGATTG GAACCCGCGA CCCCAACCTT GGCAAGGTTG TATTCTACCG 60
 CTGAACTACT TCTGCATATG CGGGTGAAGG GAGTCGAACC CCCACGCCGT AAnTTAGCAT 120

CGAACCTCTG GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT 240
 CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTT CAGTTGCTCT 300
 5 ACCAATTGAG CTAGGCCGGn CAATATGTAA GAATAAATGG TGGAGAATGA CGGGTTTCGA 360
 ACCGCCGAAC CCTCTGCTTG TnAAGGGCAG ATGGCTCnTC 400

(2) INFORMATION FOR SEQ ID NO: 3980:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3980:

20 TTACCACGTA TTTAGGTTTC TTTGGTGGCT CTAGATTTGT CCCTATTGTC ACAGCATTTG 60
 CCGCAATCTT TTTAGGTGTA TTGATGTTTT TCATTGGGCC AAGCATACAA GCCGGCATTT 120
 ATCATGTTGG TGGATTTGTA ACGAAAACAG GTGCCATCGG TACTTTTGTT TATGGCTTCA 180
 25 TCTTAAGATT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTACTTACCG TTTTGGCAGA 240
 CGGCACTTGG TGGTACTTTA GAAGTCAAAG GGCACCTAGT TCAAGGTACG CAGAACATCT 300
 TCTTTGCTCA ACTTGGTGAT CCAGATGTGA CGAnTATTAT TCCAGGTGTG TCACGCTTTA 360
 30 nGTCAGCCGT TTTAATACGA GGATGTTCCG CTAnGTGGTG 400

(2) INFORMATION FOR SEQ ID NO: 3981:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3981:

45 CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC 60
 GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 120
 CTGGAATAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GATACAATTC 180
 50 AAGTTGTTGC AACGCAAGGG AAGCGGAGAG ACAGTGTAGT GGATGGAGCA ACGTATAGTT 240
 GGATTTTACA GTTGTGCGAC CACAACCGAA CCAAGCGACT GACTGAAGAT TTGGCAAAAT 300
 GGnCATATTG ATATCACGCC TAATGAnTCC ATTCAGGACA TTTAATTAAT CCAACTCAAG 360

(2) INFORMATION FOR SEQ ID NO: 3982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3982:

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 60
 TAATGTTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAGCAAA 120
 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT 180
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG AAAATTATAG GTGTTGAACC 240
 TTCAGTGCAA GTAGTATGTA TGAATCTGTT GTGGTAAATA ATCAGGTAGT CACATTGCCT 300
 AATATCGATA AATTTGTGGG ACGGTGCATC TGTAGCTAGA GTTGCGGATA TTACATTGGA 360
 AATTGCCAAA GAAAAGTAGA GGATTACGTT CCAGTAGAGn 400

(2) INFORMATION FOR SEQ ID NO: 3983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3983:

CCACCATTAT TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT TTACCAAGCA 60
 AAACCGAGTG AATAAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA TCGCTAGTGT 120
 TCGAAAGAcG CGACAAGATT AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG 180
 CAGACAATGA GTTAAATTAT TTAAAGCAG AGTTTACTTA TGTAAATGAG CATTTAAAAT 240
 AATGAAAACG AGGCCGTATG TGGAGCGTTT GACTTATnAA AAATGGTGGG AAACATAGAT 300
 TCAAGTTATT GAAGGGCGCA CGGTGGGATG CCTTGGGCAC TAGnAAGCCG nTGGAAGGAC 360
 GTTACTAACG ACGATATGCC TTGGGGGAGC 390

(2) INFORMATION FOR SEQ ID NO: 3984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3984:

5 GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTTGC CTTGTATCTG CAAATGTTTT 60
 GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC ACAAATTCAA ATGTATCAGG 120
 10 CGTTTCTTTT ATCCATTTC AATATTTTCT TTCCGGTTGT ATCGCATAGT ATGTGCGATC 180
 TAATTCGACA ACCGGAAAAT GTCCAGCATA TGTTTTAAGT TTATCGGTTT GGC GTTCTAA 240
 ATCTTCATAT AATGAATAGT GATCACCCTA ACCTGTTAAT CCGATGTTTT ATCATATATA 300
 15 TCACCAATGT CATCATACCA TATAACTTTT ATCATnATCA TTTCAGCGAA CTTTAGGTTT 360
 GnAGGTTTTT TGGCCTGGAT TAAAnATCTT TCGGGCGGAT 400

(2) INFORMATION FOR SEQ ID NO: 3985:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3985:

30 GCATTTGCTT ATATCTTTAA AAAAGATTTT GAAGATATTG AAAGAAAAAC TAAAGAAATT 60
 ATTTCTGATA TTGAAAGTAA AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT 120
 AAAAAAnCAGC AGTAAGATAA TTTTCAATTA GAAAATATCT TACTGCTGTT CTCTATTTAT 180
 35 ACAATACTTC GTATTGAAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTTGGTCTTC 240
 GACTGGCACT GCTCCCTCAG GAGTCTCGCC ATTGAATACT ACGTATTAAC ATGTnAATTT 300
 TACTTTGGAA ATACTTTTAA AAAATAAGAC ACTTTGCCCA ACTTGGCACA TAAATGTTAA 360
 40 AATnCAATGA AATGAATTTT CTGTGTTGGG TCCCCTnCTA 400

(2) INFORMATION FOR SEQ ID NO: 3986:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3986:

55 TTCGTTCAAA GTCATCTAGG TCACATTATT CTATTTGGGA TTCTTAGTGC TGTTCTTATT 60

ATGACAATAC AAAACGTAAA AAAGTCGCAG TGATCGGTAG TATTTTAGTA TTTATCATT 180
 GTATTCCAGC AACCTTATCT TTTGGTATCT TAAAAGATGT AAGATTCCGT GCGGGAACGA 240
 5 TTTTGTATAA TATGGATTTT ATCGTTTCGA ATGTATTGAT GCCATTAGGC GCATTAGGTA 300
 CTACGCTTGT CGTAGGnCAA TTATTAGnTA AAAAAATTATT ACAnCAATAT TTTGGTAAAG 360
 AnCGATTTAG GATTATTCAG TGGTTGGTAT TACTTAATTA 400
 10

(2) INFORMATION FOR SEQ ID NO: 3987:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3987:

GGATTGGAAC CCCCGCGAGC CGTTAAGCCC CTGTCCGTTT TCAAGACCGA TCCCTTCAGC 60
 CGGACTTGGG TATTCCTCCA AAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA 120
 25 CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC 180
 TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC 240
 30 TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAG TAATATGGTG GGGACTAnCG 300
 GGATCGGAAC CGCTGGACCT CTGCGTGGC AAAGCAGGCC GCTCTCCCAG CTGGAGCTAA 360
 GnCCCCCATA ATAATnACAG TATATCnGGG AAGACAGGAT 400

35 (2) INFORMATION FOR SEQ ID NO: 3988:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3988:

CAGCTGATAA ACAAGTTGAT CTGGTCCCGA TTTGTTGGGT AAACGGTTGA TTAATGnAAA 60
 ATGTTCCGCG AAGGATTCAT AATCCGAGAG GTCTAATTCA ACGTATCATT AATCAAGATG 120
 50 CGCCTATTTA TCAATCTGAA ACAAATTATC ATTCGAAAGA TCGCGGTAAG TCTAAAAATG 180
 GTATTCAAAT GGTGTATCAA CATTTAATGA ACGGTGTATC GTTTATGGnT CCTTTTATCG 240
 TAGTTGGTGG ACTCCTTATC GCCATCGCGC TGA CTCTAG GCGGTGAACG ACCATCCAAA 300
 55

CCTTTAAATT AATGGTCCCA TACCAGnCGG GATAAACGCT

400

(2) INFORMATION FOR SEQ ID NO: 3989:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3989:

CCAGAGATT CCGAATGGG GAAACCCAGC CATGAGTTAT GTCATGTTAT CGATATGTGA 60
 ATACATAGCA TATCAGAAG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA 120
 GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCAAACGG GAAGAGCCCA AACCAACAAG 180
 CTTGCTTnGn GGTnTGTAGG ACACTCTATA CGGATTACAA AGGACGACAT TAGACGAATC 240
 ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT CGAAAATGTT GTCTCTCTTG 300
 AGTGGATCCT GAGTACGACG GAGCACGTGG AAATTCCGTC GGAATCTGGG AGGACCATCT 360
 CCT 363

(2) INFORMATION FOR SEQ ID NO: 3990:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3990:

TTTCCAAGAA CATGAGCCTG TACAGTTAAC ACCATGTnTG nTTCTTACTT CTTTATCGTG 60
 GCTCCAACGT TCTCTGTACA TTTTTTCCCA TTCTCTACTT TTTACTTTCTA GGATCGACCA 120
 ATTCCCATTA AATTTTTCTG TTGGCTTAAA GAAATTCAAT CCAAATTTTC CCATATTTAT 180
 ATCTCCTAC GTATAAAAAT ACGATGTGTA GATGTCGTGT TTTTAAATAC TTTAAAATGC 240
 CCAAGACTAT TGCTTTAATT AGATTGTACA TTTTTTCACA AACATAAAAT ATTAGGGAAT 300
 CACCTAATTA CTTAAGGnAT TCCCTATCAA TAACGGGATT TCATTGAAAT AATACACAAT 360
 CAGTAnGGTC AGCCTAATGC CAGGCTAAAT CGTTCAAATT 400

(2) INFORMATION FOR SEQ ID NO: 3991:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3991:

	AAAGTGGTTA AATATTATAG AAAACATCAA AGGATGTTAA GAAATACAAT TTATTACCCA	60
10	GCATTTAATA ATGGTGCTAT AGAAGGAATT AATAATAAGA TAAAATTAAT CAAGTGAATT	120
	TCTTTTGGTT ACAGAAATTT CAACAACCTT AAAGCAnGTA TAATGATGAT TTTCAGCTTG	180
	TACAAAGGAG AAAAAAGAA GACAACCAAG CCCAATAATG GACTGGCCGC CTAATAATnn	240
15	GAGCTCTAAA AGTTGTATTT TAAAAATAGT TCTTTAAATT ATATACCCAC CACATTTGGT	300
	GGAGAACCTA AAAAAAGCA CTTCCCAAAA ATGGAAAGTG CAAGTAGTGA GCCATAGAGG	360
	ATTCGAACCT CTGACCCCTCT GATTAAAAGT CAGATGCTCT	400

20

(2) INFORMATION FOR SEQ ID NO: 3992:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
25	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3992:

	AGTGTATGGT TATCAAAGAT TTGATACGAC GGTCAATTATT ATTACCGTTA TTGTATTAGT	60
	CATTATTGTC CAAGTGATTC AAACGCTAGG GAATGTTCTA GCTAGATTCA TACGTnGACA	120
35	TTAATGATAT ATAGTGAAGA TTTTGAAAGG AATTGATAGA ATGAAAAGAT TGATTGGGTT	180
	AGTTATCGTA GCACTTGTAT TAATTAGCAG CGTGTGCTGG TAACAATGAT AAAAAAGTAA	240
	CAATTGGTGT CGCATCAAAT GACACTAAGG CTTGGGGAGA AGGTTAAAAG AATTAGCTAA	300
40	AAAAAGATGG ATnTTGATGT GGGAGATTAA GCACTTCCTC nGGATTACAA TTTACCGGAT	360
	TAAAGCCTTn AAATGGATGG TGATATTGAT AATGAATGCC	400

45

(2) INFORMATION FOR SEQ ID NO: 3993:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 383 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3993:

TTATCAGAAG AACAAATTCGA CATTTTACTG AATCATCCAT TAATCGATGA AGAAGTAGCC 120
 AATAGTTTAA TTGAAAATGT CATCGCGCAA GgGCATTAC CCGTTGGATT ATTACCGAAT 180
 ATCATTGTGG ACGATAAGGC ATATGTTGTA CCTATGATGG TGAAGAGACC TTCAGTTGTC 240
 GCTGCAGCTA GTTATGGTGC AAAGCTAGTG AATCAGACTG GCGGATTTAA AACGGTATCT 300
 TCTGAACGTA TTATGATAGG TCAAATCGTC TTTGATGGCG TTGACGATAC TGAAAAnTnT 360
 CCGCCGGCAT TGAGAGCCTT AGA 383

(2) INFORMATION FOR SEQ ID NO: 3994:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3994:

GGTACTATGA TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTCGT 60
 GCGGGTCGGA ACTTACCCGA CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC 120
 GCCTTTACTG GGGCTTCGAT TCGTAGCTTC GCAGnnAAAC CnACTCCTCT TAACCTTCCA 180
 GCACCGGGCA GCGCTCACCC TGATACATCA CCTTACGGTT TAGCAGAGAC CTGTGTTTTT 240
 GATAAACAGT CGCTTGGGCC TATTCACGTC GGCTCTTCTG GCGGTTAACC CTGAAAGAGC 300
 ACCCCTTCTC CCGAATTACG GGGTCATTTG CCGATTCCTT AACGAGATTC GCTCGCTCAC 360
 CTTAGA 366

(2) INFORMATION FOR SEQ ID NO: 3995:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3995:

AGATATTTTA CATGTGAATC AAGTAGGTAT TCATGATAAT TTCTTTGAAT TAGGTGGCCA 60
 TTCATTAAAA GCAACGTTAT GnTGAATCGG ATAGAGGCAT CTACTGGGAA ACGATTACAA 120
 ATTGGTGATT TATTACAAAA GCCAACTGTA TTTGAACTAG CACAAGCGAT TGCTAAGGTT 180
 CAAGAACAAA ACTATGAAGT GATTCCAGAA ACTATAGTTA AAGATGATTA TGTGCTGAGC 240

GTACCTTTTT TATGGCGGTT ATnCATCAGA ACTTAATGTA GCTCAnTGCG ACAAGCATG 359

(2) INFORMATION FOR SEQ ID NO: 3996:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3996:

CAATTATTGG TATTCAACTT AAAGATCATG ATGATTTAAT ACAACTCAAA CAACGTTnAA	60
ATCATTTCGA TCCTTCCAAT ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTAA	120
TTTAACACAT AGTAAGAAAA ACAGTCATAA ATTGATTCTT AATTGAAATC ATCTTATGAC	180
TGCTTTTTAT TATACTTTAC ATTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA	240
AGCCATCTTT CTTTGTGTTT GCTTTTATTT TGACGTTTnA GACATAAAAA AAGAGACCTT	300
GCGGTCTCAA ATGCGGCTCA TCGCATCCAC TTTTnGCCTG GGCAACGTTT TACTCTAGGC	360
GGAAAnGTAAG TGGGACTTAC CATCGACGn TAAGGGGCTT	400

(2) INFORMATION FOR SEQ ID NO: 3997:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3997:

GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGACCAC TTATCGTGGT GGGAGACAGT	60
GTCAnGCGGG CAGTTTnACT GGGGCGGTCG CTCCTAAAAG GTAACGGAGG CGCTCAAAGG	120
TTCCCTCAGA TGTTGGAAA TCATTCATAG AGTGTAAGG CATAAGGGAG CTTGACTGCG	180
AGACCTACAA GTCGAGCAGG GTCGAAAnCG GACTTAGTGA TCCGGTGGTT CCGCATTGAA	240
GGGCCATCGC TCAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG	300
TTCACACGAC GGGGAGGTTT GGCACCTCGA TGTCnCTCA TCGCATCCTG GGGCTGTA	358

(2) INFORMATION FOR SEQ ID NO: 3998:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3998:

5 TAGGAGGAAT TTATATGACA TTTGAAAAAG AAACGGTCTT AAAAACATTA TTTCCTGAAG 60
 ATGTACTTAG TATTGCTAAA GGTTTAACAG ACGGTGAAGT CGAATTTTTA CAACAAGTAG 120
 ATTCATTGCT AGAAAGTAAG TACCGTGAAA ATATTAATCA ACATTGGATA GACGCTACTG 180
 10 TACCCGAGGA CTATTTTAAA GATCTGGGAG AATTAAATTA TTTTAACAAT CCATTACTTT 240
 ACAAGGATCG TCCAAACGCC AAAATGCCTA GTCAnCTATT TCAGTTTTTC ATGTCTTACC 300
 TACTCGCGCG ATTTGATATT TCCTTAGCTA CCCTACTCGG TGTTACACAA GGTTAGGGCA 360
 15 TAACACTTTC TATTTTCGGAG GTAGCAAAGA CAAATTGCGA 400

(2) INFORMATION FOR SEQ ID NO: 3999:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3999:

CGCCCCCTTAG TGCTGCACtA ACGCATTAAg CACTCCGsCT GGGGAGTACG ACCGCAAGTg 60
 30 AAACtCAAAG GAATTGACGG GGACCCGCAC AAGnGTGGAG CATGTGGTTT AATTCGAGGC 120
 AACGGtAGAA CCTTACCAAA TCTTGACATC CTTTGACAAC TCTAGAGATA GAGCTTTCCC 180
 CTTCCGGGGAC CAAAGTGACA GGTGGTGcAT GGTTGTCGTC AGCTCGTGTC GTGAGATGTT 240
 35 GGGTTAAGTC CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTa AGTTGGGCAC 300
 TCTAAGTTGA CTGCCGGTGA CAAACCCAGG AAGGTTGGGG ATGACGTCAA ATCATCATGC 360
 40 CCCTTATGGn TTTGGGTTAC ACAAGTGGTT ACAATGGG 398

(2) INFORMATION FOR SEQ ID NO: 4000:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4000:

50 TGTTCTTGCA ACGCTATTTA GTATCAGGTT TAACAACAGG TGCGACAAAA GGTTAGTTTG 60

55

GACGTTATGA TGACGATTAA AGTTGGAATC ATTGGGTGTG GTGGTATTGC GAATGGCAAG 180
CACATGCCAA GTTTACAAAA AGTTGAAAAT GTTGAAATGA TCGCATTTTG TGACGTAGAC 240
5 ATTTTCGAAAG CAGCGaGTGC GGCAGAAGCA TACGGAAC TG ACAATGsCAA aGtTTATGAT 300
GATTACmAAG CaTTGTtAAA AGATGACACG ATTGATGTTA TCCATGTTTT GTACCCCCAA 360
TGGACCCCGC ATTGTGG 377

(2) INFORMATION FOR SEQ ID NO: 4001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4001:

TCGGGTTC TC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACATGTAG GCCGTTGTCA 60
CTTAAC TTCT TGTTTTCCG ATGACAGCTT CTATTAGAG AATGTCATGA TTATTTTATA 120
25 TTCAC TTCAA TGTTATCAAT ATTAGTGCCA TCTATGACAT CTGCCATGCG ATTTTCTTGT 180
AATTTTTTGT GCAATTCAAA CGTGTACTTT CCACCGTTTT TCATTTTAAT AACAAATTTA 240
CCTGAACCAA CGTTACCGTA CAGATTATTT TTTTCAATAA GTGTTTTCTC AATTTAAAAT 300
30 CAAGTTCTTT CAAGGAAATC TGTTCTTTAG TAATCTTGAA TTCTGAAACA TCATGGGnGA 360
TTGTACCGTA TnATCTTnCC TAGTAAT 387

(2) INFORMATION FOR SEQ ID NO: 4002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4002:

CTATTACGAT TGCTGCGAAA GAAGGTATTA AAAATATACA AATAGGCATG GCTCACCGTG 60
GACGTTTAAA CGTTTTAACG CATGTCTTAG AAAAACCGTA CGAAATGATG ATTTCAGAAT 120
TTATGCATAC AGATCCAATG AAATCTTAC CTGAAGATGG TAGCTTGCAG TTAAGTCTG 180
50 GATGGACTGG TGATGTGAAA TATCACTTGG TGGGCATTAA AACTACTGAT TCATACGGTA 240
CAATGCAGCG TATTGCACTG GCTAACAAATC CAAGTCACTT GGAAATTGTT GCACCTGTTG 300

TCCATCATAA AnGCAATGnC CATTGTTGAT ACATGGCGAT

400

(2) INFORMATION FOR SEQ ID NO: 4003:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4003:

AGAAATATAT GCATTTTCGGA TATCATGGTA AAGAGAATGG ATTAAGCGGT AAATCACGTG	60
ATGAAGTGCG AGCGAAATGA AACAAAATTT AGATGTCATG CGAGACGATA ATCAAAGGGA	120
CGACAGGTGA TGGGGTTGAA AGTGTAAcGn GCTACACTGG TCATGATGCT GCTAAACTAC	180
GTGATTATAA TGAAACACAT CATGCTTTGT CTGGATATGA AATGATTGAC GCAGCAAAGG	240
TGCCATTGCA ACAAATGAAG TCAATGCTGC GATGGGTATT ATTTGTGCAC GCCAACAGCT	300
GGTTCCTCGG GTACCATTCC CGGTGCACTT TTAAATTAG GAAAAACAC ATGATTTAAC	360
AGAAGAGCAA ATGATTTGAT TTCTTATTCA CTTcAGCATT	400

(2) INFORMATION FOR SEQ ID NO: 4004:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4004:

TGAAATAGAA CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC	60
GTGCCTTTTG TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT	120
GGAGCCGTAG CGAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GACCGAAACC	180
AGGTGATCTA CCCTTGGTCA GGTGGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA	240
CTTACGTTGA AAAAGTGAGC GGATGAACTG AGGGTAGCGG AGAAATTCCA ATCGACCTGG	300
AGGATAnTGG TTCTCTCCGA ATAGTTTAGG GCTAGCCTCA AGTGTGATTA TTGAGGTAGA	360
nACTGTTTGA CGAGGGGCCC TCTCGGTAC CGAATTcAGG	400

(2) INFORMATION FOR SEQ ID NO: 4005:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4005:

	ATACTAAGGC GTTATTAGAC GaTTAGACAA TGGTGTGATT AAAGGTGCAG CACTTGATAC	60
10	GTATGAATTT GAACGCAAAC TTTTCCCAAG TGATCAAAGG GGCAAAACAC TGAACGATCC	120
	ATTGTTAGAA TCGTTGATTG ACAGGGAAGA TGTCATATTA ACACCACATA TTGCGTTTTA	180
	TACTGAAGCT GCAGTTAAAA ATCTAATTGT CGATGCATTA GATGCAACAT TAGATGTATT	240
15	GGCAGACTGG AGATACTAGG TTACGAGTAA ATTAAAAATC GAACTGATGA GATAATTTGG	300
	ATTGTTGGGG ATTCTGCATC CAGTTCGATT TTTTAAATTT GGTGTTGGAT GACGTTGnAA	360
20	TGTTGCCTAA TTTAAACGAC ATCGTAAACC nTGGATCCTC CAATGGCGTC CTnC	415

(2) INFORMATION FOR SEQ ID NO: 4006:

	(i) SEQUENCE CHARACTERISTICS:
25	(A) LENGTH: 444 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4006:

	CTAACAGAAG CTAGTATAGG AAATCGGTAC TCGTTAAGGC TGATCTGTGA TGGGGAGAAG	60
35	ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA AAGCCTCTAG ATAGAAAATA	120
	GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG	180
	AACTCTCGTT AAGGAACTCG GCAAAATGAC CCCGTAACTT CGGGAGAAGG GGtGCTCTTT	240
40	AGGGTTAACG CCCAGAAGAG CCGCAGTGAA TAGGCCCAAG CGACTGTTTA TCAAAAACAC	300
	AGGTCTCTGC TAAACCCGTA AGTGATGTAT AGGGGCTGAC GCTGCCCGGT GCTGGAAAGT	360
	TAAngAGAGT GGGTTACTTC TTGCGACTTA nCGAAATCGA GnCCCCAGTA AACGGCGGGC	420
45	CGTAACTATA ACnGTCCTAA GGTA	444

(2) INFORMATION FOR SEQ ID NO: 4007:

	(i) SEQUENCE CHARACTERISTICS:
50	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

TTTGAAGCTCT ATCAAAGCAT CAGCAATCAA AACATACGTA TCTTTACAAC AGTAATCATG 60
 CATTCTATGA TGCTTCTAAC TGAATTAAAG CATCGAACAA TCGGAAGCAT ATTTCTAAAT 120
 5 TATTTATTCA TTATAGTCTT AACATAACA TGACCTAATA TATTACTAAC CTATTAAAAT 180
 AAACCACGCA CATCTAAGTG ATATACGACA ATCAGAGCAA TAATAATTGC TTTAGAAAGT 240
 10 CGTGCCGAAC TGGAAGTTAC AAGTCTAGTT CGAACACACA CTGATGTGAG TGGTTTTCTT 300
 TATTTTAAAC ATGAACAATC AGATAAGTTA CTAGCATTAG CAAATATTAT TAAATCAAGG 360
 GCTTCGnTTC ATAAATTTAA AACATGTTAA ATTAGACGTG 400

(2) INFORMATION FOR SEQ ID NO: 4008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4008:

TATACTTGTT TTTACAAACC ACAAAAAGCT CTAAACATTA GTTTAAACCA ATGCTTAGAG 60
 CTTTCTAATT ATTTTATGCT TTAAAAGATA CTGTGTTATC TACGATGACC TTACCGTCTT 120
 30 TAATAACTTT TTCTGCGTGA TTGATACCAA AATGATATGG AATATATTCA TGATTTGGTG 180
 CATCCCAAAT TACTAAATTA GCCTTATCAC CTGTGTTAAT TGTACCCGCG TTAATGTCTA 240
 TTGCTTTAGA GCCATTGACC GTAACAGCAT TCCAACTTC ATTAGGTGAT AGCTTTAATT 300
 35 TCAAGGCTGC AATCGCCATA ACAAGTTGTA AGTTGTTTGT GGACACTACT ACCAGGGTTA 360
 TAATCAGTTG GCTAATGCCA TCGGCACCGG TTAATGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4009:

ACAAACATTG AAATTAGAGG TATATAAAAA ATGCTTCTGC AATAGATGCA ATAAACATGC 60
 AATACAATAT GGAGGCGAAG TAAATGAAAA GTATTACGTT TGAAGAACAT TATGTCATTG 120
 55 AAGATATTCA AAAAGAAACG ATGAATGCCA TATCAGCAGA TCCTAAAGGT GTACCGATGA 180

ATCATGATGA ACGTATCCAA TTTATGAATA ATCAAGACGT TCAAATTCAA GTCTTATCTT 300
 ATGGAAATGG TTCTGCTTCA AATTTGGTTG GTCAGAAAGC CATTGAATTA TGTCCAAAAG 360
 5 GCAAATGATC CATTGGGCAA ACTATATTGC ACCATATCCC 400

(2) INFORMATION FOR SEQ ID NO: 4010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4010:

ACTAGAGAAG GTATGTTACG TGACAATGAA TTAATAAATG GTATTTATTC ATCGAGTTAC 60
 20 ATCTATAGTT TATTAAAATC AGAATACGAC CAAAAATGAC AAATTAGACT TACAAAAGAG 120
 TGATGACATT TAAATGGCA GCGCTCTTTT ATTTAATTTT TGAAAATAAA AGGTTGTTGA 180
 CAGTATTATT TTATAACAAT ATAATGATTT TGATAATTAT TATCAACTAG ATGATGTTTA 240
 25 TGGGAGGATG CTTTAAAACA GCCGTTTTAA GTGTAATGTA TTATTTTAGC GTGTAGGGAT 300
 GCGAAAATAT ATTTATAGGA CACATCTTGG GGATAATnGA TTTCTATAAT GAGGTGTCAA 360
 30 ATGGAAAAGT TACCACGCTA TTATTAGCCn CCACGTTATT 400

(2) INFORMATION FOR SEQ ID NO: 4011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4011:

TnTCAATTAG AAAATATCTT ACCGCTGnCT CTATTTATAC AATCCTCGTA TTGAATGGnT 60
 CGCTTTCCTA GGGTGCCGTC TCAGCATCGG CTTGCGACTGG CACTGCTCCC TCAGGAGTCT 120
 45 CGCCATTAAT ACTACGTATT AACATGTAAT TTTACTTTGA AATACTTTAA AAAAATAAGA 180
 CACTTTGCCC AACTTACACT ACCAATAAAA ACTTCTGTTA GAATTCCTCA AAATGATATT 240
 50 TCGCGACATG TTAATGAAAT TGTGAAACG ATACCTGATA GCAAATTCGA TGAATTCAGA 300
 CATCATCGTG GCGCAACATC CTATCATCCA AAGATGATGT TAAAAATCAT CTTATATGCA 360
 TATACTCAAT CTGTATTTTC TGGTCGTAGA ATAGAGAAAT TACTTCATGA CAGTATTCGA 420

GAATCCnAAT ACTG

494

(2) INFORMATION FOR SEQ ID NO: 4012:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4012:

15	TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGACATA	60
	AAAAAAGAGA CCTCACGGTC CAACTTGCCT GGCAACGTTC TACTCTAGCG GAAGTAATTG	120
	GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTC	180
20	CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCTCTTT TCTCGTTTCG	240
	TCAGATTCAA ACGTTTTCAC TTCGCCAAGC CATTTTTCTT TGTGTTTACT TTTTATTTTG	300
	ACGTTTTAGG CATAAAAAAA AGAGACCTTG CGGTCCCAAT GCGGGCTCAT CGCATCCATT	360
25	TTTTGGCCTG GGCAACGTTC TnATnCCAGC GGAAnTnAAT	400

(2) INFORMATION FOR SEQ ID NO: 4013:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4013:

40	CGAACTGCCG AACCCGAAGA GCGGATTAC AGTCCGCCGC GTTTACCACT TCGCTACCCC	60
	TCCAGCTTAT TCATATAATT TAATAATCAA AATGGTGGAG AATGACGGGT TCGAACCGCC	120
	GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGACT	180
45	CCTACGGGAC TCGAACCCGT GTTACCGCCG TGAAAGGGCG GTGTCTTAAC CGCTTGACCA	240
	AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTAA CAGCCGATAG	300
	CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTTA CTCTnAGCGG	360
50	AACGTGAATT CGACTTACCA TCGACGnTAA GGAGCTTnAC	400

(2) INFORMATION FOR SEQ ID NO: 4014:

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4014:

	ATTAGGACCT CAAGACGATA TTACTAAATT TGAATACTTA AAAAAATCTT CTCAAAATAC	60
10	AGGTACTTCA TTATTGGTAT TCAACTTAAA GATCATGATG ATTTAATACA ACTCAAACAA	120
	CGTGTGAAAT CATTTGATC CTCCAATAT TTATATTAAT GAAAAATAAGA TGTATATTC	180
	ATTGTTAATT TAACACATAG TAAGAnAAAC AGTCATAAAT TGATTTCTAA TTGAAATCAT	240
15	CTTATGACTG CTTTACATT ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTT	300
	ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTATTTT GACGTTTTAG ACATAAAAAA	360
20	nGnGACCTGC GGTCTCAATG CGGCTTCATC GCATCCACTT	400

(2) INFORMATION FOR SEQ ID NO: 4015:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4015:

	GAATGAAAAG CTCTAAAAGT TGTATTTTAA AAATAGTTCT TTAAATTATA TACCCACCAC	60
	ATTTGGGGAG GAACCTAAAA AAAAGCACTT CCCAAAAATG GAAAGTGCAA GTAGTGAGCC	120
35	ATAGAGGATT CGAACCTCTG ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT	180
	AATGGCTCTG AATGGCTGGG CTAGCTGGAT TCGAACCAAC GAGTGACGGA GnAAAGGTCC	240
40	GTTGCCTTAC CGCTTGGCTA TAGCCCAATA TATAGATGGT GGAGGGGGGC AGATTGGAAC	300
	TGCCGAACCC GAGGAGGCGG ATTTACAGTC CGCCGCGTTT AGCCCACTTC GnTACCCCTG	360
	CCAGnTTATT CATATGA	377

45

(2) INFORMATION FOR SEQ ID NO: 4016:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4016:

ATGACGCACC TGACATCCTC TCGGTTTATA TTCAGGCATA TCCGGACCAC AACTTGGATA 120
 GTCAGTTTGT TGATTTTCCC AGGTAATCAC ACCATTTTTC ACAAATACTT TCCAAGAACA 180
 5 TGAGCCTGTA CAGTTAACAC CATGTGTTGT TTCTTACTTC TTTATCGTGG CTCCAACGTT 240
 CTCTGTACAT TTTTCCCAT TCTCTACTTT TACTTTCTAG GATCGACCAA TTCCCATTGA 300
 10 AATTTTCTG TTGGCTTAAA GAAATCAATC CAAATTTCCC ATATTTATAT CCTCCTACGG 360
 GTGAAAAATA CGGTGTGTAG AnGTCGTGGT TTTnAAAATA 400

(2) INFORMATION FOR SEQ ID NO: 4017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4017:

CTTTGAGCGC CTCCGTTACC TTTTAGGAGG CGACCGTCCC AGTCAAACCTG CCCGnCTGAC 60
 25 ACTGnCTCCC ACCACGATAA GGGCGTGGGT TAGAAAGCCA ACACAGCTAG GGTAGTATCC 120
 CACCAGCGnC TCCACGTAAG CTAGCGCTCA CGTTTCAAAG GCTCCTACCT ATCCTGTACA 180
 30 AGCTGTGCCG AATTTCAATA TCAGGCTACA GTAAAGCTCC ACGGGGTCTT TCCGTCTCTGT 240
 CGCGGGTAAC CTGCATCTTC ACAGGTACTA TGATTTTACC GAGTCTCTCG TTGAGACAGT 300
 GCCCAAATCG TTACGTCTTT CGTTGCGGGT CGGAACTTAC CCGACAAGGA ATTTTCGTTAC 360
 35 CTTAGGACCT TATAGTTACG GCCGnCTTTA ATTGGGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4018:

TGTCGATTTA AGAGGCATGC TACGAGGAAT GATTGGTCAT CCGAAAAAG ATCGAGCGGC 60
 50 ATATGAGGCA CGCCAAGCGA TTCAAACAT TAATGAAAAC AGTCCGCCAA TATTAATTGT 120
 ACATGGAGGG AAAGACCAGC AAGTTGGTAT TCATCATGCG TATTATTTAG CGGACCAACT 180
 AGAGTTAAAA GGTGCCACGC ATGnAAACAT TTTATCAAAT GGCAGAAGGA CATGTGCCAA 240

CGCATAGCTT AGTTATGGAA ACGTGGTGTG CGCATGGGGA ACTATTCAAG CTTTGGAGGA 360
 TGTGGTACTT ACATGCGTTG GAATTAGGGG TCCGGTACT 400

(2) INFORMATION FOR SEQ ID NO: 4019:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4019:

GGAGGTTTGG CACCTCGATG TCGGCTCATC GCATCCTGGG GCTGTAGTCG GTCCCAAGGG 60
 TTGGGCTGTT CGCCCATTAAG ACGCGTACCA AGCTGGGTTC AGAACGTCGT GAGACAGTTC 120
 GGTCCCTATC CGTCGTGGGC GTAGGAAATT TGAGAGGAGC TGTCTTAGT ACGAGAGGAC 180
 CGGGATGGAC ATACCTCTGG TGTACCAGTT GTCGTGCCAA CGGCATTAGC TGGGTAGCTA 240
 TGTGTGGACG GGATAAGTGC TTGAAACATC TTAAGCATGA AGCCCCCTC CAAGATGGAG 300
 ATTTCCCAAC TTCGGTTTnT AAGATCCCTC CAAAGnTGAT GGAGGTTTAA TAGGTTTCGA 360
 GGTGGGAAGC AnGGTGGACA GTTGGGAGCT GGACGAnTAC 400

(2) INFORMATION FOR SEQ ID NO: 4020:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4020:

GAAGATGTTT GTCATTCTTC AAATAAACCA GAGCTAGTTG CAATTGCTGA ACCAGCATCT 60
 AATAGACCGA AAAAGAGAAG TAGACGTGCG GCACCGGCAG ATCCTAATGC AACTCCAGCA 120
 GATCCAGCGG CTGCAGCGGT AGGAAACGGT GGTGCACCAG TTGCAATTAC AGCGCCATAT 180
 ACGCCAACAA CTGATCCTAA TGCCAATAAT GCAGGACAAA ATGCACCTAA CCGAnTnTTG 240
 TCATTTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAA CAGTTAAACG 300
 TTTGTAAATA ACTTGCCGGG CTTCACTA ATCAATGGTG GGCAAAGTAn GGGTGTTTAG 360
 TCATGCAATG GGTAAGAACG AGCATGTTTG GATTTTCAGG 400

(2) INFORMATION FOR SEQ ID NO: 4021:

(A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4021:

10 CTAAGTCATG AATGGGAAGT GGCTCGCGTT GAAGAAGGAC TGACTIONGTC TGCCACACAG 60
 CTGCTAAAC AATTATCAGA ATTAGATTTA GCGTCACATC CTTTTGTGAT GTCAGAGCAG 120
 TTTGCAAGTn TAAAAGATCG TCCATTTTCAT CCATTAGCTA AAGAAAAAAG AGGATTAAGA 180
 15 GAAGCGGATT ATCAAGTGTA TCAAGCTGAA TTAAATCAAT CATTTCTTTT AATGGTTGCA 240
 GCAGTTAAAA AGACACATAT GATTCATGGC GATACTGCAA ATATCGATGA ATTAGAAAAT 300
 TTGACAGTAC CTATAAAGA ACAAGCGACA GACATGTTAA AATGATCCAA GGTATCANT 360
 20 AGATGACTAT GTACCATTC GGTACnTCCT GGCCAT 396

(2) INFORMATION FOR SEQ ID NO: 4022:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4022:

GATTGGTCTG nAAGAAGAAT TAATGGAAAA GCTACGTGAA AAATTAGAAG CGGCATTGTA 60
 35 TACGATTTAC GAATTGTCTC AAAACCGAAA AATAGATATG AGACTTGCAg CATATATCAT 120
 AGGTATTAAA CGTACAGCAG AAGCAGCTAG ATATCGTGGT TGGGCATAAT TAATTATCAT 180
 ATGTGATTTA ACGAGCTTGG GACAGAAAAC AAAGCCCTAA GCTCGTTAAT TTTATTTTAG 240
 40 CAGTAGTTGA CTGTAAAACA ATGCCCCGTGT AAACGCTCTT TTCAAAAATA GTCGGGGCCC 300
 CAACACAGAG GCTGGTGGGA AAGTCAGCCT ACAATAGnGT GCAAGTTGGC nGGGGCCCCA 360
 45 ACACAGAGGC TGGCGG 376

(2) INFORMATION FOR SEQ ID NO: 4023:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

CAAATGGTGG AGCCATAGGA GGATTGGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT 60
 CTACCAACTG AGCTAATGGC TCTTCCATGG nGcngGCCAG AGGACTTGAA CCCCCAACCT 120
 5 ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC GGCAATATGT AAGAATAAAT 180
 GGTGGAGAGT GACGGGTTCG AACCGCCGAC CCTCTGCTTG TAAGGCAGAT GCTCTCCAG 240
 CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT TACTCTAGCG GAAnTAATTC 300
 10 GGACTACCAT CGACGCTAAA GGAGCTTAAC TTCTGTGTTC CGGCATGGGA ACAGGTGTGA 360
 CTCCTTGCTA TATCACCAGA C 381

(2) INFORMATION FOR SEQ ID NO: 4024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4024:

GCCCCTTATG ATTTGGGCTA CACACGTGCT ACAATGGACA ATACAAAGGG CAGCGAAACC 60
 GCGAGTCGAA GCAAAATCCCA TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC 120
 TACATGAAGC TGGAATCGCT AGTAATCGTA GATCAGCATG CTACGGTGGA ATACGTTCCC 180
 30 GGGTCTTGTA CACACCGCCC GTCACACCAC GAGAGTTTGT AACACCCGAA GCCGGTGGGA 240
 GTAACCTTTT AAGGAGCTAG CCGTCGAAGG TGGGGACAAA TGGATTGGGG TGAAGTCGTG 300
 AACAAAGGTAG CCGTGATCGG AAGGTGCGGC TGGGATCACC TCCTTTGCTG AAGGATGATG 360
 35 ATTTCGGnAA CATCnTTCTT CCAGAAGATG CCGGTAATAA 400

(2) INFORMATION FOR SEQ ID NO: 4025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4025:

CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGGG TGAGAATCCC GTCCACCGAT 60
 50 TGCTAAGGTT TCCAGAGGAA GGCTCGTCCG CTCTGGGTGA GTCGGGTCCT AAGCTGAGGC 120
 CGACAnGTAn GGCATGGAT AACAGGTTGA TATTCCTGTA CCACCTATAA TCGTTTTAAT 180

GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT 300

GTGTCTTCGA GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AA 352

5 (2) INFORMATION FOR SEQ ID NO: 4026:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4026:

15

TGGGGCTCTT CCCGTTTCGC TCGCCGCTAC TAAGGGAATC GAATTTTCTT TCTCTTCCTC 60

CGGGTACTAA GATGTTTCAG TTCTCCGGGT GTGCCTTCTG ATATGCTATG TATTCACATA 120

20

TCGATAACAT GACATAACTC ATGCTGGGTT TCCCCATTCTG GAAATCTCTG GATCAAAGCT 180

TACTTACAGC TCCCCAAAGC ATATCGTCGT TAGTAACGTC CTTTCATCGGC TTCTAGTGCC 240

AAGGCATCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 300

25

ANGTTAACAT GAAGTTAGGT TCTTTTATAA AAGGATTAAA nGGGTTATTA ATCTTGTGnG 360

TGTTCTTTTCG 370

(2) INFORMATION FOR SEQ ID NO: 4027:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4027:

40

TCAIGTTTCG CTTGGTTTAA TGCTGTAAAT GCGTTATCGA CACGATGTTT TTCATCTGAA 60

ATTTGTTGTG CAGTTGCATC GCCATTGTCA ATAACACGTT GAGCTGCAGT TATTTAGTT 120

TCTGCTCCG CTTCTTCGCA TTATAGTTAT CAATACTTTG TTGCGTCATA CCAGCAGTTG 180

45

ATGGTACTTG GTTCACAGAA CTTTGTAAGT TATTTTATAGA CGTTACTAAT TGGCTATTAT 240

CTTCTTTATT TTGAAGTAAT GCTTTACTTG GATCAATCTT AGTTTGTGCG CACGAACTTT 300

AGTTAGTGCG TGCAGAAACT TGTTGTGGTG TTGCACGCTC ATThATGAAG CACTGTTGGT 360

50

GCCTCCGTTT TCGCATAnTG GATTGTTGTT GCGCATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 4028:

55

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4028:

10 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGGCTAC 60
 CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 120
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA 180
 15 TTCAAACGTT TTCAC TTCG CAAGCCATTT TTCTTTGTGT TTACTTTTTTA TTTTGACGTT 240
 TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC 300
 CTGGGCAACG TTCTACTCTA GCGGGAACGn AGTTGGGCT TACCATCGAC GCTAAGAACC 360
 20 TTTCTTGGAC TTGGTGGACA AACGGnGTGG CTGCTTTTCC 400

(2) INFORMATION FOR SEQ ID NO: 4029:

- (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4029:

AGGACTTGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC 60
 35 GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC CCTCTGCTTG 120
 TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT 180
 TACTCTAGCG GAAnTAATTC GGA CTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG 240
 40 GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG TAATTTGATA 300
 CATTCAAAC TAGATAGTnA AGTGAAAAGT GATTTTGGnT TCGCAAAACC ATTTGATTTT 360
 GATTGAAGTC CTTGATCGA TTGAGTGATT CGTGCAGCTn 400

45

(2) INFORMATION FOR SEQ ID NO: 4030:

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

GATGATAAAT CATGTTTTTC ATACCAAGTC GCTGCCGGCA AAACAATGTC AGAATATAAC 60
 GGTGTTGCCG TCATTCTGAA GTCTAAAGAG ACCACTAAAT CTAACCTACC TGTTGTTTCT 120
 5 TCACGCCACG TAATTTCTTC TGGCTTTTCA TCTTCATTG GTGTAGCTAA TAACCCTGAT 180
 TTTGTGCCAA GTAAATGCTT CATAAAGTAT TCTTGACCTT TTGCAGAACT TGAAATTAAG 240
 10 TTTGAACGCC ATATAAATAA TGATTTTGA TGATTCTTTT CAAATCAGGA TCTTCTATTG 300
 CAAATTGTGG TTTGTTTGG ATTTCACTC ATCAATTGCA CGTTGCAAAA TCGCTTCATG 360
 TGAATCTATA CCCTGCATCT TGTAGCTCC 390

(2) INFORMATION FOR SEQ ID NO: 4031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4031:

TGGTTGGAAT CCAGCTAGCC CAGTTATTGG CGGCATAGCA AGTGGTAAGG CAGAGGTCTG 60
 CAAAACCTTT ATCACCGGTT CAAATCCGGT TGCCGCCTCC AGGTTTATGC GGGAGTAGTT 120
 30 CAACTTTTAG AACACGTTCC TTCCCGGAAn GAGGTATAGG TGCAAATCCT ATCTCCGCT 180
 CCATAATTTA ATAATAATGC GGGAGTATTT CAACTCTTAG AATACATTCC TTCCTGGAAT 240
 GAGGTATAGG TGTAATCCT ATCTCCGCT CCATAATTTA ATATTTGCGG GGAGTAGTTC 300
 35 CAACTTTTAG AACACGTTCC TTCCCGGGA GGAGGTATAn GTGTATCCTA TCTTCCGCTc 360
 CATAATGCCT TCCAAAGGGG AATTTTTTGG TTTnACCATT 400

(2) INFORMATION FOR SEQ ID NO: 4032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4032:

GTATCGATGA GTTTCTTCGG TGCCTCTTCG ACAGCCATTT TGACTTCGAC AAAATGCATC 60
 ACATCGGGAT GACCATTAAT TGCATTAAAC GTGTCTTGTA AATCTTTTGA TGATTCAACG 120
 55 TCATGAATTT CAACATTTTT ACCACCAAAT ACAGCTGGTA AAGCTTTATA ATCCACATG 180

TTATTAATCA CCAATAATAC CGGGTTAATA TGCTGTCTAA TCATAGTTGG AAATAGCTTG 300
 AACAGTTAGT TGGCCATGAG CCATCACCCA TTTAATAATA AGTTACGACG GATCTTTGGT 360
 5 CTGCCAATTG GGGGAnCnCA ATGTTGCAGG GnAATGGTAT 400

(2) INFORMATION FOR SEQ ID NO: 4033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4033:

CACGACGTTT TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTgGG 60
 20 ACCGACTACA GCCCCcAGGA TGCGATGAGC CGACATCGAG GTGCCAAAct CCCCCTCGAT 120
 GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCggGGTA GCTTTTATCC GTTGAGCGAT 180
 GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 240
 25 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTCC AACCATTCTG 300
 AGGGAACTTT GAAGCGCTCC GTACCTTTTA AGAnGGCGAC CGGCCCAGTC AAACCTGGCCG 360
 CTGACACTGT CTTCCAACAC GATAAGTGGT GCGGGTTAGA 400

(2) INFORMATION FOR SEQ ID NO: 4034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4034:

AATTCCATGT GTACGGTTGA AATGCGCAGA GATATGGAGG AACACCAGTG nCGAAGCGAC 60
 TTTCTGGTCT GTAACGTACG CTGATGTGCG AAACGTGGGG ATCAAACAGG ATTAGATACC 120
 45 CTGGTAGTCC ACGCCGTAAA CGATGAGTGC TAAGTGTTAG GGGGTTTCCG CCCCTTAGTG 180
 CTGCAGCTAA CGCATTAAAGC ACTCCGCCTG GGGAGTACGA CCGCAAGTTG GAAACTCAAA 240
 GGAATTGACG GGGACCCGCA CAAGCGTGGn AGCATGTGGT TTAnTTTCGAA CAACGCAGAG 300
 AACCTTACCA AATCTTGACA TCCTTTGACA ACTCTAGAGA TAAAGCCTCC CCTTCGGGGA 360
 CAAATGACAG TGGTGCAngT TGTCTCACT CGTGTCGTGA 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4035:

```

10  TTCGCTTTGC CCGTCTGTCA CATTACTGTA AAATTCTATA AATAGAATTT TTGATGACGG      60
    GTCCCTTCCT AGGGTGCCGT CTCAGCCACC CCAACCGGCA CATTGTTGTA AGCTGACTAT      120
15  ATGTCAC TTC TGTGTTGGGG CCCCTGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC      180
    CATTAATACT ACGTATTAAAC ATGTAATTTT ACTTTGAAAT ACATTAAAGC CCAAATTAAT      240
    CAAAAGCTTT CTGAACCAGA AACGAAAAAA ATCTATAGTC ATAGAAAAAT TTATGTAGAG      300
20  CCTGTTTTTG GATTATGAA GGCTATTTGG GGTTCAC TCG AATGTCAGTT CGAGGAATAA      360
    TnAAGTnAAC GAGAGCCAGG TTTGTAATTA TGGCACTnAT      400
  
```

(2) INFORMATION FOR SEQ ID NO: 4036:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4036:

```

35  TAAATGTTGA AAAAGCACGA TTAGATAGAA TTTTGAATAA CAATGAAATT CGTCAAATGA      60
    TCACAGCATT TGGTACAGGA ATCGGTGGCG ACTTTGATCT AGCGAAAGCA AGATATCACA      120
    AAATCGTCAT TATGACTGAT GCCGATGTGG ATGGAGCGCA TATTAGAACA TTGTTATTAA      180
40  CATTCTTCTA TCGATTTATG AGACCGTTAA TTGAAGCAGG CTATGTGTAT ATTGCACAGC      240
    CACCGTTGTA TAAACTGACA CAAGGTAAAC AAAAGTATTA TGTATACAAT GATAGGGGAC      300
    TTGATAAACT TAAATCTGAA TTGAATCCAA CACCAAAATG GCTATTGCAC GTACAAAGGC      360
45  TTGGAGAATG AATGCACTCC ATTTGGGAAC ACATGACCTG      400
  
```

(2) INFORMATION FOR SEQ ID NO: 4037:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4037:

TCGTCGCTAA AGACCTTTCT TGA_{CTT}GTGA CAATCGCTTG CTTCTTTCCT CTCCTTCGGC 60
 5 TCTCGCTTAC TCATTTAGCT CTA_{CTAA}ACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT 120
 CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT 180
 AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA TTTTTGCCT 240
 10 GGCAACGTTT TACTCTAGCG GA_{AT}TAAATT GGGCTACCAT CGACGCTAAG AACCTTTCTT 300
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TTCTTCGGCT CTCGCTTAC_n CATTTAGCTC 360
 15 TAC_nAAACTC GTTGCCTCTT T 381

(2) INFORMATION FOR SEQ ID NO: 4038:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4038:

CTGTTTGTCA TACTTCATAA ATCCTTTAAA TTCACCCATC GTATCTCCCC CTTTCCTTAA 60
 TACACAACGG CTGTTTATG TTTAGCATCG ATTGTTTAC TGTATCGTA AAATGCAGCT 120
 30 AACATCGCTT CATCTTCATT GTCATGTAAT GATTTGTGCA AATGAATTTT TTGCATCATT 180
 AATTGATAAT CTTTAGGAAT AACTTTAACG ACGACATCTT CAATGCGATC AAAATGTTTT 240
 35 AACACATGAA TCGCTCTCGT ACTATTCGTG TGTGACACAT GT_nCTTCCAG CATTTGCTTA 300
 ATGAATGCTT TT_nCTTCTTG GTGTTTAATC TTTGTAAACG AAAGCGTATC TAGTGATAnG 360

(2) INFORMATION FOR SEQ ID NO: 4039:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4039:

AGTGCGAACC CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC 60
 50 GCATATGTTT TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAG TGAnTGCACT 120
 CACCGCAGAT TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG 180

55

GAAGTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GCTnAGGATC 300
 CTAAGTCTAG TGGCTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC 360
 5 GAACCTCTGG ACCCTCTGGA TTAAAAAGTC AGATGCTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4040:

CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTCTCTCTCC TTCGGCTCTC GCTTACTCAT 60
 20 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 120
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTGTAGAC ATAAAAAAG 180
 AGACCTCAGC GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 240
 25 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC 300
 GGCTCTCGCh TACTCATTTA GCTCnACTAA ACTCGTTGCG CTCTTGTTCT CGTTTCGGGC 360
 30 AGATTCAAAC GnTTGTCA 378

(2) INFORMATION FOR SEQ ID NO: 4041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4041:

GTACCTTAAC AATATCTCGA AATGGACGAA CTAAATTATG AACCGCATGA AAGGATACTT 60
 GCGAATCATT TGAGCATGCT TGAATCATAA TATCACCATC GCTGTAATCG TCTATTAACT 120
 45 GATCATTCGG AAAATGCGGT AAATCTTTAA AGGCATCGGG AATTTTACTA GATAACCCAA 180
 TTTTCTTCAT CAAAGACTTA CTAATCCCAA AGGTAATCGT TAACTTGCTT GCACCTAATC 240
 50 CTATCGATTC ACCGGTATCT ACTGGTGGGC ATTAAAGGAT TGTTACTCGG GCTTGGCCAA 300
 CTGTATCACC ATCCATCATA CGATTCAGCC ATAACGGTCC ACTTTTTTAA ACATTGGCTT 360
 TATTGGCACC CnAACCTTTG GACTTCnAAT CTAACGGCCA 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4042:

GACTTGCAAA CGTTGTGATG ACGGTCAAGA AACTGGTAA CACACCAGAC GGACGTAAAG 60
 CTGGCGAACC ATTTGCTCCA GGTGCAAACC CAATGCATGG CCGTGACCAA AAAGGTGCAT 120
 TATCTTCATT AAGTTCTGTA GCTAAGATCC CTTACGATTG CTGTAAAGAT GGTATTTCAA 180
 ATACATTCAG TATCGTACCA AAATCATTAG GTAAAGAACC AGAAGATCAA AACCGTAACT 240
 TAACTAGTAT GTTAGATGGT TACGCAATGC AATGTGGTCA CCACTTAAAT ATTAACGTAT 300
 TTAACCGTGA AACATTAATA GATGCAATGG AACATCCAGA AGGAATATCC ACAGTTAACA 360
 ATCCGTGTAT CTGGTTACGC TGTAACTTC ATTAAATTAA 400

(2) INFORMATION FOR SEQ ID NO: 4043:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4043:

CTATTTTATC TAAAGTTAAA CCTGACCCAC CTAGAATTGA CGCAAACCTCT GTGACATATA 60
 AAGCAGGTCT TACAAACCAA GAAATTAAAG TTAATAACGT ATTAAATAAC TCGTCAGTAA 120
 AATTATTAA AGCAGATAAT ACACCATTAA ATGTCACAAA TATTACTCAT GGTAGCGGTT 180
 TTAGTTCGGT TGTGACAGTA AGTGACGCGT TACCAAATGG CGGAATTAAA GCAAAATCTT 240
 CAATTTCAAT GAACAATGTG ACGTATACGA CGCAAGACGA ACATGGTCAA GTTGTTCAG 300
 TAACAAGAAA TGAATCTGTT GATTCAAATG ACACTGCACA GTGAACAGTG GACACCACAA 360
 TTGACAAGCC AACTACTGAA GGCGCnGTGn TTATTAAAG 400

(2) INFORMATION FOR SEQ ID NO: 4044:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4044:

5 AAAATGGCTT GATTTGAAAA ACGACCAGCA TCGCTACTG G_nATAATAGC GAGGCTACCA 60
 TGTGTGTTTCA TCGTAG_nCGC ATGTTAGTTA ATCCAGGGAT ACAAGCATCA TGATCAATAT 120
 TAAAGCCATA TTCAAACAAT TGACCATAAG GTTCAATGTA AGCAGCGCCG GTGCACTTGC 180
 10 ATTCCAGCTG AATTAGAGCG ACGTGCAGCA TAAGCCAAGT CTTCTTTTGT AATATAGCCT 240
 TCTTTTGTTG ATGTGTTTAC GGTCCATTGG GTGGATAATA CAAAGCGATT CGAAATTTTG 300
 ATGCCATTAG GTAAGTGGAT TGATTGTAAA AGTGGTTTGT ATCGGTACAT ACTATGATTC 360
 15 C_nTTTCCATT GCAAT 375

(2) INFORMATION FOR SEQ ID NO: 4045:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4045:

GTTCCAATGA AGATAGCTAG AAATGATATC CAAAACACAT GATGCATCAC TGGTGATGCT 60
 30 CGACTAATTG TATTCCATGA TGCATTAATA ATAATGACCA ATACACATAA AATAAGCAGC 120
 CATTTATCGT TTATTTTAAA AATATAATGC AGCAAAAATC CCAAATGAT TAATTGCACA 180
 ACTGCTCGTA ATGTCGCAAC AATTAAATCT TTAATAATAT GTAAACCTTC TTTATATGAA 240
 35 ATGATAATCG GAATGACTAA AAGCAATGCC GTCAATCCAA GTGCCGTATT ACTCATGT_nG 300
 ATTCAACTCC TCTGTATTAG AAATTTGACC ATCAACAATT GTTATACGCT TTTTG_nAAGT 360
 GGTCGCATAC TTTGGGGCAT CGCTGTGGGG TAGGGGG_nC_n 400

(2) INFORMATION FOR SEQ ID NO: 4046:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4046:

CGAGTCTGAG TCGCTGTCTG AATCTGAATC GCTGTCTGAG TCCGAATCGC TATCTGAATC 60
 TGAGTCGCTG TCTGAGTCTG AATCGCTATC TGAATCTGAG TCGCTATCTG AGTCTGAGTC 120

TGAGTCTGAG TCGCTATCTG AGTCTGAGTC GCTGTCTGAA TCTGGAGTCG CTGTCTGAAT 240
 CTGGAATCGC TGTCTGGAGT CTGAATCGCT ATCTGAGTCT GGAATCGCTA TCTGAGTCTG 300
 5 AATCACTGGT CTGGAGTCCG AGTCACTGTC TGAATCTGAC TGCACnACn GGATTCTGAG 360
 TCGCTAACnG GAATC 375

(2) INFORMATION FOR SEQ ID NO: 4047:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4047:

20 ATGGGTAAAA AGGCATTAGA GTCAATCATT GATAACGCTG ATGAAACAAC TCAAGAGCGT 60
 TTACGTTT CAG GATATGAAGA TGCTGTAGAT TATAACCGTT ATGTCGGTAA TATTTATACT 120
 GGATCATTAT ATTAAAGCCT AATATCATT CTTGAAAATC GAGATTTACA AGCTGGTGAA 180
 25 ACAATCGGTT TATTCAGTTA TGGCTCAGGT TCAGTTGGTG AATTTTATAG TCGGACATTA 240
 GTTGAAGGCT ACAAAGATCA TTTAGATCAA GCTGCACATA AAGCATTATT AAATAACCGT 300
 ACTGAnGTAT CTGTTGGATG GCATATGGAA ACATTCTTCC AAACGTTTTG GATGACGGTG 360
 30 GAATTTGACG GnGGACCAAG ATGChTGTTC CAGGAGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4048:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4048:

45 CAAACCATCT GACATAATAT AACTTGGAT GTTAGATAAG GGTTTGCCAA TTGGAATCGT 60
 CTCAGGTATC AATCACCACA ATGATGTGAC CAATACGATG TGATGACTGT TGA CTCAGAT 120
 GGTCCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTTAAC AAAGGATGCC 180
 50 GTACTAGTTG CCCC GCCTGT AATCAACTTT TCAATATAAA AGTCTTCCAT AACACTACAC 240
 ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTA ACTGT 300
 TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAC 360
 55

(2) INFORMATION FOR SEQ ID NO: 4049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4049:

TCTGCATGTT CTCGAGATCC ACCAAATGTT AAATGGGTAT GTGCATCTAC TAATGCTGGG 60
 GACACTACCT TCCCACTAGC ATCAATCGTC TCAGTCGCAT CGTAGTCATC TGTATGTGTT 120
 CCAGCATATA CAATTTTGGC CATCTTTAAT GACAACTGTA CCATTTTTC AACAATTGTA 180
 ATTCACTCTAA TTCCTTACCC TTCAAAGGTT TATCTGTTGA TCTCGGTAAA ATTAATTGCT 240
 GCTATATGAT TANTATTAAA TCATTCATTA CTATCACCTG CTTATCAATC ATGGAATAGA 300
 ATACCTTTTC nTTAGCGTTT GAATAGCGAG TCATAGCCAG CATCAACATG TCGGGCAACA 360
 CCCATACCGG GGTCACTCGTC CAATACACGT TCCAAnCTnC 400

(2) INFORMATION FOR SEQ ID NO: 4050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4050:

ATCACCCATG TTCTGACTCC CAAGTTAAAT TAATTGGCAT TCGGAGTTTG TCTGAATTCG 60
 GTAACCCGAG AGGGGCCCCCT CGTCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG 120
 GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTGATT GGAATTTCTC 180
 CGCTACCCTC AGTTCATCCG CTCACCTTTT AACGTAAGTC GGTTCGGTCC TCCATTCAGT 240
 GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACAAATA 300
 CTAAACGCCT ATTCAGCTCG nTTCTGACGG CTCCACATTT ACTGCTAAAnC TTGCATCAAT 360
 CGTACTCGCG GTCAATCTAC AAAAGnACGC ATCACCAnTA 400

(2) INFORMATION FOR SEQ ID NO: 4051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4051:

5 AGTGAAAATG ACTTTATCGG GCTGTTTCAGC GATATGGATT TGAGTTCAAC GCGACTAGGT 60
 AACAAATGTCA AAGAACGTAC TGCTTTAATC TCTAAAGTCA TGGTTAATCT TGACGACTTA 120
 CCATTCGTTT ACAGTGACAT GGAAATTGAT ATGTTAGGTG ATGCATATGA ATTCCTAATC 180
 10 GGGCGCTTTG CGGCGACAGC GGGTAAAAAA GCAGGCGAGT TCTATACACC ACAACAAGTA 240
 TCTAAGATAC TGGCGAAGTT GTCACAGACG GTAAAGATnA ATTACGTCAC GTGTAACGAC 300
 15 CCAACATGTG GGnTCCGGTT CATTGTGGTA ACGTGTGGT AAAGAACGCA AGTGTATCGT 360
 TAATTCGGAC nAAGAACGTA ACAATACTAC nTACGACTTA 400

(2) INFORMATION FOR SEQ ID NO: 4052:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4052:

30 TCCTACAACC CCAACAAGCA AGCTTGTGGT GTTGGGCTCT TCCCGTTTCG CTCGCCGCTA 60
 CTAAGGGAAT CGAATTTTCT TTCTCTTCCT CCGGGTACTA AGATGTTTCA GTTCTCCGGG 120
 TGTGCCTTCT GATATGCTAT GTATTCACAT ATCGATAACA TGACATAACT CATGCTGGGT 180
 35 TTCCCATTC GGAAATCTCT GGATCAAAGC TTACTIONAG CTCCCCAAAG CATATCGTCG 240
 TTAGTAACGT CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGGC CCTTAATAAC 300
 TTAATCHnATG TTTTCCACCA TTTTTTATAA GThCAAAGGC TTCACATACG GCTTCGGTTT 360
 40 TTCATTAATT TTAAATGGCh CAATTTAACA 390

(2) INFORMATION FOR SEQ ID NO: 4053:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4053:

AACATACCGA TGTATATAAT CTATACACAA AGGATAATTA CTTATGCAAA GGCGGAGGAA 60

GTCGATTGCG AATGATTTAA GAGGGAACAT GGATGCGAGT GAATTCGTA ATTACATTTT 180
 AGGCTTGATT TTCTATCGCT TCTTATCTGA AAAAGCCGAA CAAGAATATG CAGATGCCTT 240
 5 GTCAGGTGAA GACATCACGT ATCAAGAAGC ATGGGCAGAT GAAGAATATC GTGAAGACTT 300
 AAAAGCAGAA TTAATTGATC AAAGTCGGTT ACTTCATTGA GCCACAAGAT TTATTTCAGTG 360
 10 CGATGATCGT GAAATTGAnA CGCAnGATTT CCGATATAGA 400

(2) INFORMATION FOR SEQ ID NO: 4054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4054:

GTAAGACCAT CGTACTTGAG TCTTCAAGTG TTCTTGATAA AACGGAACGA GAGACTTGTT 60
 ATTTTTCGAA CAAATCTTTC ATTAACACAC CGACCATAAT AATTACAATC GAAGCAACAC 120
 25 CTGCAGCGAA TACAAGCGCA ATACAACAAA TAACAGTAAT ACATATTAAA CTTCTACAG 180
 AATGGATGCC TTTAGAAATA GTAGTTAATA AGACTTCTAA ACATCCTGCT TTTTCTACAA 240
 30 TACCTGCAAA TGCATATCCG CAAATATCG TTACTAATAT TTGGGnCATA CTCATCATAC 300
 CACCCTGTTT TAACAAGCTT TCACACTGGA TGAATATGAG nTGATGTATC ATTGATCGTT 360
 AAACCCTAAT GTGCTTTGAA CCATCGTCAT TTGAATGTGA 400

(2) INFORMATION FOR SEQ ID NO: 4055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4055:

CGTCTACAAG TTCAAAATTC AAGTCTTCCA TAATTGGTTT AACATCACT TCTACTTGTT 60
 CTGTAATTTT ACTCATACAG GCCTCCCTTT TTGGCAAATA GAAAAGAGCG GGAATCTCCC 120
 50 ACTCTTCTGC CTGAGTTCAC TAATTTTTTAA GCAACTTAAT TATAGCATAA GTTTATGCTT 180
 GAAACAAATG ACTTCACTAT TAATCAGAGA TTCTTGTAATA AGTTTGTTCC TTTATTTTAC 240
 CATTACATTT GAATAGACTC GTAAGACATT GAAAAGAAAT ACGGGCATAA TTTTGTGTCC 300

TCATTTTACA TATCAAATAT CGGAAGTTGA GCTTTATCTG

400

(2) INFORMATION FOR SEQ ID NO: 4056:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4056:

ATTTTGTTTT ACTTCATGTT GAGTTTTAGA CATTTTAACC ATCTCCAATA TAAAAATAAA 60
 TTAAATTAAA TTCTCAGGGA CTGTCATGAC GCCACCTGTA TTTGCGCTAG TTACTAGGGC 120
 AGTATAACGA GCTAGATAAC CTGTTTTTAC TTTCGCTTTA AATGGTGTTA AAGATTCTCG 180
 GCGACGCGCT AGAACATCTT CAGGCTGGTT TACGTTTAAT GTACGATTG TTAAATCAAT 240
 AGTAATCTCA TCACCATCTT CAATTAAgGc AATTGGTCCA CCAGATGCAG CTTCAGGGGA 300
 AATATGaCCA ACTGcAATAC CTCTTGTTGgC ACCGGtAAAA ACGCCCATCA GTKaATTAAT 360
 GCaACATCTT TACCTAAGCC GCGaCCAACA ATAGAGGAAG TAGGTGCTAA CATTTTCAGG 420
 nCATACCTGG GTCCACCTTT TAGGTGCCTT TCAnTATCTn ATGGACAACG ACGTGGGCCT 480
 G 481

(2) INFORMATION FOR SEQ ID NO: 4057:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4057:

TTTTTGCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GTCGCTAAAG 60
 ACCTTTCTTG ACTTGAGACA ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC 120
 ATTTAGCTCT ACTAAACTCG TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA 180
 CTTGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GGACGTTTTA GACATAAAAA 240
 AAAGAGACCT TCGGGTCTCA ATCGGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT 300
 ACTCTAGCGG AAGTAAATTG GGCTACCAnc GACGCTAAGA ACCTTTCTTG GACTGTGACA 360
 ATCGGCTGCh TCTGTnCCT 379

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4058:

CTGCATCACT GCCATAAAAA CTACCGTCAG CAGCGATAGn CGGCCAATCA TACCAGGAAC 60
 AAGACCGGGC TTGTCAGCGA TACTAACAGC GATATATCCA GCTAGTATTG GAACCATAAA 120
 TTTAAAGGCT AAACCTACCA TGTTTTCAAT GGATTTCCAA AATGAATCAT CTGGGATGAC 180
 TAATCCTTTT GATGTCGTTT CACCGCCTAG AGTCAGCGCG ATGGCGATAA GGAGTCCACC 240
 AACTACGATA AAAGGAACCA TAAACGATAC ACCGTTTCATT AAATGTTGAT ACACCATTTG 300
 AATACCATTT TAGACTnACC GCGATCTTTC GAATGATAAT TTGTTTCAGA TGGTTAAATA 360
 GGCGCATTTG ATTTAATGAT ACGTGGATTT GGACCCTCGG 400

(2) INFORMATION FOR SEQ ID NO: 4059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4059:

TTAAAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAACTA AGTnGAnCTA CCATCGACGC 60
 TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120
 CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180
 TCGCAAACA TTTATTTTGG ATTAAGTCTT CGATCGATTA GTATTCGTCA GCTCCACATG 240
 TCACCATGCT TCCACCTCGG AACCTATTAA CCTCATCATC TTTGGAGGGA TCTTATAAAC 300
 CGAAATTGGG GAAATCTCAT CTTGAGGGGG GCTTnCATGC TTAGATGCTT TCCAGCACTT 360
 ATCCCGT 367

(2) INFORMATION FOR SEQ ID NO: 4060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4060:

TTCCGnACTC ACATAGCGAC TCAGGATTCA GACAGCGCAT TCAGATTGAG ACACCGCATT 60
 5 CAGATTGAGC ATAGCGATTG AGCATTCCGC ACAGTGACTC AGnATTCCGA CAGTGACTCG 120
 GATTGAGATA GCGATTGAGA TTCCGACAGT GACTGAGATT CCGACAGTGA CTCGAGTCA 180
 GACAGTGATT CCGATTGAGC GAGTGATTG GATTGAGATA GTGATTCCGA CTCGACAGT 240
 10 GACTCGGATT CAGATAGCGA CTCGAGTCTG GATAGCGACT CCGATTGAGA TAGCGATTCTG 300
 GACTGAGATA GCGATTGAGA ATCAGACAGC GATTGAGATT CAGACAGCGA CTCGACAGT 360
 15 GACTGAGATT CAGA 374

(2) INFORMATION FOR SEQ ID NO: 4061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4061:

AAAATCATAA TATTTGGCAA TTTTTTCAAC TTGACTCTGG TCCTTCTGCA TAACTGCCGT 60
 AAATAATTCA CCTTCATCAC ACGCTGTACC TACCAATAAT CCCTCAGGAT ATTCATCTAA 120
 30 CAATGAACGT GGAATTCGAG GTGTACGGTA GAAATACTTC ACCAATGATG CACTTACAAT 180
 TTTAAATAGA TTTTAAGAC CTTGTTGGTT TTGTACAATT AATGTGACAT GACTAGGTCT 240
 35 TGCACGTTTA TATGCATCTT CATTACTGAG TTTTtKGTtG ATTTGTTAT GATTTAATAC 300
 GCCTAAwTCy TTCATTTGTT GAACCATTTT TATGAAAATG TAAGCTGTTG CTTCTGTATC 360
 ATAAATGGCA CGGTGATGTT GCGTTAATTC TACGCCATAT TTTTtAGCCA AGAAATTCAA 420
 40 ACCATGTTTA CC 432

(2) INFORMATION FOR SEQ ID NO: 4062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4062:

TATCTTCGTT CTCAATAGAA TGATTAAAC CTTCGATTTC TTTATCTAAA TGACTACCAA 60

TTTTTCTTC AACTAAGTCA CGATATAATG TTTTGAATT TTCGTTCAAT TTCGATTTCGT 180
 GATTTTGAAT ACTTTTCTTC CACACAAATG TATACCTATT GGCATTAGCT TCTACTTTTG 240
 5 TACCATCAAT AAGATTTTGC TTAAACATT GACTATGAAA CTGGGATAAA TAAAGANTCA 300
 ATTAACGCAT CACTATTAGG GANTCACTCT AATACGATTA ATAGTTTTTA TAAGAAGGTG 360
 10 NTTGGATTG GAGCTAACCA CATCCA 386

(2) INFORMATION FOR SEQ ID NO: 4063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4063:

TAGGAGAGCG TTCTAAGGGC GTAGCATGAT CGTAAGGACA TGTGGAGCGC TTAGGAGAAT 60
 GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT AAGGTTTCCA 120
 25 GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCCTAAGC TGAGGCCGAC ACGTAGGGCG 180
 ATGGATAACA GGTGATATT CCTGTACCAC CTATGAATCG TTTTAATCGA TGGGGGGACG 240
 CATAGGTATA GGCGAGGTGA CGATTGGGAT TGCACGTCTT AAGCAGTAAG GCTGAGTATT 300
 30 AGGCAAATCC GGTACTCGTT NAAGGCTTGA GCTGTGGATG GGGAGAAGAC ATnGAGTCTT 360
 CGAGTTCGTT GGnTTTCACA ATGGCC 386

(2) INFORMATION FOR SEQ ID NO: 4064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4064:

TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT 60
 TACTCTAGCG GAACGTAAGT TGGAGCTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT 120
 50 CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT 180
 ACATTCAAAA CTAGATAGTA AGTAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 240
 AGTCTTCGAT CGANTAGTAT TCGTCAGCTC CACATGTCAC CATGCTTCCA CCTCGAACCT 300

AGGGGGGGCT TCATGCCTTT AGAATG

386

(2) INFORMATION FOR SEQ ID NO: 4065:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4065:

15	AATTCTTTTCG CTACTTGAAT GACAACACTT TGTTTTACGC CTGAAATGGC TTCTTGCCAA	60
	GCAGGTGTAT ATTTTGATTC TGCATCGTCG TATCCTTTTG ATTCTAATTT ATGATCAAAA	120
	CGACGCACGC CATATTGACT TGCCATTAAAG TCAAAAATTG TAGCAATACG GACTTTGTCA	180
20	CCATTTGCTA AAGTGACTTG TCGAGTTGGA ATTGGACGAT TGAATATCCC ATCTCCATCA	240
	CTATCAAAGT ATGGGAATTG AATTGTTTCT AATTCGTATC CACCTTCTGT CATTGATAAT	300
	GTAGGGTTAA TTTTAGAACC ATCTTCTGTT TCTAGTTTAA AGTTCCACTT CTTACCTTCT	360
25	TCCCAACGTG GACCCATGGT GCCATTAnGn ACTACTAAAC	400

(2) INFORMATION FOR SEQ ID NO: 4066:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4066:

40	ATTTTGAAAT TGAGAAAACA ACTTATTGAA AAACATAATC TTTACGGTAA CATGGGTTCA	60
	GGAACAATCG TTATTAAAT GAAAAACGGT GGGAAATATA CGTTTGAATT ACACAAAAAA	120
	CTGCAGAGCA TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA	180
45	ATATAAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAAC AAGAAGTTAA	240
	GTGACAACGG TTTACATGTT GCTTAGCTTC TTTTATTATG CGTAATGATG TAAAAAGACG	300
	nATATTCATT TGTGTGATAA AGTGGCATTG TATGTCTTAA AGTGACGnAA CTTCCAATGT	360
50	GCCCAGTGTT TGATTCACAT CAAATCCATT TTTATTTAAC	400

(2) INFORMATION FOR SEQ ID NO: 4067:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4067:

	CCTCATTCCA GGAAGGAATG TATTCTAAGA GTTGAAATAC TCCCGCATT	60
10	ATGGAGCGGA AGATAGGATT TGCACCTATA CCTCGTCCG GGAAGGAACG TGTTCTAAAA	120
	GTTGAACTAC TCCCGCATAA ACCTGGAGGC GGCAACCGGA TTTGAACCGG TGATAAAGGT	180
	TTTGACAGACC TCTGCCTTAC CACTTGGCTA TGCCGCCAAT AACTGGGCTA GCTGGATTCTG	240
15	AACCAACGAG TGACGGAGTC AAAGTCCGTT GCCTTACCGC TTGGCTATAG CCCATTAATA	300
	ATAAGGGCGG CTGAAGGGGA TCGAACCTC GAATGTCGGA ACCACAATCC GATGTGTAA	360
20	CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC	400

(2) INFORMATION FOR SEQ ID NO: 4068:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4068:

	TATCTAATAG TTTTACTTTA AGTCCAGCAT TCACAAAAAG TGCTGCCAGT TGAGCGCCCA	60
	TTGTGCCTGC GCCAAGAACG GTTACTTTAT TAATTGTCAT AGTGATTCCT CCAATTTAGT	120
35	TGAGGATAAG ATAACCATTAGATAATTGG AATAACGTTG CTATTTTATA AAATTAATTA	180
	AGTATCTTTG ACAGTCATCT TAGCCTCTTA TTTAAGGAAA AAGCTTTATG CTTAAAATAA	240
	GTCTTTTTTA GTGAAATTAA TGCATCTCAT ATAATTATTT GCTATTTATA CGAAAGCAGA	300
40	ATCTCCAGTC AAAGCGCGTC CANTACTAAG GCATTAATTT CATGTGTACC TCGTACGTGT	360
	AAATCGnTTC TGCATCAGnG AGGAAACGTG CAATATCATA	400

45

(2) INFORMATION FOR SEQ ID NO: 4069:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4069:

55

AAAAAGAAGA ATTGAAACGC CATATAAAGT AACGTAAAT AATAACGAAA AAAGGGCACT 120
 ATTCAAACAA TTAGCGTATG TTGAAGGGTT TGAAAAATAT CTTCATAAAA ACTTCGTTGG 180
 5 TGCAAAGCGT TTTTCAATTC nCGGGGTAGA CGCACTTGTA CCGATGTTAC AACGTACTAT 240
 TACGATTGCT GCGAAAGAAG GTATTAAAAA TATACAAATA GGCATGGCTC ACCGTGGGAC 300
 10 GTTTAAACGT TTTTAAACGCA TGTnCTTAGA AAAAACCGTA CGAAATGATG ATTTCh 356

(2) INFORMATION FOR SEQ ID NO: 4070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4070:

AAACGTTTAG GGAAAATTAT CACACAGATA CAACAATACA CAGATATTGA TTACCCGATA 60
 GCGATTGTCT TTCAAGCATC GTGTTTTAAC GAGTTTGTG TTAAGGGGCG TTTAAGTAAT 120
 25 ATTATTTCAA AATTGCAACA CTATTCAATT GAGGCCAAAC CAGGTATATG TATTATAGGG 180
 GAAGTTGTTG ATTATACTGA AAACACTCCT AAATCATATG ATCCTATGAA GCAATTTTAT 240
 GTAGTAAGTG GTTCTAAACA TGACGCCCTT ATGCTCTGTG AACATTATAT GACGAAGGTT 300
 30 ATGGCTGTTG CTAAACCCCA ATGATACATC GAATGGGCAC CATTATCCAn TCGTCGCAAT 360
 AATGGATTAC CCAAGGATGC CATTTAnTTA AGCCnGCCAn 400

(2) INFORMATION FOR SEQ ID NO: 4071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4071:

CCTCTGGAAA CCTTAGTCAA TCGGTGGACG GGATTCTCAC CCGTCTTTTCG CTA CTCACAC 60
 CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA CGCCCTTAGA 120
 50 ACGCTCTCCT ACCATTGTCC AAAGGnATnC CCACAGCTTC GGTAATATGT TTAGCCCCGG 180
 TACATTTTCG GCGCATGTGC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGGATGG 240
 CTGCTTCTAA GCCAACATCC TAGTTGTCTG GGnAACGCCA CATCTTTTC CACTTAACAT 300

T

361

(2) INFORMATION FOR SEQ ID NO: 4072:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4072:

ATGGTGACAA AACATCGCA TTATTACTAG GTGTCGGCAC AGGCGTTTGT GGTGCTGCTG 60
 CTATTGCCGC AGTCGCTCCA ATATTCAAAT CACGTGAAAA GGATACAGCT ATTAGTATCG 120
 GTATCATCGC ATTGATTGGT ACGATATTTT CACTTATATA TACAGCTATC TACGCTATCT 180
 TTTCAATGAC GACAAATGTT TATGGCGCTT GGTCTGGTGT TAGTCTTCAT GAAATTGnCA 240
 CACGTTGTCT TAGCTGGTGG CTTTGGTGGT AGTGATGCAC TTAAATTCG ACTTCTTGGT 300
 AAACCTGGTA GGAGTATTCT TACTGGATTC CCATTAACCA TCGTACTTAA TTTTAAATAT 360
 GCGGTTnCCG TnCATCAGG AnTCATCTAG GCAAGGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 4073:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4073:

GCGACGATCA TTTTAGAATC CGCTTGGGCG ATTAATTCTT TAGAAGTGA TGAGGCAAAA 60
 TGTTCAATTAT CAGGAACTAA AGCAGGTGCT GATATGAAAG ATGGTCTACG TATTCATGGT 120
 GAAGACATGG GTACACTTTA TACCAAACAC GTTGAATTGG AAAACAAAGG CGTCGACTTT 180
 TATGAAGGTA ATGAAGTGA TGAAGCTGAA GAAGAAGCAA AAGCTTGGAT TGATGCAGTT 240
 GTAAATGATA CTGAACCACT TGTGAACCGG AACAAAGCAAT GGTTAGTTACC AnAATTCTTG 300
 AAGCGATTTA TCCGTCTGCC AAATCCAGGC CAAAGCCATT TACTTTGGAA TAACATCnTA 360
 CCGGTAAGGG GGcncATCCT GGACCAAATT TAAAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 4074:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4074:

	TCTTCCTAAT ACCTTTCCAC GATCTTCAGC TGGCGCCTCT GCACTCGCAA ACGCACTTGA	60
10	TGCATCAACA ACACCACCAA ATAGTCCCTG CAATAACCTC ACAAGTACAA ACTGTAATGG	120
	TGTCGTACAC AATGCCATTA AAAATAAGCA TACCGCCAAA CCAAGTAACG CTCTTAACAC	180
	CATCCATTTT CGGCTGATCT TATCACCTAG CTTCCCCCAT ATCGGCGGAG TTATGCATCG	240
15	TCGTTACAGC TGGAGCAGCA ATCGCTATAC CACTCCACAA CTGTATTTCT ACGGACTGAT	300
	AGGATTTTGT AGTGATGnCC ATGATGAAAT GGGCAATAAT GGGCACAAGT ACTGTTTCAGT	360
	CCAGCCAATC GTTATGAAAC TGGACTGGGG CCATnAAATG	400

20

(2) INFORMATION FOR SEQ ID NO: 4075:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4075:

	GGTTCAGAAC GTCGTATGnA GTTCGnTCCC TATCCGTCGT GGGCGTAGGA AATTTGAGAG	60
	GAGCTGTCCT TAGTACGAGA GGACCGGGAT GGACATACCT CTGGTGTACC AGTTGTCGTG	120
35	CCAACGCATA GCTGGGTAGC TATGTGTGGA CGGGATAAGT GCTGAAACTC TAAGCATGAA	180
	GCCCCCTCA AGATGAGATT TCCCAACTTC GGTTATAAGA TCCCTCAAAG ATGATGAGGT	240
	TAATAGGTTT CGAGGTGGAA GCATGGTGAC ATnTGGAGCT GACGAATACT AATCGATCGA	300
40	AGACTTAATC AAAATAAATG TTTTGGCACA AATCCACTTT TACTTACTAT CTAGTTTGAA	360
	TGATAAATTA CATCCATATG	380

45

(2) INFORMATION FOR SEQ ID NO: 4076:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4076:

55

TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC 120
 CTACTGCGTC CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA 180
 5 TCCATCGCCT ACGCCTGTCG GCCTCAGCTT AGGACCCGAC TAACCCAGAG CGGACGAGCC 240
 TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC AnCCGTCTTT CGCTACTCAC 300
 10 AnCGGCATT CTACTTCTAA GCGGTCCACA TGTCTTACGA TCATGCTTnA AGGCCTTAGG 360
 AAGGTTCTTA CCATGGTCAA 380

(2) INFORMATION FOR SEQ ID NO: 4077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4077:

GCAGGTCTGA CTCTAGAGGA TnCCCACGCG CGCAAGATTT AAATCGAAGA AACCAGCAAC 60
 25 AGATTCTCTCA AAATAGCGCG GCGAACAACG AAACATCAAA TAGTGCACCT GCAGCTGGTA 120
 ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA TACTGCACCA AATAATAATG 180
 30 TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT ATCGACTACA CCACAAAGTA 240
 CAAGGCGGGA AnAAAGATGG TCAAAGTTTT GTAGATATAA CAACAACACA AGTCAGCACA 300
 GCTAACGAGA ACACACAAAA CATTACAGAT AAAGATGTTA AATCAATGGA AGCGGCATTA 360
 35 ACGGGCTCTT 370

(2) INFORMATION FOR SEQ ID NO: 4078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4078:

AAACATTTTA TCAAATGGCA GAAGGACATG TGCCAAGACC ACCAGCGATG GTTGAAACAT 60
 50 TGACTTATAT TAAAGAGTTT ATGAACCAAG TTGAGTCGCA TAGCTAGTAT GAAACGTGGT 120
 GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGG AATTAGGGAT 180
 CGGTACTTTA TATGAAGACG TGCTGCTTCC ATTAAATGAG TGATGCGATT TTGGCATGAA 240

TAAGAGGGGC CAACCATTTGT TAGAnATAAC AACGGTTGGC TCTTTAAntG T

351

(2) INFORMATION FOR SEQ ID NO: 4079:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4079:

15	TTGAAGTAAC TAAATTAATA TTATGTTGTT CAATTAAAAG CTTCATACAA ACCTAATCTA	60
	TTTGCACTCC ACCGCTAACA CCGAACACTT GTCCGGTTGT ATAACCTGAT TCTTCTGACG	120
	CTAATAGCAC ATAAGTTCCA CATAACTCAA CAGGTTGACC TGCACGACCT AAAGGTGTTT	180
20	TTTGACCAAA TGTTGGGATT TTACTTTGAG GTTGTCCACC AGAAATTTGT AATGGTGACC	240
	AGAATGGACC AGGCGCTACA CAGTTCCTC TAATTCCTT TGGTCCTAAT TCTTCTGAAA	300
	AACCTTTTAGT TAATGAAATA ATTGCTGCCT TTTGAAGGGG CATAATCCAT GAAGAATAnG	360
25	GCCAGGGAnT AAAACCCTGG ACnAAAGAAG CCGTGGAAT	400

(2) INFORMATION FOR SEQ ID NO: 4080:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4080:

	TCGTTGGACA CAATCTGAAA AATAAATAGA TATAAATTCG CGAGATATAT TCGTATTTAT	60
40	AGTAAAATTA AATAAGAGA TTATATAACA CGAGGAGTAG TAAGTATGAA ATTTGAGAAA	120
	TATATAGATC AACTTTTATT GAAGCCTGAG TCAACACGTA CGCAAATCGA TCAAATCATC	180
	GATGAAGCGA AACATTACAA TTTTAAATCT GTATGTGTGA ATCCAACACA TGTTAAATAT	240
45	GCAGCAGAGC GACTAGCTGA TTCAGAGGTG CTCGTTTGTA CGGTAATAGG ATTCCCATT	300
	GGTGCGTCGA CAACTGGCAA CGAAAGCATT TGAAACAGAA GATGCAATTC AAAATGGTGC	360
50	AGATGAATTG GACATGGTCA TCCACATCGG CGCATTAATA	400

(2) INFORMATION FOR SEQ ID NO: 4081:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4081:

	CGACTAGTGA GCTATTACGC ACTCTTTAAA TGATGGCTGC TTCTAAGCCA ACATCCTAGT	60
10	TGTCTGGGCA ACGCACATCC TTTTCCAATT AACATATATT TTGGGACCTT AGCTGGTGGT	120
	CTGGGCTGTT TCCCTnChCG AACACGGACC TTATCACCCA TGTCTGACT CCCAAGTTAA	180
	ATTAATTGGC ATTCGGAGTT TGTCTGAATT CGGTAACCCG AGAGGGACCC CTCGTACCAA	240
15	ACAGTGCTCT ACCTCCAATA ATCATCACTT GGAGGCTAGC CCTAAAGCTA TTTACGGAGA	300
	GAACCAGCTA TCTCCAGGTT CGATTGGAAT TTCTCCGChA CCCTCAGTTC ATCCGCTCA	359

(2) INFORMATION FOR SEQ ID NO: 4082:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4082:

30	TTTGACATTT AGTGTAAGCG TnTTACAAAT AAAGCGTGTT GTTTTTGAAT TAAATGCATT	60
	TCACATTAGT ATTCATATTA TTTTtaggag GAATTTATAT GACATTTGAA AAAGAAACGG	120
	TCTTAAAAAC ATTATTTCTT GAAGATGTAC TTAGTATTGC TAAAGGTTTA ACAGACGGTG	180
35	AAGTCGAATT TTTACAACAA GTAGATTCAT TGGCTAGAAA GTAAGTACCG TGGAAAATAT	240
	TAATCAACAT TGGATAGACG CTACTGTACC CGAGGACTAT TTTAAAGATC TGGGGAGAAT	300
	TAAATTATTT TAACAATCCA TTACTTTACA AGGGATCGTC CAAACGCCAA AnGGCCTAGT	360
40	CCAACTATTT nCAGTTTTT	379

(2) INFORMATION FOR SEQ ID NO: 4083:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4083:

	TTGAAACAGC CAGAGGTGTT TTATACCCAG GTGTTTCAGA TATGTATGAT GCGAAACAAT	60
--	---	----

55

TTGGAACATA TGGTCCTAAC AAAGATGTTG TAGGCATATC TACTCGTCTT ATTAGAGTGA 180
 CATATGATAA TAGACAAACA GAAGATTTAA CTATTTTATC TAAAGTTAAA CCTGACCCAC 240
 5 CTAGAATTGA CGCAAACCTCT GTGACATATA AAGCAGGTCT TACAAACCAA GAAATTAAAG 300
 TTAATAACGT ATTAATTAAC TCGTCCGTGA AATTATTTAA GCCGATAATA CACCATTAAA 360
 TGThCnCAAT ATTACCCnGG GTAGCGGGTT TTAGTTCCGG 400

10 (2) INFORMATION FOR SEQ ID NO: 4084:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4084:

AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCnAGGCAT CCACCGTGCG 60
 CCCTTAATAA CTTAATCTAT GTTCCATCC TACAGGAAAC GCGTTAGTAA TCTTGTGAGT 120
 25 GTTCTTTTCGA ACATAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC 180
 ACTCGGTTTT GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT 240
 TTCTTTTtag TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 300
 30 TAAATAAACA TTCAAACCTG AATACAATAT GTCACATTAT TCCGCCATCT nCTGAAGAAG 360
 ATGThnCCGA ATATnATCCT TAGAAAGGAG GTGGATCCCA 400

35 (2) INFORMATION FOR SEQ ID NO: 4085:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4085:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60
 CCTCCTGCGT GCAAAGCAGG CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA 120
 TTAATGGTGG GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT 180
 50 GAACCAGCTG GAGCTATAGG CCCATTAATT TGGAATGAAC AAACATTCAA AACTGGAATA 240
 CAATATGTCA CGTTATTCCG CATCTTCTGG AAGAAGATGT TTCCGAATAn ATCCTTAnGA 300

AAGCATTGTG TCCACCTTC GACGGCTGAG CTCCTAAAAG

400

(2) INFORMATION FOR SEQ ID NO: 4086:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4086:

GTCATTGGAA ACTGGAGnAC TTGAGTGCAG AAGAGGAAAG TGGAATTCCA TGTGTAGCGG	60
TGAAATGCGC AGAGATATGG AGGAACACCA GTGGCGAAGC GACTTTCTGG TCTGTAAC TG	120
ACGCTGATGT GCGAAACGTG GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT	180
AAACGATGAG TGCTAAGTGT TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA	240
AGCACTCCGC CTGGGGAGTA CGACCGCAAG TTGnAACTC CAAAGGAATT GACGGGCGCA	300
CAAGCGTGGG AGCATGTGGT TTAATTCGAA CCAACGnATA GAACCTTACC AAATCTTGGA	360
C	361

(2) INFORMATION FOR SEQ ID NO: 4087:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4087:

GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG	60
AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA	120
CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT	180
AGTTTGTAAG TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TCGTGCAAA	240
GCAGnCGCTC TCCAGCTGA GCTAAAGCCC CCATAAATAA TTACAGTATA TCGGGAAGAC	300
AGGATTTCGAA CCTGCGACCC CTTTCCCAAA CCAAGTGCTT TTACCAAGTT GGTACTTCCn	360
GTATAATTTA ACGGGCCCGA TAGGAGTTTCG GAACCCTTAA	400

(2) INFORMATION FOR SEQ ID NO: 4088:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4088:

10

AGCTATTATT TTTGACAGAT TCCATATCGT TCAACATTTA AATAGAGAAC TTAATAAGTA	60
TCGTGTACAA GTTATGAATG AATACCGTAA TAAAAAAGGA CCTGATTATA CAATTTTAA	120
GAATAACTGG AAAGTCCTAT TGATGGATAC TAGTAAACC ATATTTAGTA AATACAGATG	180
GAATAAATCT TTTAAGGCTT ATAAACGCTC ATCTGACATT GTAGGAATTC ATGCTTTCAA	240
AAGACGATAT ACTACGACAC TCCTACGAAC TTGTCCCAAG GGATTACGGA AAAGGCCCTA	300
AGGGTTATGT TAATTGGCCC TAAATTTATT AAATGCGTTT GAAATTCAGT TAGTTAAAAA	360
GTCTGTGAGT GAnGGGTGTA TGGGAAAGTG GTTAAAATAT	400

20

(2) INFORMATION FOR SEQ ID NO: 4089:

25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4089:

35

ATCGTTTTAG ATAAGACGGG TACATTACAA ATGGTCGTCC AGTCGTGACA GATTATCATG	60
GTGACAATCA AACGCTACAA CTACTTGCTA CTGCTGAAAA AGATTCTGAA CACCCATTGG	120
CAGAAGCCAT TGTCATTAT GCAAAAGAAA AGCAATTAAT ATTAAGTGA ACAACAACAT	180
TTAAAGCAGT ACCTGGGCCA TGGTATTGAA GCAACGATTG GATCATCACC ATATATTGGT	240
TGGTAACCGT GAAATTAATG GCTGACAATG GATATTAGCT TGCCTAAGCA TATTTnnGGA	300
TGGATTTAAC ACATTATGAA CGAGATGGTA AACTGCTAG CTCATTGCTG TTGAATTATT	360
ncATAACGGT ATCA	374

45

(2) INFORMATION FOR SEQ ID NO: 4090:

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4090:

TTAATAACGT ATTAAATAAC TCGTCAGTAA AATTATTAA AGCAGATAAT ACACCATTAA 120
 ATGTCACAAA TATTACTCAT GGTAGCTGTT TTTGTTGGT TGTGACAGTA AGTGACGCGT 180
 5 TACCAAATGG CGGAGTTAAA GCAAATCTT CAATTTCAAT GAACAATGTG ACGTATACGA 240
 CGCAAGACGA ACATGGTCAA GTTGTACAG TAACAAGAAA TGAATCTGTT GATTCAAATG 300
 ACAGTGCACC AGTAACAGTG ACACCACANT TACAAGCAAC TACTGAAGGC GCTGTATTTA 360
 10 TTAAGTT 367

(2) INFORMATION FOR SEQ ID NO: 4091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4091:

TAATATTATA TTGCTAGTAG TTGACTGAAT GAAAATGCGC TTGCAACAAG CTTTTTTCAA 60
 25 CTCTAGTCAG GGGCCCCAAC ACAGAGAATT TCGAAAAGAA ATTCTACAGG CAATGCGAGT 120
 TGGGGTGTGG GCCCCAACAC AGAGAATTTT GAAAAGAAAT TCTACAGGCA ATGCGAGTTG 180
 GGGTGTGGGC CCCAACACAG AGAATTTTGA AAAGAAATTC TACAGGGCAA TGCGAGTTGG 240
 30 GGTGTGGGCC CCAACATGAG AGAAATTGGA TTCCAATTT CTGACAGACA ATGCAAGTTG 300
 GCGGGGGCCC CAACACAGAA GCTGGACGAA AATCCTTGAA CGAATGAATG TGGCAATTGG 360
 CGGGGGCCCA ACACAGAAGn TGACGAAAAT nCTnGAACCA 400
 35

(2) INFORMATION FOR SEQ ID NO: 4092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4092:

GCATTTTCTCA TAACACAAGG AATTTCAACA AGTCCGGCTA CTGGATCACA AACTAAACCT 60
 AATAAATTAC TTATCGCTAA TGCCATAGCG TGCCCGGATG CTTCTGGTGA TCCTCCGAAT 120
 50 ATAGCTACTG CTGCAGCTGC GGCCATTGCA GATGCTGAAC CAACTTCAGC TTGGCAGCCA 180
 CCTGTTGCAC CAGCTACACT TGCATTGTTT GCTACGACAC GCCCAAACAA TGCTGAAGTG 240

CCGGGAATGG TAnCCGAGGG AAnCAGCTGT GGGCGTTGCA CAAATAATAC CCCATCGCAG 360
 CATTGACCT TCATTGGTT GCAATGGAA CCTTTGACTG 400

(2) INFORMATION FOR SEQ ID NO: 4093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4093:

TGACTTACGT ACTGTTCAAC CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC 60
 TGGTCGTGCA GTTGTAGTTC AAGAAGCACA ACGTCAAGCT GGTGTTGGTG CAGCAGTTGT 120
 AGCTGAATTA AGTGAACGTG CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC 180
 AGCAGATACA ATTTATCCAT TCACTCAAGC TGAAAATGTT TGGTTACCAA AAAAAATGA 240
 CATCATCGAA AAAGCAAAAG AAACCTTAGA ATTTTAATAC ATTTTAAAAG TTAACGAATT 300
 AGCGTATTTT AGTCTCATTG ATTAAnATGA AATGnGnTAA TTTACGGAAT CCTA 354

(2) INFORMATION FOR SEQ ID NO: 4094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4094:

CGTTAACATG AAGTTACGTT CTTTATAAAA AAGATTTAAA CGCGTTATTA ATCTTGTGAG 60
 TGTTCTTTCG AACACTAGCG ATTATTTCTT ATGAATTCAA GCTTATTTAA AACTCTTTAT 120
 TCACTCGGTT TTGCTTGGTA AAATCTATAT nTTACTTACT TATChAGTTT TCAATGTACA 180
 AATAATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGCCTGCAAA GCAGGCGCTC 240
 TCCCAGCTGA GCTAAGCCCC CAAATAGGnA TTAAATTAAT GGTGGGCCTA AGTGGACTCG 300
 AACCACCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT A 351

(2) INFORMATION FOR SEQ ID NO: 4095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4095:

5 ATTGTTGCGA CTGGCACACC CGAAGATATT GCTCAGACAA AGTCATCATA TACAGGAAAG 60
 TATTTAAAAG AAGTACTTGA ACGAGATAAA CAAAATACTG AAGATAAATA AGATTAAAAG 120
 AAGTGAAGGA TGTTATAATT TATCCTTCGC TTCTTTTAT TAATTTAGTA ATGAATAGTA 180
 10 GAAAGAAAAG ATGCGTAAAA AGAATTATGT TAAGATAGGG TCAATCTAGA GTAGTTAAAC 240
 ATAAATCGAA CTnGGAGTGG GACAGAAATG ATAAAGAATC ACTAATGATT TATTATGTAG 300
 TGGTTCTTTG TCATTAGCCA CAGCTATTTG TGTACTTAAA AnTAGGTATG CCAGTGTGCA 360
 15 CTCCTTGAGA GGAAATACTn ATTT 384

(2) INFORMATION FOR SEQ ID NO: 4096:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4096:

CTGCATCTTC ACAGGTACTA TGATTTACC GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60
 30 TTACGCCTTT CGTGCGGGTC GGAACCTACC CGACAAGGAA TTTCGCTACC TTAGGACCGT 120
 TATAGTTACG GCCGCCGTTT ACTGGGGCTT CGATTCGTAG CTTCGCAGAA AGAGCCGACT 180
 CCTCTTGAAC CTTCCAGCAC CGGGCAGGCG TCACCCTGAT GACATCACCT TACGGTTTAG 240
 35 CAGAGACCTG TGTTTTTGAT AAACAGTCGC TTGGGCCTAT TCACTGCGGC TCTTCTGGGC 300
 GTTAACCCn AAAGAGCACC CCTTCTCCCC AAATnACGG GGTCATTTTG GCCGAGTTCC 360
 TTAACGAGnA TTCGCTCGGT GCAACTT 387

(2) INFORMATION FOR SEQ ID NO: 4097:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4097:

50 CCACTCACAT TCACACATCG ATTCACACAC CGCACTCAGC ACTCAGnATA CCGCATTCAG 60

TCAGATAGCG ACTCAGATTC GGATAGCGAC TCAGACTCAG ATAGCGATTC AGATTCAGAT 180
 AGCGATTCCG ACTCAGACAG TGATTCAGAT TCAGACTCAG ATAGCGACTC AGATTCTGAC 240
 5 AGCGATTCAG ACTCAGACAG CGACTCAGAC TCAGACAGTG ATTCAGATTC AGACAGCGAC 300
 TCAGATTCAG ATnGCGACTC AGACTCAGAT AGCGACTCAG ATTCAGATAG CGATTCCGAC 360
 TCAGACAACG ACTCAGATTC AGATAGCGAT TCAGATTCAG 400

10 (2) INFORMATION FOR SEQ ID NO: 4098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4098:

TCGTACCTGA ACTACTTTGT ATTAAATAG TTACAACGAT ACCTGCAATA ACACCTAATA 60
 CTGGATTGTA TGTAATTTG TTTAAATAT CTCGTAGCCT GTCTCCTGCT GATGCTTGAA 120
 25 GCCCGTCTCC CATGATTTTT AAGCCGTAAA GGAAAATACC TAAACCACCT AAAAAGGAGA 180
 AAATGACTTC TGTAACCGAC ATTTCCATTA TTTCACCTCA AATAAGCTTT ATATTTAGAT 240
 TATCGCTTAT AATTGTAAAT TTAATGTAA GATTAGGTAA AATTATTTAA CAATATATGT 300
 30 TATTTGTATA TGACTTGTA AATATCGTCA CTTATTATGT AAATTTTCAG TGGTGGnAAT 360
 GGCCAGTTTG CCAAGCACTG GTTTGACCAn ATGGnGGCAn 400

35 (2) INFORMATION FOR SEQ ID NO: 4099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4099:

ATCCTTTTCC ACTTAACATA TATTTTGGGA CCTTACCTGG TGGTCTGGGC TGTTTCCGGA 60
 CCGAACACGG nACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCGG 120
 AGTTTGTCTG AATTCGGTAA CCCGAGAGGG CCCCTCGTCC AAACAGGGCT CTACCTCCAA 180
 50 TAATCATCAC TTGAGGCTAG CCCTAAAGCT ATTTCCGAGA GAACCAGCTA TCTCCAGGTT 240
 CGATTGGAAT TTCTCCGCTA CCCTCAGTTC ATCCGCTCAC TTTCAACGTA ATCGGTTCGG 300

(2) INFORMATION FOR SEQ ID NO: 4100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4100:

TAGAACTTGT	TGCCAAACAG	CATGCTTAAT	TTCAATATCT	TCTTTGACTG	CTTCGATATA	60
TAAATCAGCA	TCATCATTTA	CCAAGTCATC	ATCAAAATTA	CCATATGTTA	AATGACTCGC	120
TAGATTTAAG	TCGAATAGTA	GCGGCCGTTT	CTTATCTGTA	ATTTTATCGT	AAGATTTTTT	180
CGCAATGAGA	TTTGGATCGT	TTTGTCCAC	TACAATATCT	AATAGTTTTA	CTTTAAGTCC	240
AGCATTCAACA	AAAAGTGCTG	CCAGTTGGAG	CGCCCATTGT	GCCTGCGCCA	AGAACGGnTA	300
CTTTATTAAT	TGGTCATAGT	GanTCCnCCC	ATTTAGTTGA	GGGATAAGAT	AACCATT	357

(2) INFORMATION FOR SEQ ID NO: 4101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4101:

TAACTCAGGC	TGGGGACATA	AATCAATATT	CTATGCTCTA	CGAATTATAT	TGGCAGTAGT	60
TGACTGGnCG	AAAATGCGCT	TGTAACAAGC	TTTTTTCAAT	TCTAGTCAGG	GGCCCCAACA	120
CAGAGAATTT	CGAAAAGAAA	TTCTACAGGC	AATGCGAGTT	GGGGTGAGGG	CCCCAACACA	180
GAAGCTGACG	AAAAGTCAGC	TTACAATAAT	GTGCAAGTTG	GGGATGGGCC	CCAACAAAGA	240
GAAATTGGAT	TCCCAATTTT	TACAGACAAT	GCAAGTnGGG	GTGGGACGAC	GnGATAAATT	300
TTGCGAAAAT	ATCATTTCTG	TCCCACTCCC	ATCAAAAGAA	TGACAT		346

(2) INFORMATION FOR SEQ ID NO: 4102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATGATGAAA ATCAATTAGA CAAAGCAGGT AAATTAAGTG ATGTCGCGTC ATTTAAGGAA 60
 GCGATTACACA ATCGAGAATC ACAAAGTACA ACTGGTATCG GCGAAGGTAT TGCCATTCCA 120
 5 CATGCCAAAG TGGCCGCAGT TAAGTCACCA GCTATTGCGT TTGGTAAATC TAAAGCAGGC 180
 GTAGATTATC AAAGTTTGGG ATATGCAACC AGCACACTTA TTCTTTATGA TTGCAGCGCC 240
 AGAAGGTGGC CCCAAACACA TTCTAGATGC TTTACTAAAG TTGnCTGGTA TTTTAATGGG 300
 10 ATGAAAATGT ACGTGAGGAA ATtnTTACAT GGCTTCATCA nCTGAAGAAG TACTAGCGAT 360
 CAT 363

(2) INFORMATION FOR SEQ ID NO: 4103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4103:

25 GAGTGCAGCG GATAACATTA AACCGACGAC AnCTTTTTTA TGTTcAGGTT TAGCTGTGTG 60
 ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC GGCCTGACAT 120
 AAAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGga TCACCAAGTT GAGCAAAGAA 180
 30 GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC CAAGTGCCGT 240
 CTGCCAAAAC GGTAAGTAA AAATATGGTG TAAACCGAGT GGACCTAACA ATCTTAAGAT 300
 GAAGCCATAA rCAAAAGTAC CsGTTGGcAC CTGTTtTCGT TACAAATCCA CCAACATGtK 360
 35 AaTGCCGGTT TGTATGGTTG GCCCAAntGA nAACATCATA 400

(2) INFORMATION FOR SEQ ID NO: 4104:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4104:

50 AATTGAGAAT TTGTCGCTAT TTGTAAATTG TATCCTGGCT TAAGTTGGCC AAAGTGTCTT 60
 ATTTTTTTAA AGTATTTAAA AGTAAATTA CATGTTAATA CGTATATTAA TTGGCGAGAC 120
 TCCTGAGGGA GCAGTGCCAG TCGAAGCAGG GGCCCCAACA CAGAAGCTGA CATATAGTCA 180

CAAAAATTCT ATTTATAGAA TTTTACAGTA ATGTGCCAGA TGGGCATAGC GACCCATTCA 300

ATACGAnTAT nTGAnTAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG AAAATTAT 358

(2) INFORMATION FOR SEQ ID NO: 4105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4105:

GACGCGTTAC CAAATGGCGG AATTAAAGCA AAATCTTCAA TTTCAATGAA CAATGTGACG 60

TATACGACGC AAGACGAACA TGGTCAAGTT GTTACAGTAA CAAGAAATGA ATCTGTTGAT 120

TCAAATGACA GTGCAACAGT AACAGTGACA CCACAATTAC AAGCAACTAC TGAAGGCGCT 180

GTATTTATTA AAGGTGGCGA CGGTTTGTGAT TTCGGACACG TGGAAAGATT TATTCAAAAC 240

CCGCCACATG GGGCAACGGT TGCATGGCAT GATAGTCCAG ATACATGGAA GGAnTACAGT 300

CGGTAACACT TCATAAAACT GCGGTTTGTh ACCATTACCT AATnGTCAAG GGTACGGCGT 360

TAATGTTTGA AGGTTCCCGT TCCAAGGTTT TTTCCCGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4106:

GAAGTTAAGC TCCTTAGCGT CGATGGTAGT CGAACTTACG TnCCGCTAGA GTAGAACGTn 60

TGCCAGGCAG TTTTtTAATC AAATTTTGGT TAAAAAATAA AATGGACAAG ATAAAAAAG 120

TTATTGACTT AAATGTTAAT AAAATGTATA ATTAATTCTT GTCGGTAAGA AAAATGAACA 180

TTGAAAACTG AATGACAATA TGTCAACGTT AATTCCAAAA AACGTAAC TAAGTTACAA 240

ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTCATGGGA GAGTTTGGAT 300

CCTGGGCTCA GGATGGAACG CTGGGCGGCG TGCCCTAATA CATGGCAAGT CnGAGCGAAC 360

GGGACGAGAA GGCTTTGCTT CTCCTGGATG TTAACCGGcn 400

(2) INFORMATION FOR SEQ ID NO: 4107:

(A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4107:

10 GATTGTGCCA CGCTTTTAAC CGAAATACAA CATCATCATT GACAATTTGT TGATTTGAAA 60
 AATCTTTCTC TTCAATAAAT ACATACGTTT GCATCGTATG TGCTTTCATG TAACTCAATA 120
 TTGGTTTTTAA ATGCATTTCA GGAATTAAAT AATGTTTACT AGAACCTGCT GTCGCTACAA 180
 15 GTCCTATTAC CTTGTCACGA AACGCATTGA CTGGAAGTAG ATCAAACACA TTTnnCAAAG 240
 CACCAGGGAT GGAAAGCTTG AAAAATTGGA AAACCAATAA AAATCACATC AGCCTGCATT 300
 AACGACGTCG TTAATTTATA TACATCTCCT GTAGTATCTA Gnt 343

20

(2) INFORMATION FOR SEQ ID NO: 4108:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4108:

30

ATACAAAACA CCAGGTCGTG AAGATAAACA ATCACAAGCG GCTACTGCTT CAGCAACTGA 60
 ATTACCATAT GCAGTATTAG AAGCTATGGG TGGCAAAGCA AACATTAAAC ATTTAGACGC 120
 35 TTGTATCACA CGTCTACGGT TGAAGTTAAC GACAAATCTA AAGTTGATGT TCCTGGTTTG 180
 AnAGATTTAG GCGCATCTGG TGTATTAGAA GTCGGCAATA ATATGCAAGC AATTTTGGT 240
 CCTAAATCTG ACCAAATCAA ACATGAAATG CAACAGATTA TGAnTGGTCA AGTAGTAGAA 300
 40 AATCCTACTA CTATGGAAGA CGATnAAGAC GAAACTGTTG TGGGTTGGCA G 351

(2) INFORMATION FOR SEQ ID NO: 4109:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4109:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60

55

CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGnAT CACACCTTCT 180
 GCGGCACCAC GGAATAATAC ACCATGTGGG AGTACGACTG CnATGGTACC TTCATCGTCT 240
 5 AAGGTAATGT ACCCTGTGGT TGAATAAAGG CAAAATCTGC TTTGGGATTT TGGCGCAACT 300
 TTGCCCGTAA CCACTGAATC GTTCATCATT TTCAAATTTT TGAATCnGCT GGTCCATTCTG 360
 CACTGTA 367

(2) INFORMATION FOR SEQ ID NO: 4110:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4110:

GTCGTCCGAT TGAAGGATGG AGTACTGTCTG CATTTCGCGAA AGACTGGCAA GGACCACCAC 60
 GTTTGCAAAA CGGAACAAGT TGGTTCTATT TTGCAACAGA CCAATGGAAA TATGAAGAGT 120
 25 CAAATGTAGA TCGTTTAAAA TCTCCATTAG CTAAACAGA GGAGTTAAAG CATCAACATC 180
 CAGCTGATTA TAATGTTTTA GCAGCTAGAC TTGGTTGGTT ACCATCATAT CCACAATTTA 240
 ATAAAAATAG TTTGTTGTTT GCAGAAGAAG CTAAAGATGA AGGTATAGAT TCAAATGAAG 300
 30 CGATTTTGCC ACGTGCAATT GATGAAGTGA ATCAAACCA AACACCATTT GCCATAnGAA 360
 AATCCTGATT TGGAAAAGGA TCCTnCCAAA ATCCAnnATT 400

(2) INFORMATION FOR SEQ ID NO: 4111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4111:

TCAGATGAAG CTAAAAGTAA AGGTATTACA TGTGCAAGTG CAGGTAATCA TGCTCAAGGT 60
 GTTGCTTATA CAGCTAAAAA ACTTAATTTA AACGCTGTTA TCTTTATGCC AGTCACTACA 120
 CCTTTACAAA AGGTAAATCA AGTAAAGTTC TTTGGAAATA GTAACGTTGA AGTTGTACTC 180
 50 ACTGGTGATA CATTGATCA CTGTTTAGCT GAAGCTTTAA CTTATACAAG TGAACATCAA 240
 ATGAACTTTA TAGATCCATT CAATAATGTT CATACAATTT CTGGACAAGG TACGCTTGCT 300

AATTGGTGGT GCGGTTTAA TTTCCAGTAT TAGTACTAAC

400

(2) INFORMATION FOR SEQ ID NO: 4112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4112:

GCCCTTAATA ACTTAATCTA TGTTTCACCC ATTTTATATA GTCAAACGCT CACATACGGC 60
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120
 ACTCATGTGC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180
 GAGTGTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT TAAACTCTT 240
 TATTCACCTCG GntTTTGCTTG GGAAAATCTA TATTTTACnT ACTTATCTAG TnTTCAATGT 300
 ACAAATAATG GTGGGCCCAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGGCGTGC 360
 GG 362

(2) INFORMATION FOR SEQ ID NO: 4113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4113:

CAGGTGGTTT TCGGAAAAGT GAAGTATGGC GTCAAATGAT GTCAGATATA TTTGACACAG 60
 AGTTAGTGGT TCCTGAAAGT TATGAAAGTT CATGCTTAGG TGCCTGCGTG CTCGGACTTA 120
 AAGCTGTAGG TGACATTGAA GATTTTTCAA TCGTTTCATC GATGGTCGGT GCCACAAACA 180
 ATCATACGCC GATTGAAGAA AATGTCACTG TTTACCAAGA GATCGTATCC ATTTTATCA 240
 ATTTAAGTCG TTCTTTAACA GAGAATTATG ACAAATTGCA GATTCAACG CCACATATCG 300
 CTGAAATAAA ACnCCATAAA TACGnCACTC AAGCATCTTA GATAAAGTTG TnGGCCATGC 360
 TAC 363

(2) INFORMATION FOR SEQ ID NO: 4114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4114:

	GGTCTGGGCT TGGTTCCGGT TCTGGGTCTG GACTTGGTTC TGGATCTGGC GTTGGTTCTG	60
10	GTTCTGGGTC TGGACTTGGT TCTGGGTCAA CCGGCGGCCC TGGAGTTGGG TCTTTCGGAT	120
	TTACTGCTGA ATCACCATCA GCACTTCCAC CACCATAACG TACAACATTC TCATTATTCC	180
	AACCGAAAAT ACTGTAGTCT CTATTTGTGA CAGGATCAAC ATTTTCTTGA ATAACCTGAG	240
15	TTTTTAAGTT CTTACCTGTA TTGTCGTAAT GCCCTTCTAC TAATACTACA TATGTTTTAG	300
	TAATATCACC AAATTAATAC TAGCTACATT GGATGCnCAT AATAGATCTA TTTTAAATGG	360
	nCTGTACTCC TTAAGGTAGA GCATTGGACT GCAn	394

20

(2) INFORMATION FOR SEQ ID NO: 4115:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4115:

	GGCGATTATA TTAAAAAGCC AATTACAGAA TG TAGTGGTA ATGAAATATG CCAAGAATGG	60
	CTGTATCACT TAGGTGTATC AACTGACAAA ATTGAAGACT TAGCAAAACA TGCATCTAAT	120
35	ACGATTCCTG TTTATATGCC ATATATCACA TCTTATTTCA TGACGCGTGC TATCGGCGAC	180
	AGACCTTTAG TCGTCCCGCA TCAATCTCAG AACTTAGCAT TTATTGGTAA CTTTGCCAGA	240
	AACAGAGCGA GAACTGTAT TTACAACAGA ATATTCGGTT CGTACTGCCA GGGAAGCTGT	300
40	TTATCAATTA CTAATATAG ATCGTGGTAT TCCAGAAGTC ATCAATAAGT CCATTGGATC	360
	TnCGCGTnC TTAATGGGAT GGCCATATAC GAACTGGATG	400

45

(2) INFORMATION FOR SEQ ID NO: 4116:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4116:

55

TTAAAGGGCG AAATAGAAGT GCCGGGCGAT AAGTCAATGA CACACCGTGC AATCATGTTG 120
 GCGTCGCTAG CTGAAGGTGT ATCTACTATA TATAAGCCAC TACTTGGCGA ATGTCGTCGT 180
 5 ACGATGGACA TTTTCCGACT GTTAGGTGTA GAAATCAAAG AAGATGATGA AAAATTAGTT 240
 GTGACTTCCC CAGGATATCA ATCCTTTAAC ACGCCACATC AAGTATTGTA TACAGGnAAA 300
 TTCnGGGTAC GACAACACGA TTATAGGTTG TTAAGTGGGT TAGGTATTGA AAGTGGTTTG 360
 10 GTCnGGGCGA ATGTTTTCCA ATTGGGTAAA AGGCCCATGG 400

(2) INFORMATION FOR SEQ ID NO: 4117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4117:

AATAAAAAGG AACAAAACGA TGGCTATTGA TATGGACACA AATCATAAAT AGCTGCTTTG 60
 25 TTCTTTT TTTTATATA TTTAnAATAC ACATATTCAA GAGCCTCGAG ATATAAGTCA 120
 ATGTACTAGG CCACACAATT TAATATTGAC AGTAATTACC CGAACGAAAA TGCGCCCCGG 180
 GGCCCCAACA TGGGGAATTT CGAAAAGAAA TTCTACAGAC AATGCAAGTT GGCGGGGCCCC 240
 30 CAACATAGAA GCTGGCCAAT AGTTAGCTTT CAATAATGTG CCAGTTGGGG TAAGGGCCCC 300
 AACACAGAAG CTGGCCAATA GTCAGCTTTC AATAATGTGC CAAGTTGGGG TAAGGGGCCCC 360
 35 CCACCACAGG GAATTCGAA AGAAATnCT 389

(2) INFORMATION FOR SEQ ID NO: 4118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4118:

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60
 50 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAAnTAAGTT GACTACCATC 120
 GACGCTAAGG AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA 180
 GTCACCAGAC ATATGAATGT AATTTATACA TTCAAAACTA GATAGTAAGT AAAAGTGATT 240

ACATGTCACC ATGCTTCCCA CCTCGAACCT ATTAAACCTC AnCATCTTTG AAGGGGATCT 360
TATnAACCGA A 371

(2) INFORMATION FOR SEQ ID NO: 4119:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4119:

GCACTATTAG CCCAGTTAGA GAAAGATTGA CCTAATCTAT CCAACCAATC AGCCGACCAT 60
 TGAAACAGTG GTGCTAATTG CGGTGAATAC ATTGACTAAT CCGTCACCAA AACCACCTGC 120
 AGCACTTAAT AGCTTGTTAA ATACCGAAAC ACCCGTTGTA TTCATCATAT TAAAGAATCT 180
 TGAAGCTACA CTGCTATTTT CAGCCCATTn AAGCACGCTT TGAGACGCTT CTTCCATTCC 240
 TCTTGAAATA CCACTAAAAA ACGGnTGTA GCTCTGCATT GCAGTTTTAA CAGTATTTAA 300
 ACCATTGCA AGAGTTGTGA AGnTAGCGGA TTGATTTTGC T 341

(2) INFORMATION FOR SEQ ID NO: 4120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4120:

GGTTGAGAAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCCTCCAC GTAAGCTAGC 60
 GCTCACGTTT CAAAGGCTCC TACCTATCCT GTACAAGCTG TGCCGAATTT CAATATCAGG 120
 CTACAGTAAA GCTCCACGGG GTCTTTCCGT CCTGTGCGGG GTAACCTGCA TCTTCACAGG 180
 TACTATGATT TCACCGAGTC TCTCGTTGAG ACAGTGCCCA AATCGTTACG CCTTTCGTGC 240
 GGGTCGGAAC TTACCCGACA AGGAATTTTCG CTACCTTAGG ACCGTTATAG TTACGGCCGC 300
 CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGAnAAACG CACTTCCTGT TAAACCTTTC 360
 CAGCACCGGn CAGGCGTTCA CCCTnATTAC ATCAACTTTA 400

(2) INFORMATION FOR SEQ ID NO: 4121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4121:

	AATAAATCTT GCTTTATTCT TTTTACCAGT AATATCTAAA TGAGTTGGAT ATTTAACTTT	60
10	CGCATTAAATT TCAATATTAA ATTGCGTTAC CGCGACAAGC GCAAACACAA CATAcataAT	120
	AAGATTGGCT AAAAAGATAT AGTTAAAGCT AAATTCTGCG ACAAAGCCGC CCATTGCAGC	180
	ACCGACAGCC ACACCAATAT TTTGCGCTAA GTATATCGCA TTAAACGTTT GTCTTCCGCC	240
15	ATTTGCCAC ACTGCTCCAG CCATAGCGTA TATCGCAGGA ATAATCATTG CGCCACCAAA	300
	CCCTAACATT ACCAGGCCAT ACCAGCATAC CCAGGGCCAC CCGnGGAAGG AAATTAAGTA	360
	GCGGTGGTAC TACCAAnGAC CAGTGAAGG TnCCAATTAA	400

20

(2) INFORMATION FOR SEQ ID NO: 4122:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4122:

	GATAACTAAT AAAGTTTAGT TAAGTATTTT AATAACAAGT AGTATGTCAT TCTAGTAGCT	60
	AGAACAGATA TACTACTTGT TTGTTTTTGT GGAAAATTGA GTATATTCAA AAGGATAAGn	120
35	ACGAGAAATT CGTTATTAAA CTACGAATTC TCGATTTTTT TATATTTTAA GATAGGTTTA	180
	TTTCTGAAAA CTTAATAGAA AGGGGTTTGA CAAAGCTAAA GTGAAGTTTG ACGgTATAAA	240
	CGCAAATTAA ATATACTTTT ATAGAAAATT AACTCAGGCT GGGACATAAA TCAATATTCT	300
40	ATGCTCTACG GAGGTATATT GGCAGTAGTT GACTGAACGA AAnGCGCTTG TnACCAGCTT	360
	TT	362

45

(2) INFORMATION FOR SEQ ID NO: 4123:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4123:

55

CGCGAGGTGG TTTACAAGGA TTGTTGACAT TTCAAGACTT ACCAGTAACA AGTTATACAA 120
TCTGGGGTGG TGTCTCAGAT ATTGATTTAA TGTATGAAGA ACGTGTTCGAT TTAAGAGGCA 180
5 TGCTACGAAG AATGATTGGT CATCCGAAAA AAGATCGAGC GGGCATATGA GGCACGCCAA 240
GCGATTCCAA ACATTAATGA NAACAGTCCG CCAATATTAA TTGTACATnG GAGGGGAAAAG 300
10 ACCCAGCAAG TTGGGTATTn CATCATGCGT ATTATTTTAA GCGGACCAAC TA 352

(2) INFORMATION FOR SEQ ID NO: 4124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4124:

AACCAGGTGA TCTACCCTTG GTCAGGTGA AGTTCAGGTA AACTGGAATG GAGGACCGAA 60
CCGACTTACG TTGAAAAGTG GAGCGGATGA ACTGAGGGTA GCGGAGGAAA TTCCAATCGA 120
25 ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGC TAGCCTCAAG TGGATGATTA 180
TTGGGAGGTA GAGCACTGTT TGGACGAGGG GCCCCTCTTC GGGTTTACCA ATTTTCAGACA 240
AACTTCCGAA TGCCAATTAA TTTGAACTn GGAGTTCAGA ACATGGGTGA TAAGGTCCnT 300
30 GTTTCGnAAn GGGAAACAGC CCAGACCACC AGTTAAGGTC CCCAAATGTA TGTTTAAGTG 360
GAAAAGGGTT TTGGCGTTGC CCCGACAACT AGGATGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 4125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4125:

GGCTTATTAA TCAAAAAATT TATAAAGAAT ATGTAGAAAA CTTTTATTTA CATCGAGGCT 60
ACACGCTACA ACAGAAAATT AAAATTTTAA TTAGCTTATA CATTGTAATA GGTTTTTCAA 120
50 TTTATATGGT GGATGTTCTT GCAGTCCGTG TAGGATTAAT CATAATGGTT ATCATACAAA 180
CCGCTGTACT CTTTACATTT GTAAAAACAT TACCCAAATC AAATCATAAA ATAGAGGAGT 240
GATTGCCCAT GTTTATGGCA GAAATAGAT TACAATTACA AAAAGGCAGT GCGGAAGAAA 300

TTGTCACTAA AACATTAAAT ACCGGGATAC AGCCGAGTAA

400

(2) INFORMATION FOR SEQ ID NO: 4126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

AATCTATATT TTAATTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTTT GTCAAGCGCT 60
 CGCATAAGCA ATATCACTTT AACCAAAAAA TATTGAATG TTAAATAAAC ATTCAAAACT 120
 GAATACAATA TGTCACATTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA TATATCCTTA 180
 GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGGCTACC TTGTTACGAC TTCACCCCAA 240
 TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGGTT ACTCCACCGG CTTCGGGTGT 300
 TACAAACTCT CGTGGGTGTG GACGGGGCGG TGTGGTACAA nGACCCGGGG AACGtnATTC 360
 AnCGGTAGCA TGGCTGGATC TAACGATTTA CTAnCGCGAT 400

(2) INFORMATION FOR SEQ ID NO: 4127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4127:

CGAAATTTGT AGTAAAAGAT GTGCAACCAG CGAAACCAAC TGTGACTGAA ACAGCGGCAG 60
 GAGCGATTAC AATTGCACCT GGAGCAAACC AAACAGTGAA TACACATGCC GGTAACGTAA 120
 CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTACAC 180
 GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 240
 CTGGAATAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GGATACAATT 300
 CCAAGTTGGT TGCAACGCCA AGGAAGCGGA GAGACCAGTG AAGTGATTGA GCCACCGTAA 360
 TGGTTGGnTT CCCAGTTTG TCGGCAnCCA CAACCGGAAC 400

(2) INFORMATION FOR SEQ ID NO: 4128:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4128:

10

GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT GGAGATTATC TGTCGTCTTC	60
AAGTATGCGT TCATTAAATTG ATATTGGCGC ACCGTATAAC CATGTCAAAG TACCATTTGC	120
AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GCCTACGCGT TACATGAAAA ACGGAGAACA	180
AGCAGAACAA TTATTACGTC AGCTTATAGA AAAAGATGAA GCACTAGCTA AGTATGTCAT	240
GGGTTGTGAT GAAACAGCTT GGTGGTCATA TATGGGTCCA GATAATGATA TTTTCCAAGA	300
TCCATTAnGG CCATCTAACT GTTCCAGCTA AGGAAAGTAT CCCCGAAGTG GCTAAGCCCCA	360
AAAATGATTA CGCCAACCAG CTAGTGGTCC ATnGGCCAGC	400

20

(2) INFORMATION FOR SEQ ID NO: 4129:

25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4129:

35

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA TAGATGGnGG AGGGGGGCAG	60
ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC	120
CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC	180
GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGG AGCTAATTCT CCAAATAAT	240
GACTCCTGAC GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTC TTGAACCGCT	300
TGGACCAAGG GAGCCATGGC TCCAACAGGT GAGGGACTCG AACCTnACGG ACCGATTCGG	360
TnAACAGCC GGAT	374

45

(2) INFORMATION FOR SEQ ID NO: 4130:

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 431 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4130:

ATTAAATTTTC AGTTGTTGCA ATTTCTTCAT CTGTAGGTAC ATCATCGTTA AGGCCAACAA 120
 GTGCTTCAGA AACATTTTCGT GAATGATAAC CGATACGTTT AAGAACrCsA ATCATATCGA 180
 5 TATATAGTAA TCCGCCTTTT GTGTACATT CACCACGATT AAGGCGTTTA ATATGACCTT 240
 TCGTAGTTT ATGTTCAATA TTAAATGATT CTCTACTACG TTCTACAATT TCATCTTTTT 300
 TCGTTTTGTC ATAAACATCT AACATGTCGA TGGCTTTATC AAATGACTCA GCAACATGGT 360
 10 TGAATAAAT TATCCATACC GCGTTGTGCA TCTnCTGGTA ATGCGAATAT CTTCATCATG 420
 TTGGCGGTTT T 431

(2) INFORMATION FOR SEQ ID NO: 4131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4131:

TTTAGTTGAA GCGGTTGTTG TCGCATTGTC TGTTTGTTGC GGTGCTTCTA CTTTAGTTGA 60
 GGGCGGTGTT GTCGCGTTTG GTTTTGATTG CGGTGCTTCT ATTTTAGTTG AGGGCGGTGT 120
 TGATGTGGTG CTCCACTTT AGGnAAntGA GTGTTGTCGC GTTTGCTGCT TCGGTTGTCG 180
 30 TTGTGATTAC ACCTGTTGTT AAAAGGCCTA GTGCTAAACT TGTTTTAGCA ATCGTTGTTA 240
 TTTTCATAGT TGTATGCTCC ATTGTAATT ATTAGATTG TTCGATACAT TCATTGAATC 300
 ATACAGCTTT ATTATAGAGG CGTATTGCTC CATTACATT AAACCTGTnT AACCAGATTG 360
 35 GAAGCAGCGT TGAATnAAAT GAAGAAAGCC AGAAGTTCGT 400

(2) INFORMATION FOR SEQ ID NO: 4132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4132:

CCATTCACCTG TATGTCTTTG GCCACCACCT TGACGTTGTT GTTGCTGTTG TTGATTTTGA 60
 50 TTAGCTTGTT GTTGATTTTG ATTATTTTGT GCTTGATTGT TCGCTTGATT AGCGTTGTTT 120
 TGATCATTAT CAGATTCATC TTAGTCGCT TTGTCTTGAT CCTCTTTTGA TTTATCACTG 180

TCAGCATTAT TTTTATTTGT ATTCGCGATT TTATTTTCTT TTGTACCATT ATTATGATTG 300
 TTTAATGCCA TGCCTCCAAA TATCGCTAAA TGCACCGATA AATnAGTACA GCTGCAATGA 360
 5 ATGTAACAA TACTTTGGGC CAGnCACCGT TTTTACGGTn 400

(2) INFORMATION FOR SEQ ID NO: 4133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

TTGAATACTT TTCTTCCACA CAAATGTATA TCTATTGGCA TTAGCTTCTA CTTTGTACC 60
 20 ATCAATAAAA ATTGAATTAT TATCAATAAG ATTTTGCTTT AAACATTGAC TATGGAAC TG
 AATAAATAAA GATTCAATTA ACGCATCAGT ATTAGGATTC ACTCTAAAAC GATTAATAGT 180
 TTTATAAGAA GGTGTTTGAT TTTGAGCTAA CCACATCATT CGAATACTGT CATGAAGTAA 240
 25 TTTCTCTATT CTTCGACCAG AAAATACAGA TTGAGTATAT GCATATAAGA TGATTTTTAA 300
 CATCATTTTT GGGATGATAG GATGTTGCGC CACGATGATG TCTGAATTCA TCGAATTGCG 360
 TAnCGGGTAC CGTTCACCA ATTCATTAA CATATCGCGG AATATCATTT TGAGGAA 417

(2) INFORMATION FOR SEQ ID NO: 4134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4134:

GGTTTAATAT GGACCTTTCG CGTnTTTATG TTCAATATTA AATGGATTCT CTA CTACGTT 60
 CTACAATTTT ATCTTTTTTC GTTTTGT CAT AACATCTAA CATGTCGATG GCTTTATCAA 120
 45 ATGACTCAGC AACATGGTTG nAATAATTTA TCCATACCGC GTTGTGCATC TTCTGTAATG 180
 CGnAATATCT TCATCATGTT GGTTCGTTTTA ATTGAGCGAC ATACTCTTCT GTTAGCTCTG 240
 CTACTTTTAA AATAGAGCGA TTGACATCAA ACATAACTGC TAAACGCTCA ACGTCTGCCT 300
 50 TCGTAATGGC TTTTGTAGAA APTCTAACTA AATAATTTTCG AATGCTATCA TTGT 354

(2) INFORMATION FOR SEQ ID NO: 4135:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4135:

10 CTGGGATCGC CACCTTTAAG TCTAACCAACC TTGTTATATC GACGCGCTGC TTCCACGATA 60
 CAGTCATTTA TTTTTTCTTG CTGAATATGT TTTGCATACG GCTTTTTTACC AACATCGATA 120
 ATTTTCAGTAG TCAAATTCGC ATATTGTAAA ATTAACGGAT TCACTAATCG ATCATATAGA 180
 15 ATGACATCCG CTTACCGTAT TAAACGCTCA GCCTTTTTTCG TCAAATAATT CGGATTACCT 240
 GGACCCGCAC CTATCAAGTA AACCTTGCCA TATTCCTCTA CAGACATATA TATACGGTCC 300
 CGTCTGTAAC TTCTACCTCA TAAACATCTA CACAACCTTC ATCAGGTCTG GACAATACCT 360
 20 G_nATTAAACA ATTTTTGATC GTGGGGGGGC AAATACATAT 400

(2) INFORMATION FOR SEQ ID NO: 4136:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4136:

ACCACTGAAT CGTTCATCAT TTTCAAATTT TGAATCTGCT GTCCATTTTCG CACTGTATGG 60
 35 TGGGTTTCGCA ATAACCGCAT CAAATGTATT GCCTAAAAAG GCTGGATTTT CCAATGTGTC 120
 ATCATTACGG ATCTCGAAGT TCTCATAACG CACATCATGT AATAACATAT TCATGCGTGC 180
 40 TAAGTTGTAT GTAGTATTG_n TACGTTCTTG TCCGAAATAA CGATACACTT GCGTTTCTTT 240
 ACCAACACGT AACACAATG GAACCGGAnC CACATGTTGG GTCGTACACG TGGACGTAAT 300
 TTATCnTTAC CGTGCTGTGA CAATCTTCGC CAGTATCTTA GATACTTG 348

45 (2) INFORMATION FOR SEQ ID NO: 4137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4137:

TGGACAATAC AAAGGGCAGC GAAACCGCGA GTCAAAGCAA ATCCCATAAA GTTGTCTCTCA 120
 GTTCGGATTG TAGTCTGCAA CTCGACTACA TGnAAGCTGG nAATCGCTAG TAATCGTAGA 180
 5 TCAGCATGCT ACGGTGAAAT ACGTTCCCGG GTCTTGTACA CACCGCCCGT CACACCACGA 240
 GAGTTTGTA CACCCGAAGC CGGTGGAGTA ACCTTTTAAG GAGCTAGCCG TCGAAAGTGG 300
 GGACAAATGA TTGGGGTGAA TCGTAACAAG GTAAGCCGTG ATCGGnAAGG TCGGGCTGGG 360
 10 AT 362

(2) INFORMATION FOR SEQ ID NO: 4138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4138:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCCGAAAT CTCTGGATCA 60
 25 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120
 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC CATTTTTATA 180
 AGTCAAACGC TCACATACGG CTTCGTTTTT ATTATTTTAA ATGCTCATTT ACATAAGTAA 240
 30 ACTCTGCTTT AAAATAATTT AACTGCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT 300
 TTAACGCGT TATTAATCTT GTGAGTGTTT TTTGGAACAC CAGCGATTAn TTCnTGAGGA 360
 35 ATTCAAGCCT AnTTAAAACC CTTA 384

(2) INFORMATION FOR SEQ ID NO: 4139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4139:

CTCATTATGG GACGTGCACA AGATGGTTTT CTTGATCAAG ACAAATATGA CATTATTTTC 60
 50 AAAACAGCTG AAAATTTAGA CGTACCGATT TATCTACATC CCGCGCCAGT TAACAGTGAC 120
 ATTTATCAAT CATACTATAA AGGAAATTAT CCTGAAGTAA CTGCGGCAAC ATTTGCTTGT 180
 TTTGGTTATG GTTGGCACAT TGATGTCGGC ATTCATACAA TACATCTnGT nTnATCTGGT 240

TCCTTAGAAC GAATGGATGA AGCTTATCCG TGAACATTTG AACCACCCCG GAAGCAATAC 360
 TTAAAAATAA ATTTAATATC ACACCGGGTG GCATGGTACC 400

(2) INFORMATION FOR SEQ ID NO: 4140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4140:

CAACCACATT CGCTCGGCTC ACCTTAGAAT TCTCATCTTG AACTACCTGT GTCGGTTTGC 60
 GGTACGGrCA CCTATTTTCT ATCTAGAGGC TTTTCTCGGc AGTGTGAAAT CAACGaCTCG 120
 AAGACTCAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA TTTGCCTAAT 180
 ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC 240
 CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT 300
 AAGCCTGTCG GGCTCAGCTT AAGGACCCGA CTAACCCAG AACCGGAAGA GCCTTCCTCT 360
 GGAAAACCTT AGTCAATCCG TTGGACCGGG ATCTCAACCG 400

(2) INFORMATION FOR SEQ ID NO: 4141:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4141:

CATATCGATA ACATGACATA ACTCATGCTG GGTTTCCCCA TTCGGAAATC TCTGGATCAA 60
 AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 120
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA 180
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 240
 CTCTGCTTTA AAATAATTTA ACTCATGTGC TGCTAAACGT TTTCTTTTAT AAAAAGATTT 300
 AAACGCGTTA TTAATCTTGT GAGTGTCTT TCGAACATAG GCGGAGTATT TCTTAAGGAA 360
 TnCAAGCnTA TTTAAACTC TTAATCAnC GGTTTTGnT 400

(2) INFORMATION FOR SEQ ID NO: 4142:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4142:

10 GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTC 60
 TTTGTGTTTA CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA 120
 CTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 180
 15 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 240
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGGTTCGT CAGATTCAAA CGTTTCACTC 300
 GCCAAGCCAT TTTCCTTGGG TTACTTTTAA TTTGACGTTT AAGGCATAAA AAAAAGAGAC 360
 20 TTGCGGGCTC AAATGCGGnT CATCGCATCC ATTTTTGnCh 400

(2) INFORMATION FOR SEQ ID NO: 4143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4143:

TTTAAAATTG ACATTATTAC TGACCAAACA AGTGACATG ATCCGCTAAA TGGATATGTG 60
 35 CCACAAGGAA GCGAAAGTAT TGCCTGAAAA AGATCCGAAA AAATATGTTG AACTGTCACA 120
 AGCTTCAATG GCAAAGCATG TTGAATTAAT GCTTGGAATT CCAAAAACGT GCGCTGTAG 180
 CATTGATTA TGGTAACAAT ATTCGTCAAG TAGCCTTCAA TAACGGAnGn ATAAATGCTT 240
 40 TTGGAATTCC CAGGTTTTGT ACCAGCTTAC ATTAGACCAT TnATTCTGTG TAGGTTAAAG 300
 GGCCATTCCG CTTTGCTGCG TTGGAGTGGT GGATCCAAAA GATATCGAGC GTGCCGGATG 360
 45 GAGGAAATG 369

(2) INFORMATION FOR SEQ ID NO: 4144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

GGAAAGATAA ATAGCTTCAT CAATGTCATG CGTCACTAAA ATAATAGTTG ATTGCGTTTT 60
 ATGTTTTAGT TGCAC TAGTT GATCCTGAAG TTTATAACGT GTAAATGCAT CTAATGCACC 120
 5 TAATGGCTCA TCCATCAATA TAACGTTAGG CTTATGCACA TGCGCTCGAC ATAGTGCCAC 180
 ACGTTGTTTT ATACCCCGG ACAGTTGCTC GGGAAAATGC TTTCCCCTGT CTTCTAAATC 240
 AACTAATTTA AGCTGTGChT TAATCTCTTC ATCACTAATT TTCTGTTGTA ATCCAATCCT 300
 10 AATGTTGTCA TTAATCGTTT TCCAGGCAGC AAATTATGGT GTTGAAATAG CATAAACAAh 360
 CGGGAGhGGC 370

(2) INFORMATION FOR SEQ ID NO: 4145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4145:

CGAGGTAGCA AAGAACAAAT TGCGAAATAT GTACCTAAAT TACAGTCACA TGAAGTGCCT 60
 ACATGCTTTG CTTTAACTGA ACCAGAACAC GGTTCCGACG TTGCnGGAGG TCTTGAAACA 120
 GTCGCTGAAC GCCAAGGCGA TACTTGGGTT ATCAATGGTG AAAAGAAATG GATTGGTGGT 180
 30 GCACATGTAT CTGATGTCAT TCCAGTATTC GCAGTAAATA AAGAACTGG GCAAACCCCA 240
 TTGCTTTGTA GTCAGACCAG AACAGATGG GCGTCGATAT TGAAGTCATT GGATAATAAA 300
 ATCGCACTTC GGCATTGTTT CTAACGCCCT AATTTnAATT AAnTAATGTT CAAAGTAGGA 360
 35 TTGAAGCGGG 370

(2) INFORMATION FOR SEQ ID NO: 4146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4146:

TGGGGTGT TTACCAATAA AGCGTTGCAA GGTGGCGGTA GTTTAATCGA TTATGGTTGC 60
 CACTTGTTAG CTACTAGGTA AAGATATGGT GCCGCATGAA GTCTAGGAAA AACATATAAT 120
 CAATTGAGCA AACAAACGAA TCAAATTAAT GATTGGGGAA CATTGATCA TACTAAATTT 180

GAATGTTCTG GGTCTGCAAA TATCAAAGAA GATAAGGTTT ACGTTnTTTT ATCAGGAGGA 300
 GGATGGCGGT ATCCAATTTA TTTCCATTG GAAATATATG GnGCCCCGTT TTGGGAACnC 360
 5 ATTTTTTGA AAGCCAAGCT 380

(2) INFORMATION FOR SEQ ID NO: 4147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4147:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTTAGTCAA GCGCTCGCAT AAGCAATATC 60
 20 ACTTTAACCA AAAAATATTT GAATGTTAAA TAAACATTCA AACTGAATA CAATATGTCA 120
 CATTATTCCG CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAAG GAGGTGATCC 180
 AGCCGCACCT TCCGATACGG CTACCTTGTT ACGACTTCAC CCCAATCATT TGTCCACCT 240
 25 TCGACGGCTA GCTCCTAAAA GGTACTCCA CCGAnTTCGG GTGTTACAAA CTCTCGTGGT 300
 GTGACGGGCG GTGTGTACAA GACCCGGGAC GTATTCACCT GGCAGCTTgn CTGGGTTTAC 360
 nT 362

(2) INFORMATION FOR SEQ ID NO: 4148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4148:

CACCATACAT GCGAAATGGA CAGCAGATTC AAAATTGAA AATGATGAAC GATTCAGTGG 60
 TTACGGCAAG CTTCGCCAA AATCCAAAGC AGACTTTGCC TTTATTCAAC ACATGGTACA 120
 45 TTACCTAGAC GATGAAGGTA CCATGGCAGT CGTACTCCCA CATGGTGTAT TATTCCTGG 180
 TGCCGCAGAA GGTGTGATTC GTCGCTATTT AATAGAAGAA AAGAACTACT TAGAAGCCGT 240
 GATTGGGTTA CAGCCAATAT TTTCTATGGG nCAAGTATTC CAACATGTAT TTAGTATTAA 300
 50 AAATGTCGCC ACAAGACGCC ACGTACTATT ATCGATGCAT CCAATGATTT GAAAAGGAAA 360
 AATCAAACCA TTAAGCGTGC CAAGCGACGA TATnGnCnCTA 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4149:

10 CAGCTATTGA TATCGATTAC CATACTGCTG TGGATAGCGA CAGGTTACAG TTGGAGGATA 60
 CACTGAGTCC TCTGAGGAAT CAAATCCAAT TGACTTTGAA GAATCTACAC ATGAAAATTC 120
 15 AAAACATCAC GCTGATGTTG TTGAATATGA AGAAGATACA AACCCAGGTG GTGGTCAGGT 180
 TACTACTGAG TCTAACTTAG TTGAATTTGA CGAAGAGTCT ACAAAGGTA TTGTAAGTGG 240
 CGCnTGAGCG ATCATACAAC AGTTGAAGAT ACGAAGAATA TACTACTGAAG TAATCTGATT 300
 20 GAATAGTGGA TGAATACCTG AAGAGCATGn TCAGCACAAG ACCAGTCGAG GAATnACTAA 360
 AACCATCATC ATATTnCAT CTGGTTAGGA CTGAAATGGC 400

(2) INFORMATION FOR SEQ ID NO: 4150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4150:

35 AAGGACGACA TTAGACGAAT CATCTGGAAA GATAATCAAA GAAGGTAATA ATCCTGTAGT 60
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAGCACGTGA AATTCCGTCG 120
 GAATCTGGGA GGACCATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT 180
 40 ACCGTGCAGG AGAAGGTGAA AAGCACCCCG GAAGGAGTTG AAATAGAACC TGAAACCGTG 240
 TGCTTACAAG TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG 300
 GCGAGTTACG ATTTGATGCA AGTTAAGCAT AAATGTGGAG CCGTAGCAGA ACnngTTnTG 360
 45 AATAGGCGTT A 371

(2) INFORMATION FOR SEQ ID NO: 4151:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4151:

TCAGCTTTTT TGATATGTAT TTTATAATGT ACAGCTCGTT GACnntAATT TTCCTTATAT 60
 5 TAAGTGCCAT CAATACAAAA CCTAGCTCTC GTTTAACTTT ATTTATTCCT CGAACTGACA 120
 TTCGAGTGAA CCCAAAATAG CCTTCATAAA TCCAAAAGCA GGCTCTACAT CAATTTTTTCT 180
 TTGACTATAG ATGTTTTTCG TTTCTGGTTC AGAAAGCTTT TGATTAATTT GGACTTTTAAA 240
 10 GTATTCCCAA TTATAATTCT TCATGGATTT TCTTATTGGG ATTTCGAATT TGGTTTCATG 300
 CATTGATGTC TCAAAGAACA TGATGGAACA GTCCAnCACA TTCCAGATAG TTTGGAAGTC 360
 15 TCGTTT 366

(2) INFORMATION FOR SEQ ID NO: 4152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4152:

TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 60
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 120
 30 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAA CGTTTTCACT 180
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAA 240
 35 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300
 CTAGCGGGAC GTAAGTGGCT ACCATCGACG CTAAGAACCT TTCCTGGACT TGGTGACAA 360
 TCGCnTGCCT CCTTCCTCCT CCTCGGGCTC TCGGCTTACG 400

(2) INFORMATION FOR SEQ ID NO: 4153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4153:

TGATATTCCT GTACCACCTA TAATCGTTTT AATCGATGGG GGGACGCATA GGnATAGGCG 60
 ACGTGCGATT GGATTGCACG TCTAAGCAGT AAGGCTGAGT ATTAGGCAA TCCGGTACTC 120

CCGAGAAAAG CCTCTAGATA GAAAATAGGT GCCCGTACCG CAAACCGACA CAGGTAGTTC 240
 AAGATGAGAT TCTAAGGTGG AGCGAGCGAA CTCTCGTTTA AGGACTCGGG CAAATGGACC 300
 5 CCGTTACTTC GGGGAGAnGG GTGCTCTTTA nGGGTTTACG CCCAGAAGAG CCGCATTGAA 360
 TAAGGCCCAA GCGnTGTTTT ATCCAAAACA CGGTCTCTGC 400

(2) INFORMATION FOR SEQ ID NO: 4154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4154:

20 TTTTAGCAAT CATTTTAACA GTCAGTCATA TTAAAGGCTG GCTAACGATT GTTATCTnGT 60
 nCAGATTTGT AAGTTAAGAT TTCTTGTAAT GTGTATGCAG CACCATATGC TTCAAGTGCC 120
 CATACCTCCA TCTACCAAA ACGTTGTCCA CCGAATTGCG CTTTACCGCC AAGTGTTGT 180
 25 TGTGTAACAA GTGAATATGG TCCTGTTGAA CGCGCATGTA ATTTATCATC AACCATGTGC 240
 GCAAGTTTCA ACATGTACAT TACACCTACT GAAATACGGT TATCGAATGG TTCACCTGTA 300
 CGTCCATCAT AAAGTACAGT TTTACCATCA CGAGCCATAC CAGCTTCTTC AATTGTTGGA 360
 30 CCATACATCG TCATCGTTTG CACCGTCAAA TACTGGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4155:

GATCCGAAGT TACCAACAGG AGAGAAAGAG GAAGTTCCAG GTAAACCAGG AATTAAGAAT 60
 45 CCAGAAACAG GAGATGTAGT TAGACCACCG GTCGATAGCG TAACAAAATA TGGACCTGTA 120
 AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCTG AGAAAGAACG TAAATTTAAT 180
 CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG TGAGAAGACA 240
 50 ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA AGGTGAATCG 300
 AAAGAAGAAA TCACAaAAGT CCAGTTAATG AATTAACAGA TTCGGTGGCG AGAAATACCG 360

(2) INFORMATION FOR SEQ ID NO: 4156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4156:

CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTA AGTTGGGCAC TCTAAGTTGA 120
 CTGCCGGTGA CAAACCGGG GAAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180
 TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG CGAGTGCAAG 240
 CAAATCCCAT AAAGTTGTTT TCAGTTCGGA TTGTAGTCTG CAACTCGACT ACATGAAGCT 300
 GGGAAATCGCT AGTAATCGTT AGATCCAGCA TGGCTAACGG TGGATACGT TTCCCGGGGT 360
 CCTTGTTACA CACCGCCCGT 380

(2) INFORMATION FOR SEQ ID NO: 4157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4157:

TGGAGAAGGA CCCAAAAATG TTGCCGTTTC AAGGTTATGT TTTACAACAT TTCGAACTTA 60
 TGGATGATGG ATTCTGCCAA GTTAAAATAA CTGAAGATGT ATTGGAGCAA TTCGGTATTC 120
 AGCCAAATGA AGCATCTCAG TTTGTTAATA CAATTGCTGA CATCAAAGGC TTGAAAATAT 180
 GGGTATTTGC AGTCGATGGA AGGTAATGAA ATCAGATGTC GATTACGTTC TAAAGGGCAA 240
 TTGGATTATT AATGATATTG CGCAGATTTT GGTGGCGGTG GTCATCCGAA TGCGTCAGGA 300
 GTTTCAGTGG ACCAGCTGGG GTGGANTTGA GCCACTTGCT ACCAGCTTTA CGGCACCAAA 360
 ACTTACTTA TAGGAAGGGG CCCATTCCAT CCAGGTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 4158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4158:

5 AAATCTCTGG GATCAAATCT TACTTACAGC TCCCCAAAGn CATATCGTCG TTAGTAACGT 60
 CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT 120
 TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 180
 10 AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT 240
 CAAGCTTATT TAAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGn n 351

15 (2) INFORMATION FOR SEQ ID NO: 4159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4159:

AGTTAAAGGA ACTTTTAAAG TGGTTGGCCG CCGTnATTGC CTTCTnACC TTTTGTCTCT 60
 TCTCTGTtTA CTTTTTCTGT CCCTGGTGCT AAATCmGGAT TAAATTTACG TTCTTTCTTG 120
 30 AATGGAATyT CTTCTTTTTC TACAATCGAG TCTCCTTTTA CAGGTCCATA TTTTGTTACG 180
 CTATCGACCG GTGGTCTAAC TACGTCTCCT GTTTCTGGAT TCTTAATTCC TGGTTTACCT 240
 GGAAC TTCyT CTTTCTCTCC TGTGTAAC TTCGGATCAA ATTCGTCTCG ATGACCTGGT 300
 35 GTTATCGTTT CTGGTCCGTA TTCTGTTAAT TCATTAATCG GATCTTTTGT GATTTCTTCT 360
 TTTGGTTCAC CnTnACGAA TAATnACTCC AGTAAAGGAT TTTTAAAGTG TTGGTGTCGT 420

40 (2) INFORMATION FOR SEQ ID NO: 4160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4160:

ACGATAATGG TGACGGGTTA CAAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGTCCT 60
 CCACGTAATC TAGCGCTCAC GTTTCAAAGG CTCCTACCTA TCCTGTACAA GCTGTGCCGA 120

55

TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAnTCGT 240
TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAnT TTCGTACCT TAGGACCGTT 300
5 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAAn TAACCACTC 359

(2) INFORMATION FOR SEQ ID NO: 4161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4161:

ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA 60
20 GGCCGGnAAC GGTAGGGCGA TGGATAACAG GTTGATATTC CTGTACCACC TATAATCGTT 120
TTAATCGATG GGGGGACGCA TAGGGATAGG CGAACGTGTC GATTGGATTG CACGTCTAAG 180
CAGTAAGGCT GAGTATTAGG CAAATCCGGT ACTCGTTAAG GCTGGAGCTG TGATGGGGAG 240
25 AAGACATTGT GTCTTCGAGT CGTTGATTTC AACTGCCGA GAAAAGCCTC TAGATAGAAA 300
ATAGGTGCCC GTGACCGCAA ACCGACACAG GTAGTnCAAG ATGAGAAAnTC T 351

(2) INFORMATION FOR SEQ ID NO: 4162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4162:

AnCGTCCTGC TTTGCACGCC AGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTAT 60
TTTTTACACG ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT TCCAAAAAAC 120
GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT CATAATTTTT 180
45 ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA CATGCAAGTC 240
GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG AGTAACACGT 300
GGATAACCTA CCTATAAGAC TGGGGATAAC TTCGGGGAAC CGGAGCCAAT ACCGGATAAT 360
50 AnTTTGAACC GCATnGGTCC AnAAGTGAAA GACCGGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 4163:

- (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4163:

10 ATTTTATATA TGAAATAATC TGGGACAACA TTCATAAATC TTATTGTCGT CCATTTTTTTT 60
 AAAATAATAC CAATCTCATT TTTAAATTCT AAACCTGGTT TCGTATAATA CGCTCTTAAA 120
 TCTTTAAATT TAGGATTTAT TTCTGTGGT ACTTGTTTGTG TGGTTGGCGA TTGTGGTGTG 180
 15 TCTGATTTAG TAGATTGCAT TGGTTGTGGC GTGTTTGTG ATGGAGGTGT TGTCACTTTA 240
 GTTGnAAGGC GGTGTGTGCG CATTGCTGT TTGTGCGGT GCTTCTACTT TnATTGCAGG 300
 CGGTGTGTGTC GCGTTTGGTT TTGnATGCGG TGCTTCTATT TT 342

20

(2) INFORMATION FOR SEQ ID NO: 4164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4164:

30

TCACGACACG AGCTGACGAC AACCATGCAC CACCTGTCAC TTTGTCCCCC GAGGAAGGGC 60
 TCTATCTCTA GAGTTGTCAA AGGATGTCAA GATTGGTAA GGTTCCTCGC GTTGCTTCGA 120
 35 ATTAAACCAC ATGCTCCACC GCTTGTGCGG TTCCCCGTCA ATTCCTTTGA GTTTCAACCT 180
 TGCGGTGTA CTCCCAGGC GGAGTGCTTA ATGCGTTAAT GCCAGCACTA AAGGGGCGGA 240
 AACCCCTAA ACACTTAGCA CTCCATCGTT TACGGCGTGG AACTACCAGG GTATCTAATC 300
 40 CTGTTTGATC CCCACGCTTT CGCACATCAG GTCATTAAAC GACCAGAAAT CGCTTGGCCA 360
 nGGGGGTnCC nCCAAAACCT TGGGGATTTA ACGGTAAAAA 400

45

(2) INFORMATION FOR SEQ ID NO: 4165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4165:

55

GCATTAATTT CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT 120
 GCAATATCAT AATCGTCAGC TAGTATGCCA TTACCACCTG TAATACCGCG GCCCATAGCT 180
 5 ACTGTCTCAC GCAAACGTAA GGCATTTCATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA 240
 TATTACCCAT GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA 300
 10 TTAnCTTGCA TCATTGCTAG CTTTCCTGTA TTAACGGATA TTAATAATnG GTTGCCGAAT 360
 GCTTACGCTC AGGGACnTAA CnAAGTGGCA CGTAAGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 4166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4166:

AAAGTTCTTT GGAAATAGTA ACGTTGAAGT TGTACTCACT GGTGATACAT TTGATCACTG 60
 25 TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 120
 TAATGTTTCA ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAGCAAA 180
 30 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTTC 240
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG GAAAATTATA GGTGTTGGAA 300
 CCTTCAGGTG GCAAGTAGTA TGGTATGGAA TcGGTGGTG GGTAAATAAT CcGGTnGTC 360
 35 CACATTGGCC CTAATAACCG ATAAAATTTG GGGGGCCGGG 400

(2) INFORMATION FOR SEQ ID NO: 4167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4167:

CTTATAATCC ACACCCTGAG CAAACGCTnC TTATGACAGA GTATTAAAAT AAGCCGATAA 60
 50 AGATACACAC CTTTACCGAC TATTTAAAAT ACATTCACC AATTCATTTT AATTTAATGG 120
 ATTGAAGTAA CTAAATTAAT ATTATGTTGT TCAATTAAAA GCTTCATACA AACCTAATCT 180
 ATTTGCACTC CACCGGTAAC ACCGAACACT TGTCCGGTTG TATAACTGA TTCTTCTGGA 240

GT TTTTGTGA CCAAATGnTT GGGGATTTTA CTTnGTGGGT TGTCCACCAG AAATTTGT 358

(2) INFORMATION FOR SEQ ID NO: 4168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4168:

TTTCTTGACC	ATATGGACGT	AAAGAGATGT	TAGCATCACA	ACGTAAAGAT	CCCTCTTCCA	60
TCTTAACGTC	TGATACACCA	GTGTATTGAA	TAATTGAACG	CAATTTTCT	AAATATGCAT	120
ATGCTTCTTT	AGGTGAACGA	ATATCTGGTT	CAGATACGAT	TTCAATTAGC	GGTGTACCTT	180
GACGGTTCAA	GTCAACTAAT	GAATACTCAC	CTTTATGTGT	TGACTTACCA	GCATCTTCTT	240
CCATGTGGAA	GACGAGTAAT	ACCGATTCGT	TTTGTTTCAC	CGTCGACTTC	GATATCGATA	300
TATCCATTTT	CACCAATTGG	TTGATCAAAT	TGAGAAATTG	AGAGCTTnTG	GnTTAGCTGG	360
ATAGAAATAG	TTCTTACGGT	CAACTTAGAT	CCGTTGCGAT			400

(2) INFORMATION FOR SEQ ID NO: 4169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4169:

ACCATGTTTG	AATGAATCCA	TTGGAATCAT	TATTGAAGTA	AATTAAGGAA	TCTATAATGT	60
TCGTTAAATA	AAACTGATCC	CGTTGTGCTT	CACACCCGAT	AGATAGGGAT	TTACAGATAA	120
ATTCAGGTCT	CTTCCACGTC	ATATTTGGAC	CCATCGAAAA	TTCGGGTTCT	CAAATCATCG	180
AACATAACAA	AAGAAGCTAA	GCAACATGTA	GGCCGTTGTC	ACTTAACTTC	TTGTTTTTCC	240
GATGACAGCT	TCTATTTAGA	GAATGTCATG	ATTATTTTAT	ATTCACTTCA	ATGTTATCAA	300
TATTAGTGCC	ATCTATGACA	TCTGCCATGC	GATTTTCTTG	TAATTTTTTG	TGCAATCAAC	360
GTGTACnTCC	ACGGTTTTCA	TTTAAAnAACA	ATTTACCGGA			400

(2) INFORMATION FOR SEQ ID NO: 4170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4170:

	TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA	60
10	TTCCTTGTCTG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTTGGGC ACTGTCTCAA	120
	CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG ACAGGACGGA	180
	AAGACCCCGT GGAGCTTTAC TGTAGCCTGA TATTGAAATT CGGCACAGCT TGTACAGGA	240
15	TAGGTAAGGA GCCTTTGGAA ACGTGAGCGC TAnTTTACGT GGrAGGCGCT GGGTGGGGAT	300
	ACTTACCCTA AGCTGTGTG GCTTTCTAAC CCGCACCAhT TATCGTGGTG GGGAGACCAT	360
	GGTCAAGCGG GGCATTTTGA ATGGGGGGCG GTTCG	395

20

(2) INFORMATION FOR SEQ ID NO: 4171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4171:

	TACATTATAG CTTTAATCGT TTGAAGTATA GTTTGAAACC AGTAGTCACA GCTGTTCAAG	60
	GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG TACTTTACTC ACCTATTGTT GTCGCTGCAA	120
35	GTGAAACATA TATCGGTCTT GTTGAAGCAG GTGTTGGCTT ATTACCGAGT GGCGGTGGCC	180
	TTGCAGAAAT GGCTGATCGC ATATTACGCA CATCGCATAA GTTTGATGAC AAACAAGCTT	240
	CCATGACAAA AGTACTGACG AATATCGCAT TCGGAAnGCT CTACAAATGC CTTTGAGGCA	300
40	CGTCGTATGG GTATTTACCG TGGATACAGA TACGATnATT TCCAATACAG CACAACGrGT	360
	CGAAGTGGCG C	371

45

(2) INFORMATION FOR SEQ ID NO: 4172:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4172:

55

GCTGAGCTAA GCCCCCATAA TAATTACAGT ATATCGGGAA GACAGGATTC GAACCTGCGA 120
 CCCCTTGGTC CCAAACCAAG TGCTCTACCA AGCTGAGCTA CTTCCCGTAT AATTAACGCG 180
 5 CCCGATAGGA GTCGAACCCA TAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG 240
 CTACGGGCGC ATATGTTTTT ATTGAAAATn GTGCCGAGGA CnGAATGAA CCGGTACGTG 300
 ATCATTACCG CAGATTTTAA GTCCTGTGCG TCTGCCAGTT CCGCAnCCCC GACTATAAAA 360
 10 T 361

(2) INFORMATION FOR SEQ ID NO: 4173:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4173:

GTACAGATGC ATTGTTAAAC AATCAGTTGC AACAGCTGTT GAAACTGGTA GAGTATCTAA 60
 25 TGGTGATTTA ATCATTATTA CTGCTGGTGT ACCAACTGGT GAAACTGGAA CTACTAATAT 120
 GATGAAAATC CACCTAGTTG GTGACGAAAT TGCTAATGGT CAAGGTATTG GACGTGGATC 180
 AGTTGTTGGT ACTACGTTAG TTGCTGAAAC TGTTAAAGAT TTAGAAGGTA AAGATTTATC 240
 30 TGACAAAGTT ATCGTTACTA ACTCCATCGA TGAAACGTTT GTACCTTATG TAGAAAAAGC 300
 TTTAGGCTTA ATTACAGAAG AAATGGTATT nCACACCCAG TGCCATGGTT GGTTAGGAAA 360
 35 AGnAATCCCA CCGTTGTAnG 380

(2) INFORMATION FOR SEQ ID NO: 4174:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4174:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAG 60
 CTGAGCTGTG ATGGGGAGAA GACATTGAGT CTTGGAAGTC GTTGATTTCa CACTGCCGAG 120
 50 AAAAGCCTCT AGATAGAAAA TAGGTGCCCG TACCGCAAAC CGACACAGGT AGTCAAGATG 180
 AGAATTCTAA GGTGGAGCGA GCGAACTCTC GTTTAAGGAA CTCGGGCAAA ATGGACCCCG 240

55

GCCCAAGCGC TGTTTATCCA AAACACAGTC TCTGCTnAAC CGTAGGGGAT TGTATAGGGG 360
 CTTACGCCTG CCCGGTGCCT GGAAGGTTTA AAAGGGTGGT 400

(2) INFORMATION FOR SEQ ID NO: 4175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4175:

AGCCATGGCT CAGCGAGGTA GGACTCGAAC CTACGACCGA TCGGTTAACA GCCGATAGCT 60
 CTACCACTGA GCTACTGTGG ATTAATATTA TGCCTGGCAA CGTTCTACTC TAGCGGAACG 120
 TAATTCGnAC TACCATCGAC GCTAAGGAGC TTAACCTCTG TGTTCCGGCAT GGAACAGGT 180
 GTGACCTCCT TGCTATAGTC ACCAGACATA TGAnTGTAAT TTATACATTC AAAACTAGAT 240
 AGTAAGTAAA AGTGATTTTG CTTGCAAAA CATTTATTTT GGATTAAGTC TTCGATCGAT 300
 TAGTATTCGT CAGCTCCACA TGTGCACCAT GCTTnCCACC TCGAACCT 348

(2) INFORMATION FOR SEQ ID NO: 4176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4176:

CATTTTTTTA AAATAATACC AATCTCATTT TTAAATTCTA AACTTGGTTT CGTATAATAC 60
 GCTCTTAAAT CTTTAAATTT AGGATTTATT TCTGTTGGTA CTTGTTTTGT GGTTGGCGAT 120
 TGTGGTGTGT CTGATTTAGT AGATTGCATT GGTTGTGGCG TGTTTGTTGA TGGAGGTGTT 180
 GTCACTTTAG TTGAAGGCGG TGTTGTCGCA TTTGCTGTTT GTTGCGGTGC TTCTACTTTA 240
 GTTGAGGGCG GTGTTGTCGC GTTTGGTTTT GATTGCGGTG CTTCTATTTT AGTTGAGGGC 300
 GGTGTTGAnT GTGGTGCTTC CACTTTAGGG nAAGATnAGT GGTG 344

(2) INFORMATION FOR SEQ ID NO: 4177:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4177:

5 CAGAACCTTG NAATGAATCG CGATGGAATA TCTCTATCTG NAAACAGATT TCTTTTTGTC 60
 CGCCAATGGC CTTGGAATTG TTAAATAAA TCTATTTGCG CTTCTTTATC AATGTCATAA 120
 CCTAATGCTT TTAACCTCTC TGAGAAGCGT GTTTACCAGA TAATTTTCCT AATGGAAGTT 180
 10 CAGTCGTGCT TACACCAACA AGTTGAGGTG TCATAATTTC ATATGTTTCA CGATGTTTTA 240
 ATACGCCATC TTGGTGAATA CCTGATTCAT GACTAAATGC ATTTGGCCAA CAATTGCTTT 300
 ATTTCTAGGC ACTCGAATAC CTGCATATCT TGAATTAAA TCCGAGGTTT TAGTTCCTCG 360
 15 AG 362

(2) INFORMATION FOR SEQ ID NO: 4178:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4178:

GGAGCTAATA CCGGATAATA TTTGAACCG CATGGTAAAG NTGGAAAGAC GGTCTTGCTG 60
 30 TCACTTATAG ATGGATCCGC GCTGCATTAG CTAGTTGGTA AGGTAACGGC TTACCAAGGC 120
 AACGATGCAT AGCCGACCTG AGAGGGTGAT CGGCCACACT GGAAGTGAAG CACGGTCCAG 180
 ACTCCTACGG GAGGCAGCAG TAGGGAATCT TCCGCAATGG GCGAACTTn ACGGAGCAAC 240
 35 GCCGCGTGAG TGATGAAGGT CTTGGATCG TAAAACTCTG TTATTAGGGG AGGACATATG 300
 TGTAAGTAAC TGTGCACATT TTTGACGGTA CCTnATCAGG AAGCCACGGT TTACTAGGGG 360
 CCCAGAAGCC CCGGTTAATA CGTGGGTGGG nAAGGGTTTT 400

40 (2) INFORMATION FOR SEQ ID NO: 4179:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4179:

55 GTTGTTCAG CAGCGACACA GTGTATTCCA TTCTTAGAAA ATGATGACTC AAACCGTGCA 60

GTTGGTACAG GTATGGAACA CGTTGCAGCA CGTGATTCTG GTGCGGCTAT TACAGCTAAG 180
CACAGAGGTC GTGTTGAACA TGTGAATCT AATGAAATTC TTGTTCTGTCG TCTAGTTGGA 240
5 AGAGAACGGC GGTGAACAT GAAAGGTGGA TTAAGATCGC TATCCATTAG CTAAATTTAA 300
ACGTTCAAAC TCAGGTACAT GTTACAACCA ACGTCCAATC GTTGCCAGTT GGGAGATGTT 360
10 GTTGGnnnTA C 371

(2) INFORMATION FOR SEQ ID NO: 4180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4180:

AAAGGGAATC GAATTTTCTT TCTCTTCCTC CGGGTACTAA GATGTTTCAG TTCTCCGGGT 60
GTGCCTTCTG ATATGCTATG TATTCACATA TCGATAACAT GACATAACTC ATGCTGGGTT 120
25 TCCCCATTCTG GAAATCTCTG GATCAAAGCT TACTTACAAC TCCCCAAAGC ATATCGTCGT 180
TAGTAACGTC CTTTCATCGGC TTCTAATGCC AAnGCATCCA CCGTGCGCCC TTAATAACTT 240
AATCTATGTT TCCACCATTT TTATAAGTCA AACGCTCACA TACGGCTTCG TTTTCATTAT 300
30 nTnAAATGCT CATTTACATA AGTAAACTCT GCTTTAAAAT AATT 344

(2) INFORMATION FOR SEQ ID NO: 4181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4181:

CCGTGATCGG AAGGTGCGGC TGGATCACCT CCTTTCTAAG GATATATTCG GAACATCTTC 60
45 TTCAGAAGAT CGGGAATAAC GTGACATATT GTATTCAATT TTGAATGTTT GTTCATTCAA 120
ATTAATGGGC CTATAGCTCA GCTGGTTAGA GCGCACGCCT GATAAGCGTG AGGTCGGTGG 180
50 TTCGAGTCCA CTTAGGCCCA CCATTAATTT AATACCTATT TGGGGGCTTA GCTCAGCnGG 240
GAGAGCGCCT GCTTTGCACG CnGAGGTCAG CGGTTTCGATC CCGCTAGTCT CCACCATTAT 300
TTGTACATTG AAAACTAGAT AAGTGAnGTA AAAATATAGA TTT 343
55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4182:

CAGAGCCAAC TCGTATGTGA TTTGTCTGCG CCAATGTATG CATCATCAAA AGTTCTGGAC 60
 TACTACACGC AAACGCTGGT ACATTATGAT GTTCCGTAAA CCAAATTCGC TTAAAGCCAA 120
 GTCGATCTGC TAATTTTGCA AGTGTCACTG AATCTTGCAA TGCCTTTTGT GCATCCTTAC 180
 CTTCATCTAT TAAGGCATAG TCTAATACGC TTAATTTAAC CAATCCGTCA TCTCCAAACT 240
 TATCCTGTCA TGTCAAACCG ACATAACATT TTAGCGTCTT AATACCATT CTTCTTCATA 300
 TACCCACGTA TATGATAACG TTTTCAATAA CTTTATATCT TTCGCCTTAT TTnCTTTTCA 360
 TATCATATTT CAGACTACAA ATGCATCATA GTTAATTAAA 400

(2) INFORMATION FOR SEQ ID NO: 4183:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4183:

AAAGTATGAA AGATGGTAGT GACGCGGTTG GTGATTGGGC TGTATTGAAT GCACTCATTA 60
 ACACAGCTGC AGGTGGTTCA TGGATTTCAT TCCATCACGG TGGCGGTGTT GGCATGGGAT 120
 ATTCACTTCA TCGCGGTATG GTTGTGTAG CAGATGGATC AGAGCGTGCT GAAGGAAGAT 180
 TGGAACGTGT ATTGACGACT GACCCAGGTA TGGTGTGCGG CGACATGTTG nATGCTGGCT 240
 ATGACATCGC TATTCAAACA GCTAAAGAAA AAGGTATTCA nATTCCAATG ATTGGTGAAA 300
 GCAGGTGATA AGTAATGAAT GATTTAATAT TAATCAnATA GCAGAnTATT TTTACCGGGT 360
 CCAACAGATA AACCTTTGAA GGGTTAGGTA TTAGATGCAT 400

(2) INFORMATION FOR SEQ ID NO: 4184:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4184:

TTCCCTGTGC ATCGGCATCA CTATTATTAG CATGACTCAA TTATTGGCAT CACAATATGT 60
 5 CATTGCAGTT ATCATTGGTT TCGTCATATG TCGGATAGGT AATGGTTTAG TCGCAACACC 120
 TGGACTTACG ATTGCAATTT TCAGTATGCC TAATGAnAAA GTTGGTTTAG CTACAGGATT 180
 ATATAAAATG AGTGGTACAT TAGGTGGCTC CTTTGGTATA GACTAAGTA CTACAGTTTT 240
 10 CAGTATGTTA CAACTAAACT ATGCACCAAG TGTAGCTGCA ACCGTAACAT TTATAGTCAG 300
 CATTGTATTG ATGnTCCTTG GGTnCATTGT CTGCATACAT GA 342

(2) INFORMATION FOR SEQ ID NO: 4185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4185:

AAGCATACTC TGAAGCGGTG AACAAAAATA GAACAGATCA CATTAGACAT TTACTTGAAT 60
 25 TTAAAGCATG TACACCGATT GACATCGACC AAGTTGAACC GGTAAGTGAC ATTGTCAAAC 120
 GCTTTAATAC AGGGGCGATG AGTTATGGAT CGATTTTCAGC GGAACACATG AAACGTTAGC 180
 30 ACAAGCCATG AACCAATTAG GTGGAAAGAG TAATAGTGGT GAAGGTGGCG AnATGCAAAA 240
 CGTTATGAAG TACAAGTTGA TGGAAGCAAC AAAGTAAGTG CGATTnAACA AGTTGCTTCT 300
 35 GGGCGTTTTG GTGTACTAGT GATTATTAC CACCTGCCAA GGAATTCCAA TTAnACTTGC 360

(2) INFORMATION FOR SEQ ID NO: 4186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4186:

CCCAAGCGGA ATTCTAAAT GATCGTCGCT CCATTCTTCA TTTTAATAAA TCCAAACGCA 60
 50 GAATCTTCAA CTGTAAATTC ATCTGGATTC CATGAACCCC AAGCGTTTGC CGCATGATGC 120
 TGTTTATTTA ATTTATGGAA TGTGAACCC ATCACTGATT CTGGTTCATA ATTATCCATC 180
 ATCCATAACG TTAAATCTAA AGCGTGTGTA CCGATATCGA TTAATGGTCC TCCACCTTGG 240

nCTTTCCGAA GTTAAATGTC TCCTAAGTCG CCACGTTGGC GCTGCCTGGA TGGAAAATTG 360
 GACGATCTGC TCGGGAAACG AATTTGGATA AACnGATGGG 400

5 (2) INFORMATION FOR SEQ ID NO: 4187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4187:

GAATCATCTG GCAACnCCC CCAAAGAAGG TAATAATCCT GTAGTCGAAA ATGTTGTCTC 60
 TCTTGAGTGG ATCCTGAGTA CGACGGAGCA CGTGAAATTC CGTCGGAATC TGGGAGGACC 120
 20 ATCTCCTAAG GCTAAATACT CTCTAGTGAC CGATAGTGAA CCAGTACCGT GAGGGAAAGG 180
 TGAAAAGCAC CCCGGAAGGG ATGTGAAATA GAACCTGAAA CCGTGTGCTT ACAAGTAGTC 240
 AGAGCCCGTT AATGGGTGAT GGCCTGCCTT TTGTAGAATG AACCGGCGAG TTACGATTTG 300
 25 ATGCAAnGTT AAGCAGTACA TGTGGAGCCG TAGCGAAAGC GAnGTCTGA 349

(2) INFORMATION FOR SEQ ID NO: 4188:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4188:

TGGATCCTGA GTACGACGGA GCACGTGAAA TTCCGTCGGA ATCTGGGAGG ACCATCTCCT 60
 40 AAGGCTAAAT ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGGAA AGGTGAAAAG 120
 CACCCCGGAA GGGGAGTGAn ATAGAACCTG AAACCGTGTG CTTACAAGTA GTCAGAGCCC 180
 GTTAATGGGT GATGGCGTGC CTTTTGTAGA ATGAACCGGC GAGTTACGAT TTGATGCAAG 240
 45 GTTAAGCAGT AAATGTGGAn CCGTAGCGAA ACGAGTCTGA ATAGGGCGTT TAGTATTTGG 300
 TCGTAGACCC GAAACCAGGT GATCTACCTT nGGTCA 336

50 (2) INFORMATION FOR SEQ ID NO: 4189:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4189:

5 CAAAGGATGT TAAGAAATAC AATTTATTAC CCAGCATTTA ATAATGGTGC TATAGAAGGA 60
 ATTAATAATA AGATAAAATT AATCAAGTGA ATTTCTTTTG GTTACAGAAA TTTCACAAC 120
 TTAAAGCAC GTATAATGAT GATTTTCAGC TTGTACAAAG GAGAAAAAAA GAAGACAACC 180
 10 AAGCCCAATA ATGGACTGGC CGCCTAATAA TAAAAGCTCT AAAAGTTGTA TTTTAAAAAT 240
 AGTTCTTTAA ATTATATACC CACCACATT TGGTGGAGGAC CTAAAAAAA GCACTTCCCC 300
 AAAATGGGA AAGTGCAAGT AGTGAGCCnT AGGAGGGTTC GGACCCTCTn nCCCCTCT 358

(2) INFORMATION FOR SEQ ID NO: 4190:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4190:

25 TCACCAAGTT GAGCAAAGAA GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTGACTTCT 60
 AAnGTACCAC CAAGTGCCGT CTGCCAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT 120
 30 GGACCTAACA ATCTTAAGAT GAAGCCATAA ACAAAGTAC CGATGGCACC TGTTTTCGTT 180
 ACAAATCCAC CAACATGATA AATGCCGGCT TGTATGCTTG GCCAAATGAA AAACATCAAT 240
 ACACCTAAAA AGATTGCGGC AAATGCTGTG ACAATAGGGA CAnATGTAGA GCCACCAAAG 300
 35 AAACCTAAAT ACGGTGGTAA TACCATTGT GnTATTGTGT GTGAAGTATT GCGGTCATAA 360
 TA 362

(2) INFORMATION FOR SEQ ID NO: 4191:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4191:

50 TGATCACCCA TGTCTGGAC TCCCAATTGA AATTGAATTG GGCATTGCGA GTTTGTCTGG 60
 nATTGCGTAA CCCGnGCAGG GTCCCCTCGT GCCAAACAGT GCTCTACCTC CAATAATCAT 120

55

nATTTCTCCG CTAACCTCAG TTCATCCGCT CACTTTTCAA CGTAAGTCGG TCGGTCCTC 240
 CATTCACTGT TACCTGAACT TCAACCTGAC CAAGGTAGAT CACCTGGTTT CGGGTCTACG 300
 5 ACCAAATACT AAACGCCCTA TTCAGACTCG CTTTCGCTAA GGCTCCACAT TTA CTGCTTA 360
 AC 362

(2) INFORMATION FOR SEQ ID NO: 4192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4192:

20 CGTGATTAT GCCTTCTACA TTGGCCATTA TGAAACTTA TTATCAGGGT GCTGAACGTC 60
 AGCGTGCCTT AAGTTATTGG TCTATCGGTT CTTGGGGTGG CAGTGGTATC TGTTCACTCT 120
 TCGGTGGTGC AGTTGCGACA ACTATGGGTT GGAGATGGAT TTTCATCTTC TCAATTATCG 180
 25 TTGCCGTACT TTCAATGTTA CTCATCAAAG GGACGCCTGA AACGAAATCA GAAATTACCA 240
 ATACACATAA ATTTGACGTT GCAGGGCTAA TTGTTCTAGT AGTATGTTGC TAAGTTAAAC 300
 GTTGTCATTA CTAAAGGTGC AGCACTTGGn TACACATCAT TATGGGTCTT GGGTTGAATG 360
 30 CCAATCGGAA ATTGTAGCAT CnTTAATTTT CTAAAAGGTG 400

(2) INFORMATION FOR SEQ ID NO: 4193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4193:

45 AATCCCATGG ACCCTCAAAT TCTTTATCTA AATAGTACCC TAATGAAGTT TTTCTGTGCA 60
 TGTGATTAAT TCGATGAAA CCGATGACAC CAACTAGCGT TCCTTCATAC CAAATGCCAC 120
 ACTGAAATCC ATTACCATCA GCAAATTGCA AAAGTCCTCT TTTAATAAAT GCACGCGTAT 180
 50 CTGATGGTTG CTCAGTTGCA TCTACCCAAG GTAACCATTC CCTAAGTGAA TTTCTTGAAC 240
 GATTGACTAA ATTGAAAAGC GCTTCTGTGT CATGAGCTTC TAAAATTTTA ATGTTATTGT 300
 TCAATCACTT TCATTCCAAA CATACnATCA CATCCTCATT CATnTCATA TAATCCGGnA 360

(2) INFORMATION FOR SEQ ID NO: 4194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4194:

ACAAAGGACG ACATTAGACG AATCATCTGG AAAGAGAATC AAAGGTAATA ATCCTGTAGT	60
CGAAAATGTT GTCTCGAGTG GATCCTGAGT ACCACGGAGC ACGTGAAATT CCGTCGGAAT	120
CTnGGAGGAC CATCTCCTAA GGCTAAATAC TCTCTAGTGA CCGATAGTGA ACCAGTACCG	180
TGAGGAAAGG TGAAAAGCAC CCCGGAAGGG AGGTGTAAAT AGAACCTGAA ACCGTGTGCT	240
TACAAGTAGT cAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGAAT GGAACCGGCG	300
AGTTtACGAT TTgATtGCA AGGTTAAGCA GTAAATGTGG GAGCCGTA	348

(2) INFORMATION FOR SEQ ID NO: 4195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4195:

AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAAGTGCCTG GCAACGTTCT	60
ACTCTAGCGG AAnTAAGTnG GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTTCGG	120
CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA	180
TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG	240
TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGAACCTAT	300
TAACCTCATC ATCTTTGAGG GATCTTATAA nCGAGTTGGG	340

(2) INFORMATION FOR SEQ ID NO: 4196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAAATTAA TGAAAGATAC AGTAGGTGCT 60
 GATGTAGAAG TAAAAGCATC AGGTGGCGTA CGTAATTTAG AAGATTTCAA TAAAATGGTT 120
 5 GAAGCAGGTG CGACACGTAT TGGTGGGAGC GChGTGTTCA AATTATGCAA GGTTTAGAAG 180
 CAGATTCAGA TTACTAATAT ATATnAATnT TGGGAGTGAT AGCTATGACA AGACCATTTA 240
 ATCGTGTACA TTTAATCGTA ATGGATTCAG TAGGTATTGG TGAAGCGCCA GACGCAGCTG 300
 10 ATTTTTTAAAG ATGGAGGTTT ACATACTTTT A 331

(2) INFORMATION FOR SEQ ID NO: 4197:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4197:

GTAGACGTCC CGATAGCCGT TACGCATGGT TACGATGTGT ATTGGTGTCT GCATGGGTGC 60
 25 AGCTGCTATA TTTGAATATG TCGGTTAGAA TGGTTGATTT TGGATGAAGC GGATTCGTTT 120
 TGTTATTGAA TGAAGTAGGC TGAAGTTGAA GCCAGTTGAA GTTGAAGCGG GTTGAAGCAA 180
 30 TTTCGTTTTA TTGAATGAAG CTGTGTGAAA TATAGTGATT GAACAAAAAA AGTGGTTTAA 240
 TGGGATGGTG GTTATTTCCG TTTTAGAATT TAACATTTAC ACGTCTAATT TTAAATCATT 300
 GTTTTAAATT TTATGAATCG AAGCCCTTTG GATTTAATAn TATTGCTAAT GChAGTAACT 360
 35 nATCTGATTG T 371

(2) INFORMATION FOR SEQ ID NO: 4198:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4198:

GCGACCCCAA CCTTGGCAAG GTTGTnATTCTACCGCTGAA CTACTTCTGC ATATGCGGGT 60
 50 GAAGGGAGTC GAACCCCCAC GCCGTAAGCT nAGnATCCTA AGTCTAGTGC GTCTGCCAAT 120
 TCCGCCACAC CCGCAAATGG TGAGCCATAG AGGATTTCGAA CCTCTGACCC TCTGATTAA 180
 AGTCAGATGC TCTACCAACT GAGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 240

TAAGAATAAA TGGTGGAGAA TGACGGGTTT GnACCGTCGA CCCTGTGCTT GTTAAGGCAG 360
 ATGGTTTTCC CACTGGGGTA AATTTTCCGA TTAAAAATG 400

(2) INFORMATION FOR SEQ ID NO: 4199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4199:

ATCAGTTGCT GTTGCGCCTT GTGGTAATGA ATTTACTAGT CGTACACCAA TAACCTCTGG 60
 AATTGGGAAA TAAGAAGGTT GTCCAAGCAT TCCAGCTTCA GCTTCAATAC CACCAACACC 120
 CCATCCTAGT ACGCCAATAC CATTTATCAT TGTGTATGT GAATCAGTAC CAACTAATGT 180
 ATCTGGAAAT GCAGTTTTTT CACCATCTAC ATCAGGAACA TGTACAACAC TTGCTAAATA 240
 TTCTAAGTTA ACTTGGTGAA CTATTCCAGT TGCAGGAGGG AACTGCATTG TAATTATCAA 300
 ATGCTTTCGG TTGGCCCAAT TAAAAAACT GGATAACGTT CATnGTTACG TTCCAATTCC 360
 TAATTTCCnA ATTACGGTTC CAnGAGCTTC TGGGATTTTG 400

(2) INFORMATION FOR SEQ ID NO: 4200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4200:

CAACCTTTAT TGGTAAAAAC ACCCCAGCCA GGCACCTTAC GCCTACGCAT CGCTTGTACA 60
 CGTGCTACTA nAGGTTTACC AACCACACCT GATTCAATTG CTTTTTTAGC AGTAATTGCC 120
 ACATCTGTGT GACGATAATG ATATGCGACA GTTAATAATT TGTGATTTTT ATTAGCCGCT 180
 TCAATCATGC GATCACACTC TTCCGTCGTC ATCGCCATTG GCTTTTCACA CAATACATGG 240
 CACACCATGG TTCAATGCnT CTATAGAAAG ATCAGCAGGA ATTTATTAGG TGTACAAATG 300
 ACCCATCAAC AAGTTTAAAC AGCTCGCTAG GTGnC 335

(2) INFORMATION FOR SEQ ID NO: 4201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4201:

	ATGATGTGGC GGTGGTGAAA TCAGACCGAT ACCTGGCGTT GACCCTCTTG TCTTCGCAAT	60
10	CCACGGATAT ACCTTAGTAC CAGGTAATTG ACCACCTTCA CCAGGCTTTG CACCTTGCGC	120
	AACTTTAATT TGAATTTCTT TGGCATGTTG TAAATAATCA CTAGTTACAC CAAAACGCCC	180
	AGAAGCAACT TGTTTAATCG CACTTACTTT GTTGCTTCCA TCAACTTGTA CTTCATAACG	240
15	TTTTGCATCT TCGGCAACTT CACCACTATT ACTCTTTCCA nCTAATTGGG TCATGGGCTG	300
	TGCTAACGTT TCATGTGCTT CCGnTgnAAT CGATCCATAA CTCATCGGCC CCGTATTAA	360
	GCGGTTGGAC	370

20

(2) INFORMATION FOR SEQ ID NO: 4202:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4202:

	CAGCTAGCGA CTTACCTTGA CGTTTTGnGT ATTCATTCCA GCTTTGTnGG AATGAGtCGG	60
	gATATAAGCA TCTTTAGATA ATGCACCATC AACTAATGGA TATTTATGTC CAGTTGGaGC	120
35	CAGAAATCAT AAACGTCTTC AGTGTAAGCA ACAGCATCTT CaTTTAATGC CAAAATGCTT	180
	GGaTTAgTGC AATAACCATC GCAACTGnGC CAnACCTTGT GTTGGCTCGC CGCCTGAATT	240
	CAATCCATAA CGTGCTGTAT CTGTAGCAAT AACTAATACT TTTTCATTG GTCTAGTTGC	300
40	TAAATAATCT TTAGCTAATT GAATTGCTGG TGTTGCAGCA TAACAAGCTT CTTTCATTTC	360
	AAAGCAGCGT GCAAAAGGTT	380

45

(2) INFORMATION FOR SEQ ID NO: 4203:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4203:

55

GACATGTCAC CAAGAGCATT AGAAGAAGTT ATTTACTTTG CTCCTTATGT TGTTGTAGAT 120
 CCAGGTCCAA CTGGTTTAGA AAAGAAAAC TTTATTATCTG AAGCTGAATT CAGAGATTAT 180
 5 TATGATAAAT ACCCAGGTCA ATTCGTTGCA AAAATGGGTG CAGAAGGTAT TAAAGATTTA 240
 CTTGGAAGAG ATTGATCTTG ACGAGGAACT TAAATTGTTA CGCGATGAGT TGGGAATCAG 300
 CTACTGGGTC CAAAGACTTA CTCCGTGGCA ATTAACGGTT TAGAAGTTGT TnGAATCATC 360
 10 CCGTAATCCA GGGTACCACC CTCCnnGGnT GGATTTAGGA 400

(2) INFORMATION FOR SEQ ID NO: 4204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4204:

AAATTCTTCC GCCCTGTAAT TCCTTAACCG CTTCAACGGC ATCGTnAATn TCTTACATTT 60
 25 AGATAAAGAT GCATTGCAAG ATATCGTCAA CTTATTATTA GACGATGTAC AAGTTACATT 120
 AGACAAAAAA GGTATTACGA TGGACGTTTC TCAAGATGCG AAAGATTGGT TAATTGAnGA 180
 AGGCTATGAT GAAGAATTAG GTGCACGTCC ATTAAGACGT ATTGTTGAAC AGCAAGTACG 240
 30 TGACAAAATT ACAGATTACT ATTTAGATCA TACAGACGTT AAACATGTGG ATATAGATGT 300
 TGAGGATAAC GAATTAGTCG TAAAAGGTA 329

(2) INFORMATION FOR SEQ ID NO: 4205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4205:

GGTAAACAAA AACTTCCCT TTGGAAGCGA ATTATGGAGC GGAAGATAGG ATTTACACCT 60
 ATACCTCGTT CCGGGAAGGG CTGTTTCTAA AAGTTGAACT ACTCCCGCAA ATATTAAATT 120
 50 ATGGAGCGGA AGATAGGATT TACACCTATA CCTCATTCCA GGAAGGAATG TATTCTAAGA 180
 GTTGAAATAC TCCCGCATT TATTAAATT ATGGAGCGGA AGTAGGATTT GCACCTATAC 240
 CTCGTTCCGG GAAGGAGCTG TTTCTAAAAG TTGAACTACT ACCGCATAAA CCTGGTGGCG 300

(2) INFORMATION FOR SEQ ID NO: 4206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4206:

TACTTTGTGA ATCCAGAAAA CTTTGAGGAT GTCACATAATA GTGTGAATAT TACATTCCCA 60
 AATCCAAATC AATATAAAGT AGAGTTTAAAT ACGCCTGATG ATCAAATTAC AACACCGTAT 120
 ATAGTAGTTG TTAATGGTCA TATTGATCCG AATAGCAAAG GTGATTTAGC TTTACGTTCA 180
 ACTTTATATG GGTATAACTC GAATATAATT TGGCGCTCTA TGTCATGGGA CAACGAnnAG 240
 CATTTAATAA CGGATCAGGT TCTGGTGACG GTATCGATAA ACCAGTTGTT CCTGAACACC 300
 TGATGAGCCT GGTGAAATTG AACCAATCCA GGGATCAGAT CTGACCCAGG TCAGATCTGG 360
 CAGCGATCTA ATCAGnAGCG GTCAGATCGG GnAGGATCAC 400

(2) INFORMATION FOR SEQ ID NO: 4207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4207:

AAAAAGTTGA GAAAAATGTT TGAATCAGCA AACGTTGTGC AATCGAAATT TCCACACCAT 60
 CAAAACCTGC TTTAATCGCG CGTAATGTAG CATCGCnGwk ACTGCTGAAT GATGCTATTG 120
 ATTTTCTCAT GAGACATGGC GATAACATCG TGTTtCAATC GGTGAATGCA ATGwCATAGG 180
 GCTTGGTCCA TACACCTTTC CAAAATTTAA AATGGCTTGA TTTGAAAAAC GACCAGCATG 240
 CGCTACTGGG ATAATAGCGA GGCTACCATG TTGTTTCATC GTAGATCCCA TGTTAGTTAA 300
 TCCAGGGATA CAACCATCAT GATCAATATT AAAnCATATC CAACCATTGA CCATAAGGTC 360
 AATGTAACAC GCCGGTGA CT CATCCAGCT GAATAGACGC GT 402

(2) INFORMATION FOR SEQ ID NO: 4208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4208:

5 GAAGAGTTGC AGCAGCAGAT ACAATTTATC CATTCACTCA AGCTGAAAAT GTTTGGTTAC 60
 CAAACAAAAA TGACATCATC GAAAAAGCAA AAGAACTTT AGAATTTTAA TACATTTTAA 120
 AAGTTAACGA ATTAGCCGTG ATTTTAGTCT CATTGATTAA AATGAAATnG TTAATTTACG 180
 10 AAATCTTAGG AGGGCAAAAA CGTGGGCATT TGAATTTAGA TTACCCGATA TCGGGGGAAG 240
 GTATCCACGA AGGTGAAATT GTAAAATGGT TTGTTAAAGC TGGAGGATAC TATnGGAAGA 300
 AGACGATGTT TTAGCTGGAG GTACAAAACC GATAAATCAG TAGTAGAAAT CCCCATCCAC 360
 15 CAGCATCTGG TACnGGTAAG 380

(2) INFORMATION FOR SEQ ID NO: 4209:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4209:

AATAAACCTC AGGCTATTCA ATGGCATACA AATTTAACGA ATGAGCGATT CACTACTATC 60
 30 GCACATCGTG GCGCAAGTGG CTATGCACCC GAGCATACGT TTCAAGCATA TGATAAGAGT 120
 CATAATGAGT TAAAAGCATC TTATATCGAA ATTGATTTAC AACGTACCAA AGATGGCCAT 180
 TTAGTTGCTA TGCATGATGA AACTGTTAAC CGTACAACAA ATGGACACGG TAAAGTTGAG 240
 35 GATTATACCC nTGATGAATT AnAACAGTTA GATGCAGGAA GTTGGTTAAT AAAAAATATC 300
 CnAAATACGC CAGAGCAGTA TTAAAATGCT AAAGTACCAC TTAGGTGGAA TTTAGGACGT 360
 ATTGGCCCCG TGCCAACnTT TATATTGAAC CAAGCACCTG 400

40 (2) INFORMATION FOR SEQ ID NO: 4210:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4210:

CCCCACAACC ACAAAGGCTG TAGGCTACAA ATATGGAGAC GGCGGGATTT GAACCCGCGT 60

55

AAAAGTGATA AACAAACCAAC ATGATGCTAG TTTGATTAAG TTTCTTCTAA ACAGACTTCA 180
AACGGCATnG TTAGCATATC CTATTAAGGT TGAATCGCGT TAACAGCACA TAGGAAATGC 240
5 TGTTAGGCGA TGCAGAGTGC GATTAGGCAG CTA CTGCGAA ATTATTGTnT GATTTGCCAG 300
TTATTATnAA CTGTGTGGTG TTGATGACGA 330

(2) INFORMATION FOR SEQ ID NO: 4211:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4211:

AAATCATCTT ATGACTGCTT TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC 60
GTTTTCACCTT CGCCAAGCCA TCTTTCTTTG TGTTCGCTTT TATTTTGACG TTTTAGACAT 120
AAAAAAGAG ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG 180
25 TTCTACTCTA GCGGAACGTA AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCnGTG 240
TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC CAGACATATG AATGTAAATT 300
ATACATTCAA AACTAGATAG nAAGTAAAAG TGATTTTGC 339

(2) INFORMATION FOR SEQ ID NO: 4212:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4212:

GCGATGGTTG AAACATTGAC TGATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60
TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120
45 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180
CGATTTTGGC ATGAAGGTCA CCTnAAATGT ACATTGTTGT AATAAAATTG CCTATAAAAT 240
TTTTAGCACA TAAAATAAGA GGGGCCAnCC ATTTTAGACT ATAACAACGG TTGGCTCTTT 300
50 GAATTGTAAA AAGAAAACCA TACGCTATGn TATT 334

(2) INFORMATION FOR SEQ ID NO: 4213:

(A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4213:

10 CTATGATTTC ACCGAGTCTC TCGTTGAGAC AGTGCCCAA TCGTTACGCC TTTCGTGCGG 60
 GTCGTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT ATAGTTACGC CGCCGTTTAC 120
 TGGGGCTTCG ATTCGTAGCT TCGCAGAGTA nACCCACTCC TCTTAACCTT CCAGCACCGG 180
 15 GCAGGCGTCA CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA 240
 GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGGCGTTA ACCCTAAAGA GCACCCCTTC 300
 TnCCGAAGTT TACGGGGTCA nTTTGCCGAG TT 332

20

(2) INFORMATION FOR SEQ ID NO: 4214:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4214:

30

CGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTGGCT ACCATCGTCG CTAAAGACCT 60
 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATTT 120
 35 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 180
 GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TAnTTTGACG TTTTAGACAT AAAAAAAGA 240
 GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGGCAA CGTTCTACTC 300
 40 TAGCGGAACG TAAGTTGGGT ACCATCGACG CTAAGAACCT TCTTGGAnTG TGGACAACGn 360
 TGG 363

40

(2) INFORMATION FOR SEQ ID NO: 4215:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4215:

55

TTATTTGTAT TGTATAGAGA GAAATAAAAA GAAACCTTGT TTTACAAGGT TTCTAATACG 120
 TTATGTTATG TAAATAACAG TTAATTATAC CCGTGGTCGG GGTGGAACCG ACACTCCACA 180
 5 AGTGAACCG GGATTTTGTAG TCCCGCGCGT CTGCCAATTC CGCCACACCG GCTTAATGGT 240
 AAACAAAAAA CTTCCCTTTG GAAGCAATTA TGGAGCGGAA GATAGGATTT ACACCTATAC 300
 CTCGTTCCGG GAAGGACGTG TTCTAAAAGT TGA CTACC 338
 10

(2) INFORMATION FOR SEQ ID NO: 4216:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4216:

ACGGTGATCC CATAATGCTT GAACATCAAT TTCATCCATT AATGTTACAT GAGGTGCAGT 60
 ATGCTTAGAG TTAACCATTG CTTTCGCAAT TGCTCTACGC ATAGCAGGGA TTTTTCAGT 120
 25 TGTTTCTGGG AAGTCGCCTT CTAATGTTAC TGCTGCAGGT GCTGCAGGAG TTTCAGCAAC 180
 TTCTTCACTT GTAGCTGAAG CAGCTGATTC ATTTGAAGCT GTTGGTGCAC CACCATTTAA 240
 GTATGCATCT ACATCTTCTT TTGTAATACG ACCATTTTAA CCAGATCCAG AAAGTCTTTT 300
 30 AATGnTAACA CCTnTTTCAC GTGCGTATTA CGACTGAAGG CATGCCTTAA CAGTCnGGTT 360
 CACCACTCTC AGTTGAGAGC ACAGGGCTGC nCGCTGGCGC 400

(2) INFORMATION FOR SEQ ID NO: 4217:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4217:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTAATAAGA TGTTTCAGTT CTCCGGGTGT 60
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120
 50 CCCATTTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240
 TCTATGTTTC CATCCTACAG GAAACGCGTT ATTAATCTTG TGAGTGnCT TTCGAACATA 300

(2) INFORMATION FOR SEQ ID NO: 4218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4218:

GGCGCCCTCG TGCCAAACAG TGCTCTACCT CCAATAATCA TCACTTGAnG CTAGCCCTAA 60
 AGCTATTTTCG GAGAGAACCA GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA 120
 GTTCATCCGC TCACTTTTCA ACGTAATCGG TTCGGTCCTC CAnTCAGTGT TACCTGAACT 180
 TCAACCTGGA CCAAGGGTAG ATCACCTGGn TTCGGGTCTA CGACCAAATA CTAAACGCCC 240
 TATTCAGACT CGCTTTTCGCT GACGGCTCCA CATTTACTGC TTAACCTTGC ATCAAATCGT 300
 AACTCGCCGG TTGCATTCTA CAAAAGGCAC GCCATGCACC CATTA 345

(2) INFORMATION FOR SEQ ID NO: 4219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4219:

TCTTATGACT GCTTTTTTATT ATACTTTACA TTTCTCGTTT CGTCAGATTG AACGTTTTTC 60
 ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA 120
 AGAGACCTTG CGGTCTCAAT GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC 180
 TCTAGCGGAA CGTAAAGTTC GnACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG 240
 GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGGAAT GTAAATTATA 300
 CATTCAAAAC TAGATAGTAA GTAAAGTGGn TTTGCTTCGC AAACChTTAT TTTGGTTAGT 360
 CTTCGTC 367

(2) INFORMATION FOR SEQ ID NO: 4220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4220:

AAGAGCCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCACTT 60
 ACTCATTTAG CTCTACTAAA CTCGTTGCGT TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 120
 TTCCTTCGCG CAAGCCATTT TTCTTTGTGT TTGCTTTTTA TTTTGACGTT TTAGACATAA 180
 TAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 240
 TCACTCTAGC GGAATTAAGT CGAACTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGTT 300
 CGGCATGGGA ACAGGTGTGA CCCCCTGGC TATAGTCACC AG 342

(2) INFORMATION FOR SEQ ID NO: 4221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4221:

ACCGGATGAC AGCCCCAGGA TCGATGAGC CGACATCGAG GTGCCAAACC TCCCCGTCGA 60
 TGTGAATCT TGGGGGAGAT AAGCTGTTAT CCCCAGGGTA GCTTTTATCC GTTGAGCGAT 120
 GGCCCTTCCA TCGGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 180
 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACTCTAT GAATGATTTC CAACCATCT 240
 GAGGGAACCT TTTGAGCGCC TCCGTTACCT TTTAAGAGGC GACCGCCCCA GTCAAACGTC 300
 CCGCCTGACA CTGTCTCnCA CCACGATAAG TGGCGnG 337

(2) INFORMATION FOR SEQ ID NO: 4222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4222:

GGCGCTTGAC TAAAAAGAAA TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT 60
 TTACCAAGCA AAACCGAGTG AATAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA 120
 TCGTAGTGT TCGAAAGACA TCCACCAAGn TTAATAACGC GTTTAAATCT TTTTATAAAA 180
 GAAAACGTTT AGCAGACAAT GAGTTAAATT ATTTTAAAGC AGAGTTTACT TATGTAAATG 240

ACATAGATTA AGTTATTAAAG GCGGCACGGT GGGTGCCnTG GCACTTAGAA GCCGCTGAAG 360
G 361

5 (2) INFORMATION FOR SEQ ID NO: 4223:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4223:

CGGTAGAATA CAACCTTGCC AAGGTTGGCG TCGCGGGTTC GAATCCCGTC TTCTGCTCCA 60
TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC TTAAAATCCT GCGGTGAGAG 120
20 ATCACCGTAC CGGTTCGATT CCGGTCCTCG GCACCATTTT AGCGCCCGTA GCTCAATTGG 180
ATAGAGCGTT TGAACGGA TCAAGAGGTT ATGGGTTTGA CTCCTATCGG GCGCGCCATT 240
TTTAAATTAA TTGAATAACG GGAAGTTAGC TCAGCTTGGT AGAGCACTTG GTTTGGGGAC 300
25 CAAGGGTCGC AGTTCGAATC CTGTCTTCCC GATTACTCnT AAnTCCATTT AnGGGGGCTA 360
GCTCAGTGGG GAGAGCGCTG CTTGCACGCA GGAGGTCACG 400

(2) INFORMATION FOR SEQ ID NO: 4224:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4224:

40 CATAATATAC TCTTAAGTGT AAAGGGGAAT TTCCTGGGTA ATAATTCGCG TGTGCACCTT 60
GAGTGACTTC TACCATTTTA TAGTCAAATT GCTTTAGTTC GTTTGGTTTA ACGCCGACAC 120
TCGCAAATGT ATAATCAAAG AACTTCACAA TATTGTTGCC TAAGAAGCCT TTGAATTCAA 180
45 TAGTGTCAAT TCCAGCAATT TGTTCGGCAA CAATACTTGC TGCACGGGTG AGCGCCCCCA 240
GnCAAAAGGA CCACTAGCCG GTAGAATCGA CATGTCGATA ATGTGATGGT TGCCAATAAT 300
CGCCTATTGC ATAATGTTTG GACCATTGGT TCCAAATTTA TCGTTACCGG TATGAAACCT 360
50 TTCGATCCAG TTGATAATT GAACTTCGnA AATTGATTG 400

(2) INFORMATION FOR SEQ ID NO: 4225:

- (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4225:

10 GGGTTCAATT TCTGCATACC AATCGATGCC AGCTCTATTT CTGACAATAT CCATATATTT 60
 TGAAATTTTC TCTAATTCTT TGCCACTAAC CTTTTCACCA TTCAACCAAA ATTGATCCTG 120
 TGTTAACTGG TCGTTAAAAG TGACTTTCGT TTCAGTGTA AATTTTCTA ATGTAACAGA 180
 15 TATGCTATTA TTCATTGGAA TGATTAGTGC TTCATCTTTT TTACCCCAAT ATTTTATnAG 240
 TGCAATATTC GTATGTGCAC GTGCTTTGCC ACTnnTAATC AACGCATTAA CCTCCTAAAT 300
 TCTCAATCCA AGTATGTGCT GCACCAGC 328

20

(2) INFORMATION FOR SEQ ID NO: 4226:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4226:

30

TGACGGGTTC GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA 60
 TTCTCCGATT TAAAACTGCC TGGCAACGTT CTA CTCTAGC GGAAnGTAAG TTCGnACTAC 120
 35 CATCGACGCT AAGGAGCTTA ACTnCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 240
 GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 300
 40 TCCACATGTC ACCATGCTTC CACCT 325

(2) INFORMATION FOR SEQ ID NO: 4227:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4227:

GCGCAACTCA CACAACAAGG TGGCAATCAC TCTGAACAAA GTGCGGCAAn TTnTTCAACA 60

55

AACCTTACGC AAGAAGCACG TGACGGTTTA TTAGATCCAG TCATTGGTCG TGGATAAAGA 180
 AATTCAAGnA ACTGCTGAAG TTTTAAGTAG ACGAACTAAA AACAATCCTA TATTAGTTGG 240
 5 AGAAGCTGGT GTTGGTAAAA CTGCGATTGT TGAAGGTTT AGCACAGGCA ATCGTTGGAA 300
 GGAAATGTAC CAGCAGCAAT CAAAGACAAA G 331

(2) INFORMATION FOR SEQ ID NO: 4228:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4228:

20 AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCATTAATA ATAAGGGCGG CTGAAGGGGA 60
 TCGAACCTC GAATGTCGGA ACCACAATCC GATGTGTTAA CnCTTCACCA CAGCCGCCAT 120
 GGCAGGGGCA GTAGGAATCG AACCCACACC AAAGTTTTGG AGACCTCTAT TCTACCGTTG 180
 25 AACTATGCCC CTATTAATAA TAATAAATGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 240
 AGAGCGGATT TACAGTCCGC CGCGTTTAnC CACTTCGCTA CCCCTCCATA AATGGTGCCG 300
 GCCAGAGGAC TTGnAACCCC CAACCTAATG GTT 333

(2) INFORMATION FOR SEQ ID NO: 4229:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4229:

40 CTCTTACTTT GTAAACCAAA TCTTAAATTA AAATATTGAA AATGCAATGn ATCCTTAATA 60
 TTTTATTAA CCTATAATTA CTTATTAAAA ATAACACACA ATATTCATAA AGTTTTAAAA 120
 45 ATATTCTGTT TTATCACCTA CTATTAGTGG AAAAGTACAA TTGCAATTGT ATATAGTTTG 180
 CATAACGCTT CAAAAGTAAT TTCTTTTTTG TTAGTTCAA AAAAAATTTAG AGGTGATGTT 240
 ATATGAATAA CGGTTTTTTC AATAGCGACT TTGATTCAAT TTTTCGAGGA TGATGAAAGA 300
 50 TATGCAAGGT TCAATCAAG TCGGAAACAA AAGTACTATA TTnATGGTAA GGAGTTTCAC 360
 CTGAGGACTG GCGCAACTnC ACACACCAGG TGGCCATCAC 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4230:

CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTC ACTCCCCTTC 60
 CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGTTCAC TCGGTCAC T AGAGAGTATT 120
 TAGCCTTAGG AGATGGTCCT CCCAGATTCC GACGGAATTT CACGTGCTCC GTCGTACTCA 180
 GGATCCACTC AAGAGAGACA ACATTTTCGA CTACAGGATT ATTACCTTCT TTGATTCA TC 240
 TTTcCAGATG ATTCGTCTAA TGTCGTCCTT TGTAAC TCCG TATAGAGTGT CCTAsAACCC 300
 CAACAAGCAA GCTTGTGGT TTGGGnTCTT GCCGTTTCG 339

(2) INFORMATION FOR SEQ ID NO: 4231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4231:

GAAGTCATAT GCATACACTT GGTATCATT ATTCATACGT TCAATCGCAT CTGTAACTG 60
 AATTTGCTTA CCTGCGCCTT CTTTTGCGT TTTTAAATAA TCGAAAATTT CAGGCGTTAA 120
 TACATAACGT CCCATAATAG CTAGGnTTGA TGGTGCCGTA CCTGTGCTG GCTTTTCAAC 180
 AAAC TTTTTC ACTTCAGACT GACGTCCG Tn TTTAGTTAAT GGGTCAATAA TTCCATAACG 240
 ATGAGTATCT GCTTCCGGAA CTTCTTGGAC ACCTATAACT GAGTGCCCTG TnTCTTCATA 300
 AACGTCAATC AACTGTTTCA CTGCTGGCAC TTCAGAGTCA ACAATATCG 349

(2) INFORMATION FOR SEQ ID NO: 4232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4232:

CCAGGATGCG ATGACCGACA TCGAkGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120
 GAGATAAGCC TGTTATCCCC GGGGTAGCTT TTATCCGTTG aGCGATGGCC CTTCATGCG 180
 5 GAACCACCGG ATCACTAAGT CCGTCTTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAkTCA 240
 AGCTCCCTTA TGcCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACTTTGaG 300
 10 CGCCTCCGTT ACCTTTTAGG AGGCGACCGC CCAGTCAAAC TGCCCGCCTG ACACTGTCTC 360
 CCACCACGAT AAGGTCG 377

(2) INFORMATION FOR SEQ ID NO: 4233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4233:

GGCTAGCCTC AAGTGATGAT TATTGGAGGT AGAGCACTGT TTGGACGAAG GGCCCCCTCTC 60
 25 GGGTTACCGA AGTTCAGACA AACTCCGAAT GCCAATTAAG TTAACTTGG GAGTCAGAAC 120
 ATGGGTGATA AGGTCCGTGT TCGAAAGGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 180
 30 AATATATGTT AAGTGAAAAA GGATGTGGCG TGGCCCAGAC AACTAGGATG TTGGCTTAGG 240
 AAGCAGCCGT CATTTAaAGA GTGCGTAATA GCGCACTAGT CGAGTGACAC TGGGGGGAAA 300
 GGGTACCGGG GCTGAACATA TTACCGAAGC TGGTGGGTTG TCCTTTGGAC AnTTn 355

(2) INFORMATION FOR SEQ ID NO: 4234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4234:

ATCCGCCTCC CGCAATATTT TATAGGTCTC GTAGTGTAGC GnTTAACACG CCTGCCTGTC 60
 ACGCAGAGAT CGCGGGTTTCG ATTCCCGTCG AGACCGCCAT CATTACATT TTATTATGGT 120
 50 TCAGTAGCTC AGTTGGTAGA GCAATGGATT GAAGCTCCAT GTGTCGGCAG TTCGACTCTG 180
 TCCTGAACCA TTTCTTAGCC GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT 240
 AGGTTGGGGG TTCAAGTCCT CTGGCCGGCA CCATTTATGG AGGGGTAACG AnTGGGCTAA 300

TTAATAATTT TAATAAGGGG CATAnTTCAA CGGTAnAATA

400

(2) INFORMATION FOR SEQ ID NO: 4235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4235:

ATGCCATGTT CACCTTGT TT AAAATCAAGG TTTGTAATGT TTCCTTGTGT CACGATAATA 60
 GCGTAATAT CACTCTTTC ATGATTGCGG ATGTAGTCTA AATCAAAGTT GATTAATAAA 120
 TCACCTTCTT TAACTnnTTG ACCTTCCTCA ACATGTAAAG TAAAGCCTTC TCCGTTTAAT 180
 TTAACAGTGT CTAACCGAT GTGGATTAAT AGTTCTAAAC CACTATCTGA TACAAGACCA 240
 ATTGCATGnT TTGTTGGGAA AATCATTTGT ACTTTACCGT TGAATGGTGC ACGAACTTCA 300
 CCTTGTGAGG TTTGATAGCG ATACCGTCAC CCATGCATTT T 341

(2) INFORMATION FOR SEQ ID NO: 4236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4236:

GTTGATGCAG CCCGTTGAGC TCTAAACCAA CTGAGCTAAA GGTCCTAAAT ATAATTTTAC 60
 AACTAATAAA TAGTGGCGGT GGAGGGGATC GAACCCCGA CCTCACGGGT ATGAACCGTA 120
 CGCTCTAGCC AGCTGAGCTA CACCGCCTTA TATAGTTTGT AAATAATATG GTGGAGACTA 180
 GCGGGATCGA ACCGCTGGAC CTCCTGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAG 240
 CCCCCATAAT AATTACAGTA TATCGGAAG ACAGGATTCTG AACCTGCGAC CCCTTGGTCC 300
 CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGnGC CCGTAGGAGT 360
 TGAACCCATG AACCTnTTGA TCCnTAGTnC AAACGGTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4237:

5 nAnTTCTTGA CCTGACATCA CCTGAAATTG AATGGACATG GTCCACCAGG TCATATACTC 60
 TAATCCATGG GTCGCCGATA CCTTCAACGn ACAACATCTA CACCACTATT TCTAATACAG 120
 AATCTTTCTC CTGCACTACC GTTAATAAAT GCCTTACCAC TTGTCGCACC ATAGAATGAG 180
 10 ACGTTACCAG CAATAATTTT ATTTTGTTCG TCTTCAAAAG GTGCTTTGAC AATGACCGTA 240
 CCACCAGATA ATCCTTTACC AACATAGTCA TTCGCATCTC CAGTATGATG AATCATTAAAG 300
 CCTTTCCGGTG CATATGCTGC AAGACTTTGA CCAGCATGAC CATTTCGTATA AACATTAATT 360
 15 GTATTTTCAG GAAGTC 376

(2) INFORMATION FOR SEQ ID NO: 4238:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4238:

25 CGATTTAAAG CTAAGCCCAT TTTCGCTCTT TCTCCATAGC CTAACCAAGC AATACGTGAT 60
 GGTAGTCCTT GATATGAAAT TTTTCTTCA GCTAAATCAA GCCATCTTAA TAACTTTTCA 120
 30 TTTTCTGGGA AAAGTTGCG CATTCTTCA TCCGCACGCT CGATATCTTT TGGATCACCA 180
 CTCAACGCAG CAAAGCGGAA TGGCCCTTTA CCTTCACAGA ATAATGGTCT AATGTAAGCT 240
 35 GGTACAAAAG CTGGGAAGTC AnAAAGCATT TTCACTCCG TATTGAAGGC TACTTGACGA 300
 TATGnTACCA TAATCAATGC TACAGCGCCA CGTTG 335

(2) INFORMATION FOR SEQ ID NO: 4239:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4239:

45 CCACAnTTAC AAGCAACTAC TGAAGGCGCT GTATTTATTA AAGGTGGCGA CGGTTTTGAT 60
 50 TTCGGACACG TAGAAAGATT TATTCAAAAC CCGCCACATG GGGCAACGGT TGCATGGCAT 120

55

TTACCTAATG GTCAAGGTAC GCGTAATGTT GAAGTTCCAG TCAAAGTTTA TCCAGTTGCT 240
 AATGCAAAGG CGCCATCACG TGATGTGAAA GGTCAAATTT TGCTGTTGGA CGGATGCGAT 300
 5 GAACTACATT ACATTTGTCC AATACAACAC AGATnGTATC ACTGCAGC 348

(2) INFORMATION FOR SEQ ID NO: 4240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4240:

TTGATGTTAA AGATTTAGCA AGGGGCGAGA GAACTGGAGA AGAGGTTGCC AAACGAATGG 60
 AACGTGCTTC TGTATTGGCC CAAGTAGATA TTCATCGTGC AGCAACACAT AATAAAGGTG 120
 TTATGAATGG CATACTGCT GTTGTTTTAG CAACAGGAAA TGATACGCGT GGTGCAGAAG 180
 CAAGTGCACA TGCATTACGC GAGTTCGTGA CGGACAGTAT CGTGGTATTG CTACATGGCG 240
 TTACGATCAA GATCGTTCAA CGATTTGATT GGTACATTGG AAGTGCCTAT GACATTGGCA 300
 ATCGTTGGCG GTGGGTACAA AAGTATTACC AATTGCTAAG CCTTCATTAG GAGnTACTAA 360
 ATGGTAGAGT CCGCCCCAAG AATTAnGnCC CTGTA 395

(2) INFORMATION FOR SEQ ID NO: 4241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4241:

ACTAATGATT TATTATGTAG TGGTCTTTG TCATTAGCCA CAGCTATTGT GTACTTAAAA 60
 ATAGGAATGC ATGAGTGCAA CTCTAnAnGn AGCATACTAA TTTCTAAAGA AAAAGTATTT 120
 CTTTATGTTG GGGCCCCGCC AACTTGCATT GTTTGTAGAA TTTCTTTTCG AAATTCTTTA 180
 TGTGTTGGGCC CCGCCAACTT GCATTGTTT TAGAATTTCT TTTCGAAATT CTTTATGTTG 240
 GGGCCCCGCC AACTAATTCC AATATATCAT TGTAGAGCTT AGGTCATTGA TTTTGGCTC 300
 GGACTTTTAT GGCGATATGA ACCATGTAAA T 331

(2) INFORMATION FOR SEQ ID NO: 4242:

(A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4242:

10 TGCATTGCAT TATTGTACTG CGTAATTGTA CCTGGCTTTT TACCTTCAGT GCTTACTGGA 60
 TCATCTAAAT GATTTTTAGC TGTGATTAACT TCACGTTTAT CCGCTTTTGT GAAAATGGAC 120
 TCTTGTA CTTTCTAGTACT ACCATCATTG TAAGTTACTG TCACAGGAAT CGTCGTTGTG 180
 15 CTACCACCAG CTAATTAGT AGGCATTGCT GTGCCATTTT TAATCGTTGC AGTACGTTTA 240
 TTAGCAACTT GAACTGCATT GTTAATTTCA GCTGCTGTGA CATTGGAACC ATAATCTTTC 300
 ACAATTn CAG TTGTGTTGAC AGATGAGnGG CGGTGCAGTA AGGACTGGAT ACACTACGAG 360
 20 TGACCGGACT GCTTCGGGnA ATGTGATGA 389

(2) INFORMATION FOR SEQ ID NO: 4243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4243:

35 ATACGCATGT TAACGATCGA ATGCTTAATG TCCCGGGAAA TAAATCTATC ATAAGTTACT 60
 TTAATGAAGT TGTCTCACGA CAAGGTAATC ATGTTGCGCT ATCATGAATG ATTTGACAAT 120
 GACGTATGAA CATTACGCAA CTATGTGGAT GCCATTGCGC ACATGCTCCT ATCAAATGGT 180
 40 GTGGGCAATG GTCAACGGGT TGCCTTGTTT ACAGAACGTn TTTTGGAAT GATTGCGGCG 240
 ATGTTGGCGA CAGTTAAAGT AGGTGCATCT TATATACCTA TCGATATTGA TTTTCCGAAT 300
 AAACGACAAG GTGCAATTTT GG 322

(2) INFORMATION FOR SEQ ID NO: 4244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4244:

CAGTTCTCCG GGTGTGCCTT CTGTATATGC TATGTATTCA CATATCGATA ACATGACATA 120
 ACTCATGCTG GGTTCCTCCA TTCGGAAATC TCTGGATCAA AGCTTACTTA CAGCTCCCCA 180
 AAGCATATCG TCGTTAGTAA CGTCCTTCAT TGGCTTCTAG TGCCAAGGCA TCCACCGTGC 240
 GCCCTTAATA ACTTAATCTA TGTTCACACC ATTTTATAA GTCAAACGTT AACATGAAGT 300
 TACGTTCTTT TATAAAAAGA TTAAACGCG TTATTAATC 339

(2) INFORMATION FOR SEQ ID NO: 4245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4245:

CCATTAACGG GCTCTGACTA CTTGTAAGCA CACGGTTTCA GGTTCTATTT CACTCCCCCTT 60
 CCGGGGTGCT TTTCACCTTT CCCTCACGGT ACTGGTTCAC TATCGGTCAC TAGAGAGTAT 120
 TTAGCCTTAC GAGATGGTCC TCCCAGATTC CGACGGAATT TCACGTGCTC CGTCGTACTC 180
 AGGATCCACT CAAGACAGAC AACATTTTCG ACTACAGGGA TTATTACCTT CTTTGGATTG 240
 ATCTTTCCAG ATGATTGCTC TAATGTCGTC CTTTGTAAGT CCGTATAGAG TGTCTACAA 300
 CCCCACAAG CAAGCTTGTT GGTnTTGGGC nACTTCCCCG TTTCGGTTCG GCCGnAA 358

(2) INFORMATION FOR SEQ ID NO: 4246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4246:

AAAGAGACCT TGCGGTTAGA TGCGGCTCAT CGCATCCATT TTTGCCTGG CAACGTTCTA 60
 CTCTAGCGGA ACGTAAGTnG AnCTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG 120
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180
 TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTGATTAAG 240
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGGAACCTA 300
 TTAACCTCAT GCATCTTTGA GGGGnGCTTG ATAACCGA 338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4247:

CCCCGGGTAG CTTTATCCG TTGAGCGATG GCCCTTCCAT GCGGAACCAC CGGATCACTA 60
 AGTCCGTCTT TCGACCCTGC TCGACTTGTA GGTCTCGCAG TCAAGCTCCC TTATGCCTTT 120
 ACACTCTATG AATGATTTC AACCATTCTG AGGGAACCTT GAGCGCCTCC GTTACCTTTT 180
 AGGAGGCGAC CGCCAGTCA AACTGCCCCG CTGACACTGT CTCCCACCAC GATAAnGGCG 240
 GGGGTTAGAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCTCCACG TAACTAnCGC 300
 TCACGTTTCA AAGnTCTACC TATCCTGTAC A 331

(2) INFORMATION FOR SEQ ID NO: 4248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4248:

ATAATCATAC AGATGGCAAT ACAACAGCAA CTGAGACAGT GTCAAACGCT AATAATAATG 60
 ATGTAGTGTC GAATAATACC GCATTAAATG TACCAACTAA AACAAATGAA AATGGTTCAG 120
 GAGGACATCT AACTTTAAAG GAAATTCAAG AAGATGTTTG TCATTCTTCA AATAAACCAG 180
 AGCTAGTTGC AATTGCTGAA CCAGCATGCT AATAGACCGA AAAAGAGAAG TAGACGTGCG 240
 GCACCGGCAG ATnCCTAAAT GCAACTTCCA GCCAGATCCA GCGGCTGCAG CGGTAnGGAA 300
 ACGGTGGTGC CACCAGTTTG CCAATTTACA GCGCCCATAT TACGCCAACA ACTGGTnCCC 360
 TAATGCCCAA T 371

(2) INFORMATION FOR SEQ ID NO: 4249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATTGCATGG CATAACATCG GCGATTAAAA GATGGACGTT TTGATGATGT ACAACAAGAC 60
 ATTGAAGCAG TGGTGAAAGC TCGGAAGGTC ACACAGTAAA AGTGATTATT GAGACGGTAT 120
 TGTGACCA TGACGAAATT GTAAAAGCGA GTGAATTAAC AAAAGCGGCT GGTGCGGACT 180
 TCGTTAAAAC TTCAACAGGT TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAATTAAT 240
 GAAAGATACA GTAGGTGCTG ATATAGAAGT AAAAGCTCAG GTGGCGTACG TATTnTAGAA 300
 GTTTCAATGA AnGGTTGAAG CAGGTGCGAC ACGTAnTGGT GCGAGCGCAG CGTTCAA 357

(2) INFORMATION FOR SEQ ID NO: 4250:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4250:

GAGCCCAAAC CAACAAGCTT GCTTGTTGGG nGTTGTAGGA CACTCTATAC GGAGTTACAA 60
 AGGACGACAT TAGACGAATC ATCTGGAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT 120
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAACACGTGA AATTCCGTCG 180
 GAATCTGGGA GGACCATCTC CTAAGGCTGA ATACTCTCTA GTGACCGATA GTGAAGnAGT 240
 ACCGTGAGGG AAAGGTGAAA AGCACCCCGG GAAGGGGAAG TGAAATAGAA GCTGGAAACC 300
 GGTGTGCTTA CAAGGTAGTC AnAGCCCGTT AATGGGTGAT GCGTGCCTT TT 352

(2) INFORMATION FOR SEQ ID NO: 4251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4251:

CATTTACTGC TTAACCTTGC ATCanATCGT AACTCGCCGG TTCATTCTAC AAAAGGCACG 60
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTCAC 120
 TCCCCTTCCG GGGTGCTTTT CACCTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 180
 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTC ACGTGCTCCGT 240
 CGTACTCAGG ATCCACTCAA GAGAGACAAC ATnTTCGACT ACAGGATTAT TACCTTCTTT 300

(2) INFORMATION FOR SEQ ID NO: 4252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4252:

TATTTGATAT TTTGTGCATT GCAGTCAAAC CATGGCGGAA ATTGAACCAA TACCATTGCT 60
 AATTTTTTCT GTGTATGTAA GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTnGC 120
 TTGTATCTG CAAATGTTTT GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC 180
 ACAAATTCAA ATGTATCAGG CGTTTCTTTT ATCCATTTCa ATATATTTCT TTCCGGTTGT 240
 ATCGCATAGT ATGTCGCATC TAATTCGCAA CCGGAAAATG TCCAGCATAT GTTTTAAGGT 300
 ATCGGTTTG GCGTTCTAAA TCTGCATATA ATGAATAGTG ATCACCCCAA CCTGTAAAT 360
 CGATGGTTA TCCAnATGAT GATCACCATG TCATCAnACC 400

1

15

2

C

2

20

2

1

25

C

(2) INFORMATION FOR SEQ ID NO: 4253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4253:

AAGGTATCA AAGATGTAA AGTTACTTTA TTAAATGAAA AAGGCGAAGT AATTGGnACA 60
 ACTAAAACAG ATGAAAATGG TAAATACTGC TTTGATAATT TAGATAGCGG TAAATACAAA 120
 TTATTTTTTG AnaAGCCTGC TGGCTTAAAC ACAAACAGTT ACAAATACAA CTGAAGATGA 180
 AAAGATGCA GATGGTGGCG AGTTGACGTA ACAATTACGG ATCATGATGA TTTCACACTT 240
 ATAACGGAT ACTTCGAGGG GATGACATCA GACAGCGATT CAGACTCCAG ATAGTGACTC 300
 GnCAGCGAC TCAGACTTCA GACAGCG 327

2

40

2

C

1

45

C

2

(2) INFORMATION FOR SEQ ID NO: 4254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4254:

5 AGATGACATT AAATAGCATC TCCTCGTGTT GATTATTTTG GTTGGCTGAC CAATATTTAT 60
 TCTAGCACGT AGAGATGCAT TTTTGTGAC AATGGTAGAA CCTTTTCTGA ACCATACGCA 120
 TAGGATTGTn CTnTTTACA ATTAAAGAGC CAACCGTTGT TATAGTCTAA CAATGGTTGC 180
 10 CCTCTTATTT TATGTGGCTA AAAATTTATA GGCAATTTTA TTACAACAAT GTACATTTAA 240
 GGTGACCTTC ATGCCAAAAT CGCATCACTC ATTTAATGGA AGCAGCACGT CTTCATATAA 300
 AGTACCGATC CCTAATTCCA ACGCATGTnG 330

(2) INFORMATION FOR SEQ ID NO: 4255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4255:

25 ATTAGTGATT GTAAAAAGT AAAACTATTC TTGGGAGTCG GACATAAATC AATGTCTAGA 60
 CTCTATAGTG TTGTATTTGG CAGTAGTTGA CGGGGCCCCA ACATAAAGAA ATACTTTTTTC 120
 30 TTTAGAAATT AGTATTTCTT ATACATGAGT TTTACTCAGG ATATCCTATT TTTAAATACA 180
 CATTAGCTGT GTTTAATGAT AAAGAACCAC TACATCATAA ATCTTTAATG GTTCTTTATC 240
 AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTTAAATCAA TATAATTCAA AAAAGGGTCG 300
 35 AAGATATGAn ATCACATCTT CGACCCTTnn TTGTACTAAT TTAA 344

(2) INFORMATION FOR SEQ ID NO: 4256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4256:

50 CCAGTAATAT CTAAATGAGT TGGATATTTA ACTTTCGCAT TAATTTCAAT ATTAAATTGC 60
 GTTACCGCGA CAAGnCATnA CACAACATAC ATAATAAGAT TGGCTAAAAA GATATAGTTA 120
 AAGCTAAATT CTGCGACAAA GCCGCCATT GCAGCACCGA CAGCCACACC AATATTTTGC 180
 55 GCTAAGTATA TCGCATTAAA CGTTTGTCTT CCGCCATTG GCCACACTGC TCCAGCCATA 240

TACCAAGGCC ACCCGTGGAn AGA

323

(2) INFORMATION FOR SEQ ID NO: 4257:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4257:

GCTGACTTTC CACCAGCCTC TGTGTTGGGG CCCCAGACTAT TTTTGAAAAG AGCGTGTTAC 60
 ACGGTCATTG TTTTACAGTC AACTACTGCT AAAATAAAAT TAACGAGCTT AGGGCTTTGT 120
 TTTCTGTCCC AAGCTCGTTA AATCACATAT GATAATTAAT TATGCCCAAC CACGATATCT 180
 AGCTGCTTCT GCTGTACGTT TAATACCTAT GGATATATGC TGCAnTCTGC ATATCTATTT 240
 TTCGGTTTTG AGACAATTCG TAAATCGTAT CAAATGCCGC TTCTAATTTT TnCACGTGGC 300
 TTTTGCATTG AACTTCTTCT nGCAGGACCA ATAATAACCT TGGATTATTT TGTGACCCAT 360
 GCGGAGTGA 369

(2) INFORMATION FOR SEQ ID NO: 4258:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4258:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60
 TTTTTAAATA CTAAATACA TGTTGGAATA CTTGTCCCAT AGAAAATATT GGCTGGTAAC 120
 CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGAAT CACACCTTCT 180
 GCGGCACCAC GAATAATACA CCATGnGGAG TACGACGCCA nGTACCTTCA TCGTCTAGTA 240
 ATGTACCACT GTTGAATAAA GCAAAGTCTG CTTTGATTTT GCGGCAACTT GCCGTAACCA 300
 CTGAATCGTT CATCATTTCA AATTGAACT GCTGT 335

(2) INFORMATION FOR SEQ ID NO: 4259:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4259:

5 ATTTTCGCTAC CTTACGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTTCGTA 60
 GCTTCGCAGC nACAACCACT CCTCTTAACC TTCCAGCACC GGGCAGGCGT CACCCTATAC 120
 ATCACCTTAC GGTTTAGCAG AGACCTGTGT TTTTGATAAA CAGTCGCTTG GGCCTATTCA 180
 10 CTGCGGnTCT TCTGGGCGTT AACCTAAAG AGCACCCCTT CTCCCGAAGT TACGGGGTCA 240
 TTTTGCCGAG TTCCTTAACG AGAGTTCGCT CGCTCACCTT AGAnTTCTCA TCTTGACTAC 300
 CTGTGTCGGT TTGCGGTACG GGCA 324

(2) INFORMATION FOR SEQ ID NO: 4260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4260:

25 AAGCGGTTGT TAGACAATGC ATTAAGAAAA ATTAAAGCGG AGTTTACTTT TGTAATGAG 60
 CATTTGATTT TTTGAAAATA AAGCAGTATC GGGCGCTTGA CTAAAAAGAA ATTGTACATT 120
 30 GAAACTAGA TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 180
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ACGAGCAAGA 240
 TTAATAACGC GTTTAAATCT TTTTATAAAA GAAAACGTTT AGCAGACAAT GAGTTAAntT 300
 35 ATTTTAAAGC AGAGTTTACT TATGTnAATG GAGCATTGAA AATnATGAAA ACGAGCCCGT 360
 ATGTGGAGCG TTTGGACTTA TAAAAATGGT GGGAAACATA 400

(2) INFORMATION FOR SEQ ID NO: 4261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4261:

50 AATTAATGTG CGAGTTGGGG TGGGACGACG ATAAAGAAAT ACTTTTCTA TAGAAATTAG 60
 TATTTCTTAT GCATGAGTTT TACTCAGTAA TTCCTATTTT TAAGnACACA TTAGCTGTGG 120

CTCCCCTGAG AAGTTTAAAA TTTTATATGT TGGCTTGTTA TGTTAAGGGA ATTAACATGG 240
 TTGTCTTGTT TATATTATGT GATTCAAACA TTACTAGTCT TGGTAAATCT AATTCGTAAA 300
 5 ATGCTAAATC TAACCATCTA TTAAATTTAA AACC 334

(2) INFORMATION FOR SEQ ID NO: 4262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4262:

TTTCGGTCAT ATTCAAACGT TTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT 60
 20 ATTTTGACGT TTAGGCATA AAAAAAGAG ACCTTGGCGG TCTCAATGCG GCTCATCGCA 120
 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGnAGTA ATTGGGCTAC CATCGTCGCT 180
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGcncTTTC CTCTCCTTCG GCTCTCGCTT 240
 25 ACTCATThAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT 330

(2) INFORMATION FOR SEQ ID NO: 4263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4263:

GAGGTATACC CCGGGACGGC TGAAGGGGAT CGAACCCTAC GnaATGTCGG AACCACAATC 60
 CGATGTGTTA CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC GAACCCACAC 120
 45 CAAAGGTTTT GGAGACCTCT ATTCTACCGT TGAATATGC CCCTATTAAA AATAATAAAT 180
 GGAGGGGGGC AGATTGGAAC TGCCGAACCC GAAGAGTCGG ATTTACAGTC CGCCGCGTTT 240
 AGCCACTTCG CTACCCCTCC ATAAATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 300
 50 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 339

(2) INFORMATION FOR SEQ ID NO: 4264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4264:

	GTATTTCAAA GTAAAATTAC ATGTTAATAC GTGnTTAATG GGCGAGACTC CTGAGGGAGC	60
10	AGTGCCAGTC GAAGCCGAGG CTGAGACGGC ACCCTAGGAA AGCGAGCATT CAATACGAGA	120
	TnTnATGAAA TAGAGAACAG CAGTAAGATA TTTTCTAATT GAAAATTATC TTA CTGCTGT	180
	TTTTTAGGGA TTTATGTCCC AGCCTCTTAC TCTAATTATA TTCACTATCA ATTAGACAAA	240
15	ATGGCCATTT TCAAATATCA CGCGTTGTTT CTGACCTTGA ATATATTTAT TATAATTCTC	300
	TTTTTGAAAA ATCAGTTAAC ATTAATTTAG ATGTACCGTA TTTTAAACAC T	351

20

(2) INFORMATION FOR SEQ ID NO: 4265:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4265:

30	ATTTTCACTT TAAAACCTGC TTCTTTGGCT TTTTGCATAT AATGTTGCGA TTGTTCTATT	60
	GTAAATACAC CTGTTTCACA GAAAATATCC GCAAAGTCTG CATATTGTTT TACTTCCGGA	120
	AGTAACGCAA TCATTTCTTC TAAAAATGCC TCATTTGAAC TTGCCTCTTT AGGTACAGCA	180
35	TGAGGCCCTA GGAAAGTATG TTTTCATGTCT AAATCATATT TCTCAGCTAA ACGnTTAGAC	240
	ACTTTCAATT GCTTCAGTTC ATTTTCTCTA TCTAATCCAT AAACCACTCT TGACTTTCAA	300
40	CTGCAGTCAC GCCGTGTTTn AATCCATAGT AAGACAAAnC ATGACT	346

40

(2) INFORMATION FOR SEQ ID NO: 4266:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4266:

	TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT TTATTGAAAA TGGTGCCGAG	60
55	GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGGAT TTTAAGTCCT GTGCGTCTGC	120

55

CCAACCTTGG CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA 240
 GTCGAACCCC CACGCCGTAA GGnTGAGATC CTAAGTCTAG TCGCTCTGCC AATTCGGCCA 300
 CACCCGCCAA TGGTGAGnCA TAGAGGnTTC GAACCTCTGA CCCTCTG 347

(2) INFORMATION FOR SEQ ID NO: 4267:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4267:

GACTTGTTCT CTTGGACCTA TATCATGTC TTTATTTTCT AATGCAGGAT CTTTAATTGC 60
 ATCTTTAAGT GATTCATCCG CTGCAGGATA GTTTTTCGCA GTGTTTGCTG GTTGCGTGAG 120
 GThTGTGTTT GATTGTATC CTTAGGTGGC TGAGTTGTAG TTGCATTATT ATTTTGATTT 180
 TCCGAGATTT TATCTGAAGT ATTTGTATTT TCTGCTGCTT GTGCTTGATG TTGAGAAGTA 240
 ATTAAAAATA GTGTACTGAC AATGACCGAT GCAACGCCTA GAGTTGATTT TCTAATAGAA 300
 TAGGAAAGAC CnThAATTTT GGGTGGATGT TTGTTCA 337

(2) INFORMATION FOR SEQ ID NO: 4268:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4268:

ATACATGTTG GAATACTTGT CCCATAGAnA ATATTGGCTG GTAACCCAAT CACGGCTTCT 60
 AAGTAGTTCT TTTCTTCTAT TAAATAGCGA CGAATCACAC CTTCTGCGGC ACCACGGAAT 120
 AATACACCAT GTGGGAGTAC GACTGCCATG GTACCTTCAT CGTCTAGGTA ATGTACCATG 180
 TGTTGAATAA AGGGCAAAGT CTGCTTTGGG ATTTTGGCGC AACTTGCCG TTAACCACTG 240
 GAATCGTTCA TCATTTTCA nATTTTGGA TCTGGCTGGT TCCATTTTCG GCACTGGTAT 300
 GGTGGGGGTT TCGGCAATAA ACGGCATTCA AATGGTATTT GGCCTAAACA AGGCCGGGAT 360
 TTTTCCAATG GGGGTCATCA TTAAnGGGAT CnTCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 4269:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4269:

10 GGCTCATCGC ATCCTGGGGC TGTAGTCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG 60
 CGGTACGGAG CTGGGTTTCAG AACGTCGTGA GACAGTTCGG TCCCTATCCG TCGTGGGCGT 120
 AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 180
 15 TACCAGTTGT CGTGCCAACG GCATAGCTGG GTAGCTATGT GTGGACGnGA TAAGTGCTGA 240
 nAGCATCTAA GCATGAnGCC CCCTCAAGAT GAGATTCCCA ACTTCGGTTA TAAGATCCCT 300
 CAAAGATGAT GAGGATATAG GTCGAGGTTG GAGCATGGTA CATGT 345

20

(2) INFORMATION FOR SEQ ID NO: 4270:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4270:

30 AAGAATTAAT TATACATTTT ATTAACATTT AAGTCAATAA CTTTTTTTAT CTGTGCCATT 60
 TTATTTTTTA ACCAAAATTT GATTAAAAA CTGCCTGGCA ACGTTCTACT CTAGCGGAAn 120
 35 TAAGTCGaCT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 180
 TGACCTCCtT GCTATAGTCA CCAGACATAT GaATGTAATT TATACATTCA AAAGTAGATA 240
 40 GTAAGTAAAA GTGGATTTTG CTTGCAAAc ATTTATTTTG ATTAAGTCTT CGATCGATTA 300
 GTATTCGTCA GTCcCaCATG GTCACCAGCT TCCACCTCGA ACCTATTGGn CGCATCATCT 360
 CGCAGGGAnC 370

45

(2) INFORMATION FOR SEQ ID NO: 4271:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4271:

55

ATTAACAAAA GGCATTGATT TAGAAGGGCG GACATTTTTA CACAATTATG ATTGGCGTAA 120
 AGATAAAGAT GGCACATTAT TAAATACCAT CATTTCTGGT CCGGCACTTG TGGCACAATG 180
 5 GaTTAATTTA CAATATTATG CGTCGACAGT TGCGCCGCAT TTTTaCGGtA ATGGGAATAA 240
 AGCGACACAA ACCGTCACGT CAGTGTGGT GTCATGCAAG GTAATGCGAG TGCATCTGAT 300
 GTAGGGCTTA TCATGGCCAA TCTGTTA 327

(2) INFORMATION FOR SEQ ID NO: 4272:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4272:

CATTCTTTAA ACTCTGTAAG TACTTCTTCA ATCTCAGGGG CATCTACTAA CATATCATCA 60
 GTAATATGCG TCAAATTGAT AATCGTTTCC GATAATCGTT CATGCGGATT ACTAAACCTT 120
 25 TCAAACCTTAT CGATGATTTT ACCGTTATGA ACTTTTACAG CTGCAAnTCG ATGATTTTAT 180
 CATACTGATT TGATAAACCA GTTGTCTCAA CGTCGAACAC AACATAAGTA GCATCTTTTA 240
 ATACGACATC TTGTGGGTTG TATGCAATCG GGAACACCAT CATCAACTAA CATACTTCC 300
 30 ATACCGGnAT ATCATTTTAA nGCCA 325

(2) INFORMATION FOR SEQ ID NO: 4273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4273:

TCCGGCCTTG ACCTGAAGAA CACTTGTCTT GTCGTTAAGA TGACTCTAGA CTCTTATGTT 60
 45 TATTATCAAC CGTTAATAAA CTTACCATCA AGAGTGCACC TACCCATACT GACAGTGCAG 120
 TATAGAATGG TGTCATACCT GAACCATAAT CCTTAACCTG GAAAACATCA ACAGTCTTCT 180
 TATTAATAGG ATTTGCAATA ATACCCGCTT GCTTTTTTCAA ATCATTCTTA AGTGTGTCGA 240
 50 TnAATTTGTC GACTGCATCA TCTnTGTCTA ATTTCTTGAA AATTTTGATT CGCTTTTTTC 300
 CAAATCCTTn TCCAACATCA GGCAATTTTA TTTTGAGAAA AATCAGCCAA ATCCGGA 357

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4274:

```

10  ACGTTAGCAC AAGCCATGAA CCAATTAGGT GGAAAGAGTA ATAGTGGTGA AGGTGGCGAA      60
    GATGCAAAAC GTTATGAAGT ACAAGTTGAT GGAAGCAACA AAGTAAGTGC GATTAAACAA      120
15  GTTGCTTCTG GCGGTTTTTG TGTAAGTAGT GATTATTTAC AACATGCCAA AGAAATTCAA      180
    ATTAAAGTTG CGCAAGGTGC AAAGCCTGGT GAAGGTGGTC AATTACCTGG TACTAAGGTA      240
    TATCCGTGGA TTGCGAnGAC AAGAGGGTCA ACGCCAGGTA TCGGTCTGAT TTCACCACCG      300
20  CCACATCATG ATATTTnATT CCATAnGAGG ATTTAGCCGC CACCTGATAC CTGGATTTTG      360
    GAAAAATGGC GAATTAAGGT TGCnGATTTT CCCCggGTAA      400
  
```

(2) INFORMATION FOR SEQ ID NO: 4275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4275:

```

35  AACGTCGTTA ATTGAATAAC GCTTATGTTA TAAGAGCACT CATACCAAAC CATAATCATC      60
    TATAGATATA ACAATTCACG ATATAAGGGC TGTGTTTGGC ATAGCCTTTA GATATACACT      120
    TAATTCCTAT TAAATAGTA GGGATTAAAA GGGGGCTTGT CATGGATTAA AATTCAACAA      180
40  TTACAACATC ACTTTGGATC ACATAAAGTA ATTCATAACT TTAATTTGGA CATTAGCAAG      240
    GGAGAAATAG TCACTTTCAT AGGGGAAAAG TGTTGCGGA AAGTCTACTT TACTCAATAT      300
    TATCGGTGGA TTTnTTCCAT CCATCGnCTG GTCGTGTCCA n      341
  
```

(2) INFORMATION FOR SEQ ID NO: 4276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TAGTGATATA CGACATCACA GCATAATATT GCTTTAGAAA GTCGTGCCGA ACTGGAACCTT 60
 ACAAGTCTAG TTCGAACACA CACTGATGTG AGTGGTTTTT TTTATTTTAA ACATGAACAA 120
 5 TCAGATAAGT TACTAGCATT AGCAAATATT ATTAAATCAA AGGGCTTCGA TTCATAAAAT 180
 TTAAACAAT GATTAAAATT AGACGTGTAA ATTGTTAAAT TCTAAAACGG AAATAACCAC 240
 CATTCCATTA AACCACTTTT TTGTTTCATCA CTATATTTCA CACnGCTTCA TTAATAAACG 300
 10 GAATGCTTCA nCCGCTTCAA CTTCAACTGG CTTCAACTTC nGCCTACTTC ATCATAACCA 360
 ACGGTCCG 368

(2) INFORMATION FOR SEQ ID NO: 4277:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4277:

25 ATGGAAGTAC GTGACGTTCA CTACTCTCAC TATGGCCGTA TGTGTCCAAT TGAAACACCT 60
 GAGGGACCAA ACATTGGATT GATTAACCTCA TTATCAAGTT ATGCACGTGT AAATGAATTC 120
 30 GGCTTTATTG AAACACCATA TCGTAAAGTT GATTTAGATA CACATGCTAT CACTGATCAA 180
 ATTGACTATT TAACAGCTGA CGAAGAAGAT AGCTATGTTG TAGCACAAGC AAACCTCTAAA 240
 TTAGATGAAa ATGGTCGTTT CATGGGATGA TGAAGTTGTA TGTCGTTTCC GTGGTAACAA 300
 35 TACAGTnATG GCTAAAGn 318

(2) INFORMATION FOR SEQ ID NO: 4278:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4278:

CACTTGTA CT TCTGATGTT GAGCCAGACT CTGATGTACT TACCGATGTA GATAAACTTG 60
 50 CAATGGTCGA CATGCGGTTT GAAGTTGATG TACTTAGCGA ATCACTTAAT GATGCTGATG 120
 TGCTTTGTGA ATCGGATTCG CTCGTGCTTG TACTTGTTGA GTTTGAGGCA CTTTGGCTTG 180
 CTGAGTTTGA GTCTACTCCG CTTTGATTCA TTGAGGCACT TAGTGACAAT GATGTACTCG 240

TACTTATGCT CATTGGATGT TGAATCGGAT TTACTTTTAC TTGAATGATG TTGAGTCGGA 360
 TTCACTTTCA CTTGTAGAAC CACTTAATGA TGTGGGATGT 400

(2) INFORMATION FOR SEQ ID NO: 4279:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4279:

TTTGTACTION GATTTAAAAG ATATTAGACA TAAAATCTAA AAnCAGCAGT AAGATGATTT 60
 ATGATTAAAA ACTATCTTAC TGCTGTTTAC TTTTATAAT ACTTCTGAAT GTCTTCACTT 120
 ATACTTCTAG TCACAGATTT AAATAATCAA AAGTGCACAT TATTAAAAATA TCAATTTTAC 180
 ACTCAATGCG GCTCATCGCA TTCATTTCTT GTCTAGCAAC GTTCTACTCT AGCGGAAGTA 240
 AGTTAGCTAC CATCCTCGCT AAGAACCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC 300
 CTCTCCTTCG GCTCTCGCTT ACTC 324

(2) INFORMATION FOR SEQ ID NO: 4280:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4280:

CTCACTAGTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60
 GTGGATTGTC CTTTGGCATG TGnTTAGGAG AGCGTTCTAA GGGCGTTGAA GCATGATCGT 120
 AAGGACATGT GGAGCGCTTA GAAGTGAGAA TGCCGGTGTG AGTAGCGAAA GACGGGTGAG 180
 AATCCCGTCC ACCGATTGAC TAAGGTTTCC TGnGGAAGGC TCGTCCGCTC TGGGTTAGTC 240
 GnGTCCTAAG CTGAGGCCGA CAGTAGGGCG ATGGGATAAC AGGTTGATAT TCCTGTACCA 300
 CCTATAATCG TTAAATCGAT GGGGGG 326

(2) INFORMATION FOR SEQ ID NO: 4281:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4281:

5 TCGAACATGA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACCTCG 60
 GTTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG 120
 GTGGGCCTAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGCGTGCG CTCTAACCAG 180
 10 CTGAGCTATA GGCCCATTTT TTTGAATGTT AAATAAACAT TCAAACTGG AATACAATAT 240
 GTCACGTTAT TCCGCATCTT CTGAAGAAGA TGTTCCGAAT ATATCCTTAG AAAGGnAGGT 300
 15 GATCCAGCCG CACCTTCCGA TACGGGCTGA CTTGTGAC GACTTGCACC CCAAGCATTT 360
 GTGCCCAAnCh 370

(2) INFORMATION FOR SEQ ID NO: 4282:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4282:

30 GAGAGATGAC ACGGnACTGA ATTGGTTTGA CACCACGTGA TGAATGTGAT CGTCGGCCTT 60
 CTTACAGATT GnAATACTTT TACATCAAGA ACGATACCGC CAGCGCCGTG AGGTACACGT 120
 AATGAAGTAT CTCTAACTTC ACGTGCTTTT TCACCAAAGA TTGCATGTAA CAATCTTTCT 180
 35 TCGGCAGTTA ACTCAGTTAC ACCTTTAGGC GTTACTTTAC CAACTAAAT ATCTCCATCT 240
 TTTACTTCTG CACCAATATA AACGATACCA CGATCGTCTA AGTTCTTAAG TGCACTTTCA 300
 GAAACATTAG GnATATCTCT TGTGATTTCC TCAGGGCCTA ACTTAGTATC ACGTGCCTCT 360
 40 GAATCCATAC TCCTTCAATA TGAATAGAAG TATACACGGn 400

(2) INFORMATION FOR SEQ ID NO: 4283:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4283:

55 AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA AAGAGAAATT GGATTCCCAA 60

TCTGTCCCAC TCCCGATTAT CTCGTGCGAA TATTTTTTTC AAAGCGATT AAATCATTAT 180
 CATGTCCAAT CATGATTAAA ATATCACCTA TTTCTAAATT AATATTTGGA TTTGGTGAAA 240
 5 TGATGGACTC TTTGCCTCGT TTAATTGCCA TAATGTTAAT nCCATATTGT GCTCTTATAT 300
 CTnAATCCAT GATAGACTGn CCCG 324

(2) INFORMATION FOR SEQ ID NO: 4284:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4284:

20 AAATCGTAAC GAGTGAACCTT TCTTATTTAG GTGGCGAAGT AACTTACTAG CACCTGACGA 60
 AACGGTTTTA GATCGTATTC AATTGAAAAG GCCGGTATTG AATGAATCAC ACTTAGCAGC 120
 GATTGATCAG GAACATTTTA AATTAACCTA TTTATCAACG GTATATGAAG GGGATTTGGC 180
 25 AAGATGCGTT ATAAGCATTG GGCCGTAGAA GCAGTGAAAT GCTGTnAAAC AAGGGCGCTC 240
 AAATTCTAGT GTTAGATGAT AGTGGATTAG TTGGATAGCA ATGGCTTTGC AATGCCGATG 300
 TTTACTCGCA ATGAAGTGCA TGTGCCATGC AATTGACTTC TTTAAAGCCA GATTTACGTG 360
 30 ATGTCTAACA AGTTTTnTnC GCTAAAATCn GGGTGGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 4285:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4285:

45 CATTTTTCTT TGTGTTTACT TTTTATTTTG ACGTTTTAGA CATAAAAAAA GAGACTCAGC 60
 GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 120
 TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCATCTTT CCTCAnCATC GGnTnTAGCT 180
 TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT 240
 50 TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA 300
 AAAAAAAGAG ACCTTGnCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA 360

TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA 480
 ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTCACTTCG CCAAGCCATT 540
 5 TTTCTTTGTG TTTACTTTTT 560

(2) INFORMATION FOR SEQ ID NO: 4286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4286:

GTAACACTCG GnATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GTAGCTAATA 60
 20 CCGGATAATA TTTTGAACCG CATGGTTAAA AGTGGAAAGA CGGTCTTGCT GTCACCTATA 120
 GATGGATCCG CGCTGCATTA GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA 180
 TAGCCGACCT GAGAnGGTGA TCGGCCACAC TGGAAGTGA ACACGGTCCA GACTCCTACG 240
 25 GGAGGCAGCA GTAGGGAATC TTCCGCAATG GGCGAAACTG GACGGAGCAA CGCCGCGTGA 300
 TGNATGGAAG GTCTTCGGAT CGTAAAACTC TGTATT 337

(2) INFORMATION FOR SEQ ID NO: 4287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4287:

CAATCGTGCT CAnTGCGCAT CGTnACTCAT CTGTATGTGT TCCAGCATAT ACAATTTTGC 60
 CATCTTTAAT GACAACTGTA CCATTTTTCA CAACATTTAA TTCATCTAAT TCCTTACCCT 120
 45 TCAAAGGTTT ATCTGTTGAT CTCGGTAAAA TTAATTCTGG CTATATGATT AATTATTAAA 180
 TCATCATTAC TTATCACCTG CTTTATCAAT CATGGAATAT GAATACCTTT TTCTTTAGCT 240
 GTTTGAATAG CGATGTCATA GCCAGCATCA ACATGTCGGG CAACACCCAT ACCTGGGTCA 300
 50 GTCGTCAATA CACGTTCCAA TCTTCTTTCA GCACGCTCTG AATCCATCTG G 351

(2) INFORMATION FOR SEQ ID NO: 4288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4288:

CTATTCACTG CGGCTCTTCT GGGCGTTAAC CCTAAAGAGC ACCCCTTCTC CCGAAGTTAC	60
GGGGTCATTT TGCCGAGTTC CTTAACGAGA GTTCGCTCGC TCACCTTAGA ATTCTCATCT	120
TGACTACCTG TGTCGGTTTG CGGTACGGGC ACCTATTTTC TATCTAGAGG CTTTCTCGG	180
CAGTGTGAAA TCAACGACTC GAAGACACAA TGTCTTCTCC CCATCACAGC TCAGCCTTAA	240
CGAGTACCGG ATTTGCCTAA TACTCAGCCT TACTGCTTAG GACGTGCAAT CCAATCGCAC	300
GGTTTnGCCT ATCCTA	316

20

(2) INFORMATION FOR SEQ ID NO: 4289:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4289:

TTnTTTATGT CTAAAACGTC AAAATAAAG CAAACACAAA GAAAGATGGC TTGGCGAAGT	60
GAAAACGnTT GAATCTGACG AAACGAGAAA TGTAAGTAT AATAAAAAGC AGTCATAAGA	120
TGATTTCAAT TAGAAATCAA TTTATGACTG TTTTCTTAC TATGTGTTAA ATTAACAATG	180
AATATAACAT CTTATTTTCA TTAATATAAA TATTGGAAGG ATCGAnATGA TTFACACGTT	240
GTTTGAGTTG TATTAAATCA TCATGATCTT TAAGTTGAAT ACCAATAATG ACAGTACCTG	300
TATTTTGAGA GATTTTTTAA GT	322

40

(2) INFORMATION FOR SEQ ID NO: 4290:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4290:

TCATTTAGCT CTAATAAAT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT	60
CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT AGGCATAAAA	120

55

CTCTAGCGGA AntAATTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC 240
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCnACT AAACCTCGTTG 300
 5 CGCTCTTnTC TCGTTTCGTC AGATTTCAAA CGTTTTCA 338

(2) INFORMATION FOR SEQ ID NO: 4291:

- (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4291:

AATTGGTTTA CACCAGGTGA TAATGTATCG TCGCCTTCTT CACGATTGAA TACTTTTACA 60
 20 TCAAGAACGA TACCGCCAGC GCCGTGAGGT ACACGTAATG AAGTATCTCT AACCTCACGT 120
 GCTTTTTCAC CAAAGATTGC ATGTAACAAT CTTTCTTCGG CAGTTAACTC AGTTACACCT 180
 TTAAGGCGTT ACTTTACCAA CTAAAATATC TCCATCTTTT ACTTCTGCAC CAATATAAAC 240
 25 GATACCACGA TCGTCTAAAG TTCTTGAAGT GCACTTTnCA GAAACATTGA GGGAAATGATC 300
 TCTTGTGATT TCTTCCAGGT CCTAACTTGA GTGATCACGT GGCTTCTGGA TTGCAGACGC 360
 30 TTGCAAGATG GAATGAGAAG TGAnACACGT GCATCCTTGC 400

(2) INFORMATION FOR SEQ ID NO: 4292:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4292:

AAACGTTTTC ACTTCGCCAA GCCATTTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTA 60
 GGCATAAAAA AAAGAGACCT TCGGGTCTCA AATGCGGCTC ATCGCATCCA TTTTTGCCT 120
 45 GGCAACGTTT TACTCTAGCG GAACGTAATT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 180
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC 240
 50 TACTAAACTC GTTGCCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA 300
 GCCATTTTTTC TTTGTGTnna CTTTnT 326

(2) INFORMATION FOR SEQ ID NO: 4293:

(A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4293:

10 GGGGACAATT CCCTGGGGGT TCAAGTCCTC TCGGGCCGGC ATCAAAATTC TTAATTTAAA 60
 TAAGCGGGTG TAGTTTAATG GCAAAACCTC AGCCTTCCAA GCTGATGTTG TGGGTTTCGAT 120
 TCCCATCACC CGCTCCATAG ATAATTTTAA TGAACATTGA AACTGAATG ACAATATGTC 180
 15 AACGTTAATT CCAAAAACGT AACTATAAGT TACAAACATT ATTTAGTATT TATGAGCnAA 240
 TCAAACATCA TAATTTTTAT GGAGAGTTTG ATCCTGGCTC AGGATGAACG CTGGCGGCGT 300
 GCCTAATACA TGCCAGTCGA GCGAACGGAC GAGAAGCCTG CCTCnCnGAT GTTAGC 356

20

(2) INFORMATION FOR SEQ ID NO: 4294:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4294:

30

TTATCACCCA TGTTCTGACT CCCAAGTTAA ATTAATTGGC ATTCGGAGTT TGTCTGAATT 60
 CGGTAACCCG AGAGGnCCCC TCGTCCAAAC AGTGCTCTAC CTCCAATAAT CATCACTTGA 120
 35 GGCAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTCGATT GGAATTTCTC 180
 CGCTACCCTC AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCCT CCATTCAGTG 240
 TTACCTGAAC TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT 300
 40 AAACGCCCTA TTCA 314

(2) INFORMATION FOR SEQ ID NO: 4295:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4295:

AAGTGAAAGA ACTCGGCGTG ACACCTATTG CACGATTCGT TGGTTTTAAG GCAGTAGGCG 60

55

GCAATCTATC TGTTGAAGAC ATTGATTTGA TCGAATTGAA CGAAGCATT T GCTTCTCAAA 180
 CGATTGCATC TATTAAAGAA GTAGGTCTAG ATATATCAGC TACGAATGTG AATGGTGGCG 240
 5 CTATTGCTTT AGGTCATCCA TTAGGTGCTA CAGGCGCCAA TGTTAACCCG CGCGTTTACC 300
 TAATGAAATG GGGTAAACCG nCCCGATAGn CCGTAnCGCA AGGGT 345

(2) INFORMATION FOR SEQ ID NO: 4296:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4296:

20 TAAATTGATT TCTAATTGAA ATCATCTTAT GACTGCTTTT TATTATACTT TACATTTCTC 60
 GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATC TTTCTTTGTG TTTGCTTTTA 120
 TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 180
 25 ACTTTTTGCC TGGCAACGTT CTA CTCTAGC GGAAnTAATT CGnACTACCA TCGACGCTAA 240
 GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGGCT ATAGTCACCA 300
 GACATATGAA TGTrAATTGA TACATTGCAA AACTAGGATA GTGAAGTAAA AGTGATTTTG 360
 30 C 361

(2) INFORMATION FOR SEQ ID NO: 4297:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4297:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAAC TTTTCACTT CGCCAAGCCA 60
 45 TTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG 120
 TCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 180
 AAAGACCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 240
 50 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300
 TTCACTTCGC CAAGCCATTT TrCTTTGTGT nTACTnT 337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4298:

GTATTCCTCC ATTATTATAG GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA 60
 CGGGAATCCT GCGTGACAGn CAGGCGTGTT ACCGCTACAC TACGAGACCA TTAGTAAAC 120
 GGAGGAAGAG GGATTCGAAC CCCCGCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA 180
 TCCCTTCAGC CGGACTTGGG TATTCCTnCA AAATTATATG GACCTnGCAG GACTCGAACC 240
 TGCGACCGAA CGTTATGAGC CTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT 300
 TTTTACAACT AATAAAATAG TGG 323

(2) INFORMATION FOR SEQ ID NO: 4299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4299:

CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT CCATTAAATG 60
 AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTGTAAAT AAAATTGCCT 120
 ATAAATTTT AGCACATAAA ATAAGAGGnG CCAACCATTG TTAGACTATA ACAACGGTTG 180
 GCTCTTTAAT TGTA AAAAAGA AAACCATACG CTATGnTGTT ACAAnGAAAA AGGTTCTACC 240
 ATTGTCACAA AAAATGCATC TCTACGTGCT AGAATAAATA TTGGTCAGCC AACCAAATA 300
 ATCAACACGA GGAGATGCTA TTT 323

(2) INFORMATION FOR SEQ ID NO: 4300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4300:

TGAATCCAGA TAAAATTGGA ATGATTAACG CGAATCACTT TTACTACCAA TGTTCCAAAG 120
 CTGCTCTGCA AACGCATTGT ACTCTGAGCT TTTTGATTAA AATGAATTTG CTCCAAATAA 180
 5 AAATACAATT GCCATTAAAA TACCACCAGA TATTACAAGT GGCAACATGT TAGAAACACC 240
 GTTnCATTTGA AGTGTTTGAT AGAATGCTTT ACCTGGGGCT TGAATTTTTC TTGGACTGTG 300
 CATTTGAGTT ACCTTTTCTT TGGACCATCA CGGGGCAACA AAAGGTTTGA CGACTTGTGA 360
 10 GCTGAATGGC TThGnTGAAT GAATT 385

(2) INFORMATION FOR SEQ ID NO: 4301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4301:

TCCTGTACCA CCTATAATCG TTTTAATCGA TGGGGGGACG CATAGGAATA GGCGACGTGA 60
 25 CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 120
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC AACTGCCGA 180
 GAAAAGCCTC TAGATAGAAA ATAGGTGCCC GTACCGCAAA CCGACACAGG TAGTCAAGAT 240
 30 GAGAATTCTA AAGTGAACGA ACGAACTCTC GTTAAGGGAC TCGGCAAAAT GAnCCCGTAA 300
 CTTGCGGGAA AAGGTTnCTC TTTAnGGTTA ACGCCCCAAA AAACCGCT 348

(2) INFORMATION FOR SEQ ID NO: 4302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4302:

AATGGAACGT GCTTCTGTAT TGGCCCAAGT AGATATTCAT CGTGCAGCAA CACATAATAA 60
 AGGTGTTATG AATGGCATAc ATGCTGTTGT TTTAGCAACA GGGAAATGAT ACGCGTGGTG 120
 CAGAAGCAAG TGCGCATGCA ThACGCGAGT CGTGACGGGA CAGTATCGTG GTATTGCTAC 180
 50 ATGGCGTTAC GATCAAGATC GTTCAACGAT TGATTGGTAC AATTGCAAGT GCCTATGGAC 240
 ATTGGGCAAT CGTTGGCGGT GGTACAAAAG TATTACCAAT TGCTAAAGCT TCCATTAGn 300

TTTTGAGCGG CAAAAACTTT GnCAG

385

(2) INFORMATION FOR SEQ ID NO: 4303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4303:

15	AGTGCGACGA TTGGTATTTT ACAAGAATTT TATCAACAAG ATTTAATTAG CTTAAACGCA	60
	GCAATCCCTG TGTTACTAGG CGATAACATT GGTACCACGA TTACAGCTAT CTTAGCTAGT	120
	TTAGCCGGCT CAATCGCTGC AAAACGTGCG GCGCTTGTA CCGTCATCTT TAACTTAATC	180
20	GGGGTAATTA TCTTCACAAT TTTCTTGCCA GTTGTGATTC ATTTGATTAG TTTGTTACAA	240
	GATTTATGGG CACTTAAAC CAGCGATGAC GATTGCAGTA TCACATGGnA TCCTTCAACA	300
	TAACCAATAC CTTGGATTCC ATTTACCAAT TTGTAGCCnG GTTTAGCATn GGATTGGTTA	360
25	CCAAGCCTTG TCCC	374

(2) INFORMATION FOR SEQ ID NO: 4304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4304:

40	AAAACAGGAT ACTTCGATAA GTTAATGATT TCTGTTGTGA ATCGCGCACC ACGTTTCTTA	60
	ATTTTACCGA CTATTATATT AATTGGTATT TTAGGTAGTA CAGCCGGCGA TGCTGCGACA	120
	ATTTCTTGCC GCGCTTGCA GCAATGCTTT TTATTAAAAT TGGCTATCAC CCTATCGCTG	180
45	GACTAACGAT GGCATATGCT TCCGCTGTTG GAGGATTTGC AGCAAATATA GTTGTGGTA	240
	TGCAAGATGC TTTGGTCTAT TCATTTACAG AACCGGCAAC ACGTATCGTT TCAGATTCTA	300
	TTAAAACAAA CGTT	314

(2) INFORMATION FOR SEQ ID NO: 4305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4305:

5 CGTTGCAGAA TGTGTTGAAA TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG 60
 CCATTAATTT ACGGTTACCA ACCAATATAT GGTGATGATC AATCGTTGCT TCAATACCAT 120
 GGCCAGGTAC TGCTTTAAAT GTTGTGTCT CAGTTAATAT TAATTGCTTT TCTTTTGCAT 180
 10 AATTGACAAT GGCTTCTGCC AATGGGTGTT CAGAATCTTT TTCAGCAGTA GCAAGTAGTT 240
 GTAGCGTTTG ATTGTCACCA TGATAATCTG TCACGACTGG GACGACCATT TGTAATGGnA 300
 nCCGTCCTTA TCTAAACGA TGGGTATCAA TTTGATGnGG GCGG 344

(2) INFORMATION FOR SEQ ID NO: 4306:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4306:

25 AGTTTCCCTG AAAATTAATC AAGGACTTAA CATTGCGAGT CAAGGTATTG ATCAAGCTAA 60
 TGGACAGTTA AATGATGCCA AAGCTTCGTC ACACAAGTTA GAAGTAGAGT CGGTGATTAT 120
 30 CAAGATGCAA TTCGACGCGC GCAAGATTTA AATCGAAGAA ACCAGCAACA GATTCCTCAA 180
 AATAGCGCGG CGAACAACGA AACATCAAAT AGTGCACCTG CAGCTGGTAA TGGTGTAGCA 240
 35 TCAACGCCAC CAAGTGCACC AAGTGGCGAT ACTGCACCAA ATAATAATGT TACGCAAAAT 300
 ACCGCACCAG ATGAGTGAAT AATGCGCCTG TATCGACTAC ACCACAAATG ACAnnCCGGG 360
 GAAAnAGATGG TCAAATTT 378

(2) INFORMATION FOR SEQ ID NO: 4307:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4307:

50 GGACTTGGGT ATTCTCCAA AATTATATGG ACCTGTCAGG ACTCGAACCT GCGACCGAAC 60
 GGTTATGAGC CGTTAGCTCT AACCAACTGA GCTAAAGGTC CTAnATATAA TTTTACAACT 120

CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG 240
 GATCGAACCG CTGGACCTCC TGCCTGGCAA AGCAGnCGCT CTCCCAGCTG nGCTAAGCCC 300
 5 CCATAATAAT TACAGTAT 318

(2) INFORMATION FOR SEQ ID NO: 4308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4308:

TGTACGTTTA ATACCTATGA TATATGCTGC AAGTCTCATA TCTATTTTTTC GGTTTTGAGA 60
 20 CAATTCGTAA ATCGTATCAA ATGCCGCTTC TAATTTTTTCA CGTAGCTTTT CATTAACTTC 120
 TTCTTCAGAC CAATAATAAC CTTGATTATT TTGTACCCAT TCGAAGTAAG AAACCGTTAC 180
 ACCACCAGCA CTTGCTAATA CGTCTGGAAC TAATAATATA CCACGTTTACG TTAATAATACG 240
 25 TGTGCTTCT GGTGTTGTAG GTCCATTAGC AGCTTCAACA ACGATACTAG CTTTAATATC 300
 ATGTGCATTG TCCTCnGTAA TTGGGTTGAA TAGCGnGGGA CTAAATGCAC ATCnAATCAA 360
 30 CAATCCTATT GGATGTCCCA AnAATTGTAC GACCAACACC 400

(2) INFORMATION FOR SEQ ID NO: 4309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4309:

CAAATAAACC AGAGCTAGTT GCAATTGCTG AACCACATCC TAATAGACCG AAAAAGAGAA 60
 GTAGACGTGC GGCACCGGCA GATCCTAATG CAACTCCAGC AGATCCAGCG GCTGCAGCGG 120
 45 GTAGGAAACG GTGGTGACAC AGTTGCAATT ACAGCGCCAT ATACGCCAAC AACTGATCCT 180
 AATGCCAATA ATGCAGGACA AAATGCACCT AACGAATnGT TGTTCAATTG ATGACAATGG 240
 50 TATTAGACCA AGTACCAACC GTTCTGTGCC ACnTnAAACG TTGTTAATAA CTTGCCGGGC 300
 TTCACACTAA TCAATGGTGG CAAAGT 326

(2) INFORMATION FOR SEQ ID NO: 4310:

- (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4310:

10 TCAAAGCGCC AATAACATCT TCTACTGAAG TTTCTTTAGA TTTAGCATTG AGTGATAATG 60
 TTATTGTTGC TTTTCTTCC ATTGGAATAC TTTGATGAAT CGTTAATACA GATAGTTCTA 120
 ACTTTGATAT AACATCTAGT ACACGTGCCA ACATACCAAC AATATCAGTT ACATATAAAA 180
 15 TTAATGTAAA TTCTCGATGG TCAAGCATT TATCGGCTAC TGGAAATATC GTTTCTCTAT 240
 ATnTATAAnA AGCACTTCTA GATAGATCAA ACTGTTTAAC GGCATCATAA ATGGnCAATG 300
 TCGGATCACT TTT 313

20

(2) INFORMATION FOR SEQ ID NO: 4311:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4311:

GGTTCGAATC CAGCTAGCCC AGCCATTAGA GCCATTAGCT CAGTTGGTAG AGCATCTGAC 60
 TTTTAATCAG AGGGTCAGAG GTTCGAATCC TCTATGGCTC ACTACTTGCA CTTTCCATT 120
 35 TTGGGAAGTG CTTTTTTTTT GGTCTCCAC CAAATGTGGT GGGTATATAA TTAAAGAAC 180
 TATTTTTTAAA ATACAACTTT TAGAGCTTTT ATTATTAGGC GGCCAGTCCA TTATTGGGGC 240
 TGGTTGTCTT CnTTTTTTCT CCTTTGTACA AGCTGAAAAT CATCATTATA CGTGCTTAAA 300
 40 GTGGTGAATT CTGAACCAA GAATCACTTG ATAATTTATC TATATAATCC TCnATAGACC 360
 ATATAATGCT GGAATAATGG ATCTACAnCC TGAGTTCCAn 400

45

(2) INFORMATION FOR SEQ ID NO: 4312:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4312:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 120
 AGGCATCCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 180
 5 ACGCTCACAT ACGGCTTCGT TTTCAATTATT TTAAATGCTC ATTTACATAA GTAAACTCTG 240
 CTTTAAAATA ATTAACATCAT TGTCTGCnAA ACGTTTTcNt TTATAAAAAG ATTAAACGCG 300
 TTATTAAncT GTGGAGTG 318

(2) INFORMATION FOR SEQ ID NO: 4313:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4313:

ACGGTGATCA CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCCAGTTCCG CCACCCCGGC 60
 ACTATAAAAA TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG 120
 25 TATTCTACCG CTGAACTACT TCTGCATATG CGGGTGAAnG GAGTCGAACC CCCACGCCGT 180
 AAGGCATAGA TCCTAAGTCT AGTGCGTCTG CCAATTCGCG CACACCCGCA AATGGTGAGC 240
 30 CATAGAGGAT TCGAACCTCT GACCCCTCTGA TTAAAGTCA GATGCTCTAC CAACTGAGCn 300
 AATGGnTCTT CCATGG 316

(2) INFORMATION FOR SEQ ID NO: 4314:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4314:

AGGAAAAGTC GTTGTGATAC ATCAACCAGC TGAAGAAGTA CCACCAGGTG GTGCTAAAAC 60
 45 AATGATTGAA AATGGTGTAT TAGACGGTGT TGATCATGTA TTAGGTGTAC ACGTCATGAG 120
 CACAATGAAA ACAGGTAAAA GTGTATTACC AGACCTGGTT ATGTTCAAAC AGGACGCGCA 180
 50 TnCTTCAAAT TGAAAGTCAA GGTAAAGTGG TCATGGTTCA TCACCACATA TGGCCAATGA 240
 TGCCATTGTT GCAGGTAGCT ACTTCGTCAC AGCGTTACAA ACAGTGTATC TAGACGACTA 300
 GGCCATTTGA ACCGGTGGTT TCACATCGGT CATTTnCCGT AAAAGnCCAT TCCATG 356

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4315:

TATCAGCATT TGTAAGTGT ATTGTTTATA ACTTCTGTGT GAAGCGCAAT ATTACAATTA 60
 AAATGCCGAA AGAAGTACCG CCGAATATTT CACAAGTATT TAAGGACTTA ATTCCATTTT 120
 CAGCGGTAAT CATCATTCTT TATGCATTAG ATTTAGTCAT CGCAACAGCT TTAAATCAAA 180
 TGTAGCGGAA GGnATTTTAA AATTATTCCA ACCATTATTT ACAGCAGCAG ATGGGATGGA 240
 TTGGTGTAC AATTATCCTT GGnGGCCTTT GCATATTCnG GGTGTAGGG AATCAGGTCC 300
 GTCAATGTAG AGCCAGCAAT TGCAGCCATT ACATATGCCA TATCGGAGCG GACTTCAAGT 360
 TGCCTCAGCG GAGGACACGC 380

(2) INFORMATION FOR SEQ ID NO: 4316:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4316:

GCTCTAGGAT GACTGATTGA ATGTCCATGA ATGAACAACC CCTTTGTTTA ATATCGAGTT 60
 TGGCAAATTT ACGTTTATCA GCGTTTCTAT GATCAGTACT TCTACGGGTA GCGTTTCTAT 120
 GTAATTIACA TCATCTTAAC ATATAAATAC TTCGCTATTT AATTGAAAAC ATATCCTATT 180
 ATTCTTTGTC CGTTCTGACG TTAAATATCT AGCCTTAGGC ATTTCACTTG TTAATGAATT 240
 TAACCTTCTT CCACTAACCG TCCCTAAACC CAATCCCGCA ACAGTTTTTA ACTTTTTTCGT 300
 TGTGTCTCTG ACATCTCATT AAGAAAGTTT ATTCTGCTTA AACTTATAA TCCACACCCT 360
 GAGCAAACGn TnCTTATGAC AGAGTATTAA AATAAGCCGn 400

(2) INFORMATION FOR SEQ ID NO: 4317:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4317:

CCTTATTGAT AATGGTATGA GAATATTTGT TCGAGATGGA TGAAGGTAAT GAGTGAGAAA 60
 5 CTGGATTTTT AAAGTATGAG ACAATATTTT AAAAAGTTCA ATTATTAACT TATAAGCAAA 120
 TAATTGCTAT AAAAAAGTTT GGACGTGTAC AATTGCAATA TGAAGATTTT AAATTAATTG 180
 TAAAGTATCG TGGAGTGGGT AACGTGTCAG AACATGTATA TAATCTTGTG AAAAAGCATC 240
 10 ATTCTGTTAG AAAATTTAAG AATAAACCTT TAAGTGAAGA CGTTGTTAGG AAATTGGTAG 300
 GAGCTGGGCA AAGCGCTTCG ACGTCAAGTT TCCTGCCAGC ATACTCCATT ATTGGTTCGG 360
 15 CGGTGGGAGG TTAAnGGAAT TTACGGGGAG GTTCTGGGCA 400

(2) INFORMATION FOR SEQ ID NO: 4318:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4318:

TAACTACGTC TCCTGTTTCT GGATTCTTAA TTCCTGGTTT ACCTGGAAC TCTCTTTCT 60
 30 CTCCTGTTGG TAACTTCGGA TCAAATTCGT CTCGATGACC TGGTGTTATC GTTTCTGGTC 120
 CGTATTCTGT TAATTCATTA ATCGGATCTn TTGTGATTC TTCTTTCGAT TCACCTGTAC 180
 TAATAATTC TCCAGTTAAT GGATTTTTTA GTGTGGCGT CGTTATTGTC TTCTCACCTn 240
 35 TTTGTCCTTC TCTTGTAAC TTTTCTGTCC CGGTGCTAAA TnCGGATTAA ATTACGGTCT 300
 TTCTTGAAGG AATCTCTTC 319

(2) INFORMATION FOR SEQ ID NO: 4319:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4319:

50 AGGTGCATTG AGAGAATTTG TAAATGACGT ATTAGGACCT CAAGACGATA TTAATAAATT 60
 TGAATACTTA AAAAAATCTT CTCAAATAC AGGTACTGTC AATTATTGGT ATTCAACTTA 120
 AAGATCATGA TGATTTAATA CAACTCAAAC AACGTGTnAA ATCATTTCGA TCCTTCCAAT 180

ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC TGCTTTTTTAT TATACTTTAC 300
 ATTTGCTCGT TTCGTCAGAT TGCAAACGTT TTCACTTCGC CAAGCCCATC TTTCnTTGGn 360
 5 GTTTGCCT 368

(2) INFORMATION FOR SEQ ID NO: 4320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4320:

TAAGTTAGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60
 20 TCCTCTCCTT CGGCTCTCGC TTAATCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180
 TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT CTCAACTTGC CTGGCAACGT 240
 25 TCTACTCTAG CGGAAnTAA GTTGGnCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300
 GACAATCGCT TGCTTCTTTT CCTCTCCTnC GGCTCTCGGT TAACTCA 347

(2) INFORMATION FOR SEQ ID NO: 4321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4321:

GGGCAAGTTA CAGTGGTGCA TGGTTGTCGT CACTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 CnCAACGAG CGGCAACCCT TAAGCTTAGT TGCCATCATT AAGTTGGGCA CTCTAAGTTG 120
 ACTGCCGGTG ACAAACCGTA GGAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180
 45 TTTGGcTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGC GAGTCaAGCA 240
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGaCTaC ATGaAGCTGG 300
 50 aATCGCTaGT aATCgTGGTC CAGCATGCTA CGGT 334

(2) INFORMATION FOR SEQ ID NO: 4322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4322:

CTGTTAAACG ACTACAGGAA GTATTTACAA TCAAAC TAAG CAAAAGTATT CAGATGCCTC	60
AGATAAAGCT TGGGCGCATT CAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA	120
CGATATAAAA GTGCAAAGGG TTGGCTAATA GATATGGCTA ATAAATCGCG CTCGAAATGG	180
GATAATATTT CTAGTACAGC ATGGTCGAAT GCAAAATCCG TTTGGAAAGG AGCATCGAAA	240
TGGTTTAGTA nCTCATTACA AnTCTTTAAA GGGTTGGA CT GGGGATATGT ATTCAGAGCC	300
CACGATCGTT TTGATGCATT TCAGTTCGGC	330

(2) INFORMATION FOR SEQ ID NO: 4323:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4323:

CAATGATGCC ATGAGCAGTG CCTCCTTTAA TAGCATTTTA GCACTGTTTT GTCGTATTTT	60
TAAATATAAA TTTGGAATGA ATAATAAAGT AGTGATTAAA TTAAGTTGTG TGATAGGAAA	120
CTTGGACATC AATCAAAGTA ATAGGCACTA CAACGCTTAT TGGCGGGGCC CCAACAAAGA	180
AGCTGACGAA AAGTCACTTG CAATAATGTG CAAGTCnGGG ATGGGCCCCA ACATAGAGAA	240
ATTGGGTCCG nAATTTCTAC AGACAATGCC AGTTGGCGGG GCCCCACAT AGAGAATTTT	300
GAAAAGGAAT TCTACCAGCA ATGCCAGTTG GGGGAnG	337

40

(2) INFORMATION FOR SEQ ID NO: 4324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4324:

TTACTTACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG ACTATAGCAA	60
GGAGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG TCGATGGTAG	120

55

GCATTGAGAC CGCAAGnTCT TTTTTTTATG TCTAAAACGT CAAAATAAAA AGCAAACACA 240
 AAGAAAAATG GCTTGGCGAA GTGAAAACGT TTGAATCTGC CGAACGAGAA AGAGCGnACC 300
 5 GAGTTTAGTA GAnTAAATGA GTAAGCGAGA 330

(2) INFORMATION FOR SEQ ID NO: 4325:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4325:

15 TTCATCCGCT CACTTTTCAA CGTAATCGGT TCGGTCCTCC ATTCAGTGTT ACCTGAACTT 60
 20 CAACCTGACC AAGGGTAGAT CACCTGGTTT CnGGTCTACG ACAAATACTA AACGCCCTAT 120
 TCAGACTCGC TTTGCTACG GCTCCACATT TACTGCTTAA CCTTGACATC AAATCGTAAC 180
 TCGCCGGTTC ATTCTACAAA AGGCACGCCA TCACCCATTA ACGGGCTCTG ACTACTTGTA 240
 25 AGCACACGGT TTCAGGTTTCG ATTTCACTCC CTTCCGGGG TGGCTTTTCA nCTTTCCCTC 300
 ACGGnACTGG TTCAC 315

(2) INFORMATION FOR SEQ ID NO: 4326:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4326:

40 TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT TAnATGCGGC TCATCGCATC 60
 CACTTTTTCG CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGAACTAC CATCGACGCT 120
 AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC TATAGTCACC 180
 45 AGACATATGA ATGTAAATTA TACATTCAAA ACTAGATAGT AAGTAAAAGT GTTTTGCTTC 240
 GCAAAACCAT TTATTTTGAT TAAGTCTTCG ATCGnTTAGT ATTCGTCAAC TCCACATGTC 300
 ACCATGCTT 309

(2) INFORMATION FOR SEQ ID NO: 4327:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 311 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4327:

AAAGCTTATA AACGCTCATC TGACATTGTA GAATTCATGC TTTCAAAAGA CGATATACTA	60
CGACACTCCT ACGAACTTGT CCAAGGATTA CGAAAAGACC TAAGGTTATG TAATTnGCCT	120
AAATTTATTA ATCGTTTAAA TTCAGTTAGT AAAAAGTCTG TGAGTAAGGG TGTATGGAAA	180
GTGGTTAAAT ATTATAGAAA ACATCAAAGG ATGTTAAGAA ATACAATTTA TTACCCAGCA	240
TTTAATAATG GTGCTATAGA AGGAATTAAT AATAAGATnA AATTAATCAA GTGAATTTCT	300
TTTGGTTnCA G	311

(2) INFORMATION FOR SEQ ID NO: 4328:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4328:

TAGCTTCTGC GAGCTAGCGG AATCGAAGCC CCAGTAAACG GCGGCCGTAA CTATAACGGT	60
CCTAAGGTAG CGAAATTCCT TGTCGGGTAA GTTCCGACCC GCACGAAAGG CGTAACGATT	120
TGGGCACTGT CTCAACGAGA GACTCGGTGA AATCATAGTA CCTGTGAAGA TGCAGGTTAC	180
CCGCGACAGG ACGGAAAGAC CCCGTGGAGC TTTACTGTAG CCTGATATTG AAATTCGGCA	240
CAGCTTGTAC AGGATAGTAG GAGCTTTGAA ACGTGAGCGC TACTTACGTG GAGGCGCTGG	300
TGGGATACTA CCCTAGCTGT TTTGGTnTCT nACCCGACCA	340

40

(2) INFORMATION FOR SEQ ID NO: 4329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4329:

50

AATCCATAGC GAAATGTATA CCATCACCCA TGCGTCCTTC TAAAGGTAAA TCTCTACCTT	60
TTTGTGCACC AGTACATAAT ATAATGGCAT CATACTCAGA TTCTAACGTT GCTTTATCAA	120

55

TACGACGTCG AACCACATCT TTATCAAGTT TCATATTCCG AATACCATAC ATTAATAAAC 240
 CGCCTGATTG TCTAGCACGT TCATAAATAG TTAAGTTCTT 300
 5 CAGCAGCAGT AATCCTGnTG GACCG 325

(2) INFORMATION FOR SEQ ID NO: 4330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4330:

CACTTCACCA CAGCCGCCAT GGCAGGnGCA GTAGGAATCG AACCCACACC AAAGGTTTTG 60
 20 GAGACCTCTA TTCTACCGTT GAACTATGCC CCTATTAAAA ATAATAAATG GAGGGGGGCA 120
 GATTGCAACT GCCGAACCCG AAGAGCGGAT TTACAGTCCG CCGCGTTTAA CCACTTCGCT 180
 ACCCCTCCAT AAATGGTGCG GGCGnGnAGG ACTTGAAACC CCCAACCTAC TGATTACAAG 240
 25 TCAGTTGCTC TGACCAATTG AGCTAAGGCC GGCTAAGAAA TGGTTCCAGG ACAGAGTCGA 300
 AACTGCCGAC ACATGGGAGC TTTCAAT 327

(2) INFORMATION FOR SEQ ID NO: 4331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4331:

GCATCATTTT CAGCTTCCCA CTTCCACATT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 60
 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAAACAATA CAGGTTGGTA ATGCCCAATA 120
 ATAATGACCA TTTCCCAAAT GCCTAAGAAA ATAATAAATG TGATAATAGG TAATATAAAT 180
 45 TTGTTATTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 240
 AGTCATCATA TGCAGGTGGA TTAAACAAAT GATGTTGTTT TACCAATGTC GTAATTTCTT 300
 GGATAGCCGG ATGnTTTAAA TTGTTAAAAT CACCATAGGG TGTCCnGCC GTGGACTGTG 360
 50 GTTAAAAACG TCACGGACTT TGTTTAAAAn GGTGCGTCAT 400

(2) INFORMATION FOR SEQ ID NO: 4332:

(A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4332:

10 CTGGTATGCA GATTTACCAC CTGCCTCTCC ACAAnTnnGG GGAGAGCAAA CAGATGTGCC 60
 TGAATCAAGT GACTGGTATA ACGCATCATA CATTATTATG TGGGGCTCTA ATGTACCTTT 120
 AACACGTACT CCGGATGCAC ATTTTATGAC TGAAGTCCGC TATAAAGGTA CAAAAGTCAT 180
 15 TTCAGTAGCA CCAGATTACG CAGAAAATGT GAAATTTGCA GATAACTGGC TAGCACCGAA 240
 TCCTGGTTCA GATGCTGCAA TTGCACAAGC AATGACGGCA TGTATTTTTA CAAGGAACAT 300
 TATGTTAAAT CCAACCTGAA TGAACGGTTT TTATTAAATT ACGGTAAAA CCATTATTAC 360
 20 CAGGAT 366

(2) INFORMATION FOR SEQ ID NO: 4333:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4333:

TATTATTTCA TTGAGCAGAA AGAAAATTAT GGCACCAAAC TTTAATATTT TTTTCAATGT 60
 35 CATTCTTTTG AnGGGAGTGG GACAGAAATG ATATTTTCGC AAAATTTATT TCGTCGTCCC 120
 ACCCCAACCTT GCATTGTCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCATC 180
 CCCAACTTGG CACATTATTG TGAAGCTGAC TTTTCGTCAC TTGCTGTGTT GGGGCCCTCA 240
 40 CCCCAACTCG CATTGCCTGT AGAATTTCTT TTGGAATTC TCTGTGTTGG GGCCCCCTGGA 300
 CTGAGAATTG GAAAAAGCT TGTGACAAG CGChATTTTC GTTCCATGCA ACTGACTGCC 360
 45 AAGAGAAChT CGTGAGAGCh ATGAAGAAGA TTGGATTTGA 400

(2) INFORMATION FOR SEQ ID NO: 4334:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA ACGCGTTATT AATCTTGTGA 60
 GTGTTCTTTC GAACnTATGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACTCTTTA 120
 5 TTCACTCGGT TTTGCTTGGT AAAATCTATA TnTTACTTAC TTATCTAGTT TTCAATGTAC 180
 AATTTCTTTT TAGTCAAGCG CTCGCATAAG CAATATCACT TTAACCAAAA AATATTTGAA 240
 10 TGTAAATAA ACATTCAAAA CTGAATACAA TATGTCACAT TATTCCGCCA TCTTCTGnAA 300
 GAAGATGTT 309

(2) INFORMATION FOR SEQ ID NO: 4335:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4335:

nAGGACTTTT CTCGGTCAGT GTGAAAATCA ACGCACTCGT AnACACAATG TCTTCTCCCC 60
 25 ATCACAGCTC AGCCTTAACG AGTACCGGTA TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA 120
 CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC CCCCCATCGA TTAACGAT 180
 30 TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCG GnCTCAGCTT 240
 AGGACCCGAC TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA 300
 CGGGATTCTC ACCCGTCTTT CGCTACTCA 329

(2) INFORMATION FOR SEQ ID NO: 4336:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4336:

CAAAGTGACA GGTGGTGCAI GGTTGTCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 45 CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTA AGTTGGGCAC TCTAAGTTGA 120
 CTGCCGGTGA CAAACCGnnn GAAGGTGGGG ATGACGTCAA ATCATCATGC CCCTTATGCA 180
 50 TTTGGGCTAC ACACGTGCTA CAATGGGACA ATACAAAGGG CAGCGAAACC GTGAGTGCAA 240
 GCAAATCCCA TTAAGTTGT TCTCAGTTCG GATTGTAGTC TGCAACTCGG ACTACATGAA 300

(2) INFORMATION FOR SEQ ID NO: 4337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4337:

```

CCAGCACCGG GGCAGGCGTC ACCCTCATAC ATCACCTTAC GGTTTAGCAG AGACCTGTGT      60
TTTTGATAAA CAGTCGCTTG GGCCTATTCA CTGCGGCTCT TCTGGGCGTT AACCTAAAG      120
AGCACCCCTT CTCCGAAGT TACGGGGTCA TTTTGCCGAG TTCCTTAACG AGAGTTCGCT      180
CGCTCACCTT AGAATTCTCA TCTTGACTAC CTGTGTCGGT TTGCGGTACG GGCCTATTT      240
TCTATCTAGA nGGCTTTCTC GGCAGTGTGA AATCAACGAC TCGAAGACAC AnTGGCTnCT      300
CCCATCAGAG CTCAGCCTTA ACGA                                             324

```

(2) INFORMATION FOR SEQ ID NO: 4338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4338:

```

CGGACATCAA ACGGATGCTG CTCGATTGGC AAATGCATAT AACTAGTAAC ATGATCATCG      60
ACATCAAATT TAGATGATCA AATGTcCCCA ATcATTAAATT TGATTCGGTT GTTTGCTCAA      120
TTGATTATAT GTTTTTCTTA GCACTTCATG CGGCACCATA TCTTTACCTA GTAGCCACAA      180
AGATAAGTCT AACAAAGTGGC AACCATAATC GATTAAACTA CCGCCACCTT GCAACGCTTT      240
ATTGGTAAAA ACACCCCAGC CAGGCACTTT ACGCCTACGC ATCGCTTGTA CACGTGCTAC      300
TAAAGGTTTA CCAACCACAC CTGATTCAAT TGCTTTTTTA GCAGTAATTG CCACATCTGT      360
GTGACGATAA TGATATGCGC CAGTAATAnT TTGTGnTTT                             399

```

(2) INFORMATION FOR SEQ ID NO: 4339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4339:

5 TGAGGCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120
 CTAAGTGGAC TCGAACCACC GACCTCACGC nTATCAGGCG TCGGCTCTAA CCAGCTGAGC 180
 10 TATAGGCCCA TTTnTTTGAA TGTAAATAA ACATTCAAAA CTGGAATACA ATATGTGCAC 240
 GTTATTCCGC ATCTTCTGAA GAAGATGTTn CCGAATATAT CCTTAGAAAG GAGGTGATCC 300
 AGCCGCACCT TCCGGATACG GCT 323

(2) INFORMATION FOR SEQ ID NO: 4340:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4340:

25 GGCTAGCCCT AAAGCTATTT CGGAGAGAAC CAGCTATTTT CAGGTTTCAT TGGAATTTCT 60
 CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCCGTC CTCCATTCAG 120
 30 TGTACCTGA ACTTCAACCT GACCAAGGGT AGATCACCTG GTTTCGGGTC TACGACCAAA 180
 TACTAAACGC CCTATTCAGA CTCGCTTTTCG CTACGGCTCC ACATTTACTG CTTAACCTTG 240
 CATCAAATCG TAACTCGCCG GTTCATTCTT ACAAAGGCA CGCCATCACC CATTAAACGGG 300
 35 CTCTGAACTA ACTTGGTAAA GCnCCGGTTT nCnGGTCCAA TTTT 344

(2) INFORMATION FOR SEQ ID NO: 4341:

- (i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4341:

45 TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGnGATAGGC GAACGTGCGA 60
 50 TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC 120
 TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA 180
 AAGCCTCTAG ATAGAAAATA GGTGCCCCGA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240

TTCnGGGAAA AAGGGnTCCC CTTTAAGGGT TAACCGCCCC AAAAAACCCC C

351

(2) INFORMATION FOR SEQ ID NO: 4342:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4342:

AATAATGACT	CCTACGGGAC	TCGAACCCGn	GTTACCGCCG	TGAAAGGGCG	TGTACTTAAC	60
CGTATGACCA	AGGAGCCATG	GCTCACCAGG	TAGGACTCGA	ACCTACGACC	GATCGGTAA	120
CAGCCGATAG	CTCTACCACT	GAGCTACTGT	GGATTAATAT	TATGCCTGGC	AACGTTCTAC	180
TCTAGCGGAA	nTAAATTCGA	ACTACCATCG	ACGCTAAnGA	GCTTAACTTC	TGTGTTCCGGC	240
ATGGGAACAG	GTGTGACCTC	CTTGCTATAG	TCACCAGACA	TATGAATGTA	ATTATACAT	300
TCAAACTAG	ATAGTAAGTA	AAAGTGA				327

(2) INFORMATION FOR SEQ ID NO: 4343:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4343:

ACCGCTTGGG	CTGACATTTT	TGGCTTGTTA	AGCAGCTTGC	CTACITTTTTT	GGCAATAGCA	60
CCATACGTTG	TTAGAGTCCC	ATAAGGAACC	TGTCTTAATT	CATTCCAAAC	AACTGTTGA	120
AAATGACTAC	CTGTTGGCTT	TAAAGGTATT	GTGATTTTCAG	GATTGTCACC	TTTAAATAC	180
GCGTCTAACC	ACTGTGTCGC	CTCTCTAAAT	ATCGCTAAAG	ACGTATTTTC	TTCCCTAGTA	240
CCATCACCTT	GTTGATTTTC	AAACAAAACA	GCGGTCAGAC	TTACCCCATC	ACTCAAAAGT	300
TCCAAnCGTC	CTGACAGGCG	AAnCAGAGTG	AACGCTGAGA	CTCCAGAAAA	ATCCCCCTnT	360

(2) INFORMATION FOR SEQ ID NO: 4344:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4344:

ATTCCGACAT CTTCTGAAGA AGATGTTnCC GAATATATCC TTAGAAAGGA GGTGATCCAG 60
 5 CCGCACCTTC CGATACGnCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 120
 GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT 180
 10 GACGGGCGGT GTGTACAAGA CCCGGAACG TATTCACCGT AGCATGCTGA TCTACGATTA 240
 CTAGCGATTG CAGCTTCATG TAGTCGAGTT GCAGACTACA ATCCGAACTG AGAACAACCT 300
 TATGGGATTT GCT 313

(2) INFORMATION FOR SEQ ID NO: 4345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4345:

ATTTTATCGT AAGATTTTTT CGCAATGAGA TTTGGATCGT TTTGTCCAC TACAATATCT 60
 25 AATAGTTTTA CTTAAGTCC AGCATTCAACA AAAAGTGCTG CCAGTTGAGC GCCCATTGTG 120
 CCTGCGCCAA GAACGGTTAC TTTATTAATT GTCATAGTGA TTCCTCCAAT TTAGTTGAGG 180
 30 ATAAGATAAC CATTAAGATA ATTGGAATAA CGTTGCTATT TTATAAAATT AATTAAGTAT 240
 CTTTGACAGT CATCTTAGCC TCTTATTTAA GGnAAAAGCn TTATGCTTAA nATAAGTCTT 300
 35 TTTTA 305

(2) INFORMATION FOR SEQ ID NO: 4346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4346:

GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGCA AGTCTTACGG CATCTTCTAT 60
 TTTTAAGCTT GAATTTAACA AATCATAAGC CGTATGAATA TTTAAATATG CCACCATGAT 120
 50 TGAATGGnCC CTTTCTATTA GTTAAGTTTG TGCGTAAAGC TGTAGCAAGT TGCTCAAATT 180
 CATCCCCAGC TGTCCACTGA AACTCCTGGA CGCATTTCGGA TGAnCAACGC CAACCAAAAT 240

AnTACCTTCA TCGACTGCAA ATACCCATAA TTTCCAGCCT TGATGTCAGC AATGTAATAA 360
 CCAACTGAGA TGCTCATTGG CTGATACGAT GntCCATACA 400

(2) INFORMATION FOR SEQ ID NO: 4347:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4347:

TCTGGGTTGA GTCGGGTCCT AAGCTGAGGC CGACACGTAG GCGATGGATA ACAGGTTGAT 60
 ATTCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT 120
 GGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT 180
 AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA GTCGTTGATT TCACACTGGC 240
 CGAGAAAAGC CTCTAGATAG AAATAnGTGC CCGTACCGCA ACCGACACAG GTAGTCCAAG 300
 ATGAGATTCh TAAGGTGGAG CGACGAATCT CCGTTAA 337

(2) INFORMATION FOR SEQ ID NO: 4348:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4348:

GTTAAGACAC CGCCCTTTCA CGGCGTAACA CGGGTTCGAG TCCCGTAGAG GTCACCATTT 60
 TTTAGGTCTC GTAGGTAGC GATTAACACG CCTGCCTGTC ACCGAGAGAT CGsGGGTTCG 120
 ATTCCCGTCG AGACCGTACA AATGCCTATC CAAGAGGATA GnATTTTTTTT TCGGTTTAAT 180
 ATTATATTAA TAAAGATAT ATGGACGAAT GATAATCATA TTGATTTATC TGTTCTGTTCA 240
 TTTCTTTAA AATGTATGAA CCTCAAGTAA CTTAGTGGTT GGATATGAAA GATAAACGTn 300
 GACAATAAAA TCTTTATT 318

(2) INFORMATION FOR SEQ ID NO: 4349:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4349:

CTTTAAAGCA CGTATAATGA TGATTTTCAG CTTGTACAAA GGAGAAAAAA AGAAGACAAC 60
 CAAGCCCAAT AATGGACTGG CCGCCTAATA ATAAAAGCTC TAAAAGTTGT ATTTTAAAAA 120
 TAGTTCCTTA AATTATATAC CCACCACATT TGGTgNAGnA ACCTAAAAAA AnGCACTTCC 180
 CAAAAATGGA AAGTGCAAGT AGTGAGCCAT AGAGGATTCG AACCTCTGAC CCTCTGATTA 240
 AAAGTCAGAT GCTCTACCAA CTGAGCTAAA TGGCTCTAAA TGGCTGGGCT AGCTGGGATT 300
 CGAACCAACG AGTGACGGA 319

(2) INFORMATION FOR SEQ ID NO: 4350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4350:

ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 60
 GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC 120
 CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 180
 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACCGATCGGT 240
 TAACAGCCGA TAGCTCTACC ACTGnAGCTA CTGTGGATTG AATCATTATG CCTGGCAACG 300
 TTCTTACTAT AGCGGAAnGT CAAGTTCCGC ATnACCATAC GAAGCT 346

(2) INFORMATION FOR SEQ ID NO: 4351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4351:

ACGTCCTTCA TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT 60
 ATGTTTCCAC CATTTTTATA AGTnAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAA 120
 ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG 180

ACTTACTTAT CTAGTTTCA ATGTACAAAT AATGGTGGGA GACTAGCGGG ATCGAACCGC 300
TGACC 305

(2) INFORMATION FOR SEQ ID NO: 4352:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4352:

GTTTCATCAAT TGCTAATTCC AGTCCGCCTA ACGGATCAAT TTCATCCGCA TGTATTTTCA 60
CTTTAAAACC TGGCTTCTTT GGCTTTTTCG ATATAATGTT GCGATTGTTT TATTGTAAAT 120
ACACCTGTTT CACAGAAAAT ATCCGCAAAG TCTGCATATT GTTTTACTTC CGGAAGTAAC 180
GCAATCATTT CTTCTAAAAA TGCCTCATTT GAACTTGCCT CTTTAGGTAC AGCATGAGGC 240
CCTAGGAAAG TATGTTTCAT GTCTAAATCA TATTTCTCAG CTAAACGATT AGnCACTTTC 300
AA 302

(2) INFORMATION FOR SEQ ID NO: 4353:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4353:

TCTACCGCTG AACTACTTCT GCGGGTGAAG GGAGTCGAAC CCCCACGCCG TAnnTGAGGA 60
TCCTAAGTCT AGTGCGTCTG CCAATTCGCG CACACCCGCA AATGGTGAGC CATAGAGGAT 120
TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AAtGGCTCTT 180
CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA 240
CCAATTGAGC TAGGCCGGCA ATATGTAAGA ATAAATGGTG GAGAATGACG GGTTCGAACC 300
GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC CGnTTTAAAA 360
CTGCTGGCnA CGGTCTAnTC TAAGGGGACG TAAGGTGAC TACCATCGAC G 411

(2) INFORMATION FOR SEQ ID NO: 4354:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4354:

TGCTTAGATG	CTTTCAGCAC	TTATCCCGTC	CACACATAGC	TACCCAGCTA	TGCCGTTGGa	60
CGACAACTGG	TACACCAGAG	GTATGTCCAT	CCCGGTCCTC	TCGTACTAAG	GACAGCTCCT	120
CTCAAATTC	CTACGACCAC	GACGGATAGG	GACCGAACTG	TCTCACGACG	TTCTGAACCC	180
AGCTCGCGTa	CCGCTTTAAT	GGGCGAACAG	ACAAGCCCTT	GGGGACCGAC	TACAGCCCCA	240
GGATGCGATG	AGCCGACATC	GAGGTGCCAA	ACCTnCCCGT	CGATGTGAac	TCTTGGGGGA	300
GATAAGnCTG	TTATCCCCGG	GGTAACTTTT	ATCCGTTGAG	CGATGGGCCC	TTACCATGCG	360
GAAACCA						367

20

(2) INFORMATION FOR SEQ ID NO: 4355:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4355:

30

GTATTTTAAA	TCATAGTGGT	TTATGCGTCT	TTTTCAAATT	CTATAAAAAA	TCGGATGACG	60
TGTAATCTGC	CATAGATTAA	CACATTCATC	CGATTTATAA	TAATAAGATA	GACTAACATT	120
TATTGAGAGC	GGGACGGAAA	TGATAAAGAA	CGACTAATGA	TTGATTATGT	AGCGATTCTT	180
TATCATTAGT	CACAGCTAAT	GTGTACTTAA	AAATATGAAT	GCATGAGTTA	CACTCAnATT	240
AGAGGAAATA	CTAATTTCTA	AAGAAAAAGT	ATTTCTTTAT	GTTGGGGnCC	ACCCCAACTT	300
GnCATTTGTCT	GTT					313

40

(2) INFORMATION FOR SEQ ID NO: 4356:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4356:

GGGCTGGGTT	CAGAACGTCG	AGGCAGTTCG	yTCCCTATCC	GTCGTGGGCG	TAGGAAATTT	60
------------	------------	------------	------------	------------	------------	----

50

55

TCGTGCCAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AGATCCTGAA 180
 GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG 240
 5 ATGAGGTTAA TAGGTTTCGAG GTGnGAAGCA TGGTGACAGT GGnAGCTGAC GAATACTAAT 300
 CGATCGAGGA CTTAATCAAA ATAAATGTTT TGCGA 335

(2) INFORMATION FOR SEQ ID NO: 4357:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4357:

20 GCTCTAAAAG TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTGGTGn 60
 nGAACCTAAA AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT 120
 TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA 180
 25 ATGGCTGGGC TAGCTGGATT CGAACCAACG AGTGACGGAT nAAAGTCCGT TGCCTTACCG 240
 CTTGGCTATA GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 300
 AGAG 304

30 (2) INFORMATION FOR SEQ ID NO: 4358:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4358:

40 ATAATGGTGA CGTTGATGAT GCATTAACAC AAGGTAAAGC AGCAATTGAT GCTATTCAAG 60
 TAGATGCTAC TGTTAAACCT AAAGCGAACC AAGCTATTGA AGTTAAAGCA GAAGATACGA 120
 45 AAGAATCTAT TGATCAAAGT GACCAGTTAA CTGCTGAAGA AAAAAGTCAA GCATTAGCAA 180
 TGATTAAACA AATTACAGAT CAAGCTAAAC AAGGTATTAC TGATGCAACA ACAACTGCTG 240
 AAGTTGAAAA AGCGAAACTC AAGGACTTGA AGCATTGAT AACATTCAnn TCGACTCAnC 300
 50 AG 302

(2) INFORMATION FOR SEQ ID NO: 4359:

(A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4359:

10 GGTGGGAAA TCATTGCATG AGAGTGTGAA AGGGCATAAG GGGAGCTTGG ACTGCGAGAC 60
 CTACAAGTCG AGCAGGGTCG AAAGAGGACT TAGTGATCCG GTGGTTCCGC ATGGAAGGGC 120
 CATCGCTCAA CGGATAAAAG CTACCCCGGG GATAACAGGC TTATCTCCCC CAAGAGTTCA 180
 15 CATCGACGGG GAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCCTGGGG CTGTAGTCGG 240
 TCCAAGGGT TGGGCTGTTC GCCCATTAAA GCGGTACAnG GCTGGGTTCa GAACGTCGTn 300
 AGAAAGITTCG GTCCCTATCC GTCCTGGGGC GTAGGAAATT TnGAGAGGAG 350

20

(2) INFORMATION FOR SEQ ID NO: 4360:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4360:

30 AGCTCCTAAA AGGTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC 60
 GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTAGTAGCGA 120
 35 TTCCAGCTTC ATGTAGTCGA GTTGCACT CACAATCCGA ACTGAGAACA ACTTTATGGG 180
 ATTTGCTTGC ACCTCGnGGT TTCGCTGTCC CTTTGTATTG TCCATTGTCA GCACGTGTGT 240
 40 AGCCCCAAATC ATAAGGGGCA TGATGATTG GACGTTTCATC CCCAnCTTCC TCCGGnTTGT 300
 ACACCGGCAG TTCAACTTAG AGTGCCCAA 329

40

(2) INFORMATION FOR SEQ ID NO: 4361:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4361:

55 AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA CTCTAGCGGA 60

CTnTCCTCTC CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCCTCTTTT 180
 TCTCGTTTCG TCAGATTCAA ACGTTTTTCAC TnCGnCAAGC CATTTTTCTT TGTGTTTACT 240
 5 TTTTATTTTG ACGTTTTTAGG CATAAAAAAA wGAGAcCTTG CGGTCTCAAT GCGGCTCATC 300
 GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG GCTAACAACG 360
 10 TCGCCAAAGA CCTTCTTGA CTTGTGACAA TCGGCTTGCT TCTTTCCTCT CCTTCGGCTC 420
 TCGC 424

(2) INFORMATION FOR SEQ ID NO: 4362:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4362:

CACAACAAGT ATCTAAGATA CTGGCCGAAG ATTGTCACAG ACGGTAGGGG AAGGGGGTCA 60
 25 CGTGTACGAC CCAACATGTG GTTCCGGTTC ATnGTTGTTA CGTGTGGTA AAGAAACGCA 120
 ATnAnTCGT TATTTCCGAC AAGAACGTAA CAATACTACA TACAACTTAG CACCATGAAT 180
 30 ATGTTATTAC ATGATGTGCG TTATGAGAAC TTCGAGATCC GTAATGATGA CACATTGGAA 240
 AATCCAGCCT TTTTAGGCAA TACATTGAT GCGGTTATTG CGAACCATAC AGTGCGAAAT 300
 TGGACAGCAG ATTCCA 316

(2) INFORMATION FOR SEQ ID NO: 4363:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4363:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT 120
 50 ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 180
 AGGCATCCAC CGTGCGCCCT TGAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG 240
 55 TTGATTAATC TTGTGGAGTG TTCTTTCGAA CATAGCGATT ATnTCTTATG GAATTCAAGC 300

(2) INFORMATION FOR SEQ ID NO: 4364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4364:

```

nTGCACTTAA GAACTTAGAC GATCGTGGTA TCGTTTATAT TGGTGCAGAA GTAAAAGATG      60
GAGATATTTT AGTTGGTAAA GTAACGCCTA AAGGTGTACT GCAGTTAACT GCCGAAGANA      120
GATTGTCACA TGCAATCTTT GGGTGAAAAA GCACGTGAAG TTAGAGnATA CTTCAATTACG      180
TGTACCTCAC GGCCTGGCG GGTATCGTTC TTGCATGTTA AAAGTATTCC AATCGTGCAA      240
GAAGGGCGAC GATACATTAT CCACCTGGTG TTAAACCAAT TTTAGTACGT GGTATATATC      300
GTTCCAAAAA CGT                                                              313

```

(2) INFORMATION FOR SEQ ID NO: 4365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4365:

```

AACCATTGGA TGCAATAGCG TCATTCTTGG ATATTAATCC CTAAATTGCC GTGATATCCC      60
GCGTCTATCT TGGCCTGTTT CAATCACTAA ATGCGTTTTA CTAATTACAC CACTACGGGC      120
TAGTTAATAG TCCGACATAG CCCTCTGGTA TGCTTACAGC TACATCTGTn TTAATCACTG      180
CCTTTTCTTG TGGCTCAAGT ACGACAGTTC AGCTGAGAAT ATGTCATAAC CTGCATCCGn      240
CTTATGATTT CGTTCGGGCA TTCTAGCATT TTCTGATAAT AGCCTTACTT GTAATGTGTn      300
AGTCATTTTC                                                              310

```

(2) INFORMATION FOR SEQ ID NO: 4366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AGTGGTACTT CTGTTAATTG GTGAATTTGG ATACTGGTTA TATTCAGCTG CACCGCAAGC 60
 AACTTCTATT GATGGCCTAA CTGCCTTTTT ACCTCAAGCA ATGGGTATGG TAATTGTTGC 120
 5 AGTCATTTAT GGCTTTATGA ATATGAAAGC AGAGAATCCA TTCCGTAATA AAATTACGTG 180
 GTTACAAATT ATTCAGGTT TCTTCTTTGC ATTTGGTGCT TTAACATATC TTATTTTCAGC 240
 10 ACAACCTAAT ATGAATGGTT TAGCACTGGA TTTATCCTTC TCAACATCCG TGGTGCTGCT 300
 ACATTAAAGG TATTAATTCT TAAACCACAT AAACGTCAAA GAATGGTAAT ACAATCACGG 360
 CTAGTACCAT TTAGTAGCCG CTCCGTACCG NAATTATAAA 400

(2) INFORMATION FOR SEQ ID NO: 4367:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4367:

CACCTGGACG AAACGGTTTT AGATCGTATT CAATTGAAAA GGCCGGTATT GAATGAATCA 60
 CACTTAGCAG CGATTGATCA GGAACATTTT AAATTAAGTT ATTTATCAAC GGTATATGAA 120
 30 GGGGATTTGG AAGATGCGTT AGAAGCATTG TGCCGAGAAG CAGTGAATGC TGTAAACAAG 180
 GCGCTCAAAT TCTAGTGTTA GATGATAGTG GATTAGTTGA TAGCAATGGC TTTGCAATGC 240
 CGATGTTACT CGCnATAAGT CATGTGCATC AATTACTTAT TAAAGCAGAT TACGnATGnC 300
 35 TACAAATTTA ATCGCTAAAT CTGGTG 326

(2) INFORMATION FOR SEQ ID NO: 4368:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4368:

ATTATAGCCG AAATGCCCAA AATAGATTTT GACGAATATT ACGAATGGTT GCTTTACTTG 60
 50 CATAAATGGC TTTAGGAATA AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCTT 120
 CAATGGCAAC TTCTGTACCT GTAnCAATGG CGATACCGAT ATCAGCTTTA ACTAATGCAG 180
 GTGCATCATT TACACCGTCA CCAAnCCATCG CAACCTTCTT ACCTTGTTGC TGTAGTTTCG 240

GTTTTGC

307

(2) INFORMATION FOR SEQ ID NO: 4369:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4369:

15	TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCAC CGGGTGTGCC TTCTGATATG	60
	CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTTCGGAAAT	120
	CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA	180
20	TCCGCTTCTA GTGCCAAGgC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT	240
	CCTACAGGAA ACGCGTTATT AATCTTGTGA GTGTTCTTTC GAACaYTAGC GATTATTTCT	300
	TATGAATTCA AGCTTATTTA AAACCTCTTA TTCAATCGGT TTTGCTGGG TAAAATCCTA	360
25	TATTTTACnT ACCnTATCGA GTTTTCAATG TAACAA	396

(2) INFORMATION FOR SEQUENCE: SEQ ID NO: 4370:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4370:

CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT	60
CGTATTGAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT	120
GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACA TGTAATTTTA CTTTACATA	180
CTTTTAAAAA ATAAGACACT TTGCCAAACT TGCACATAAA TGTTTAATTC AATAATTTGA	240
ATTTTCTGTG TTGGGTCCCT TCGTATAATT TAATAAATAC CACTAAACTA AaTTArTGAA	300
GTGCCTTATG TATAA	315

40

45

(2) INFORMATION FOR SEQ ID NO: 4371:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4371:

5 GTCGTCAAAT GTACCTTCAC CAAGTAGTGA TGTACATATT TACCGCCTTG TTCAACAGCA 60
 CGTGTCGGCG CACCTGTAAT CGCAATGACA GGTATGCGTT CAnATATGAA CCTGCGATAC 120
 CGTTGACGGC ACTTAATTCG CCAACACCAA ATGTAGTAAC TAATGCAGCG AGTCCATTAA 180
 10 GACGGGCATA ACCGTCCGCT GCGTAACTTG CGTTTAATTC ATTTGTATTT CCTACCCAAT 240
 CTACAATGGG GTTGCTGATA ATATCGTCTA GAAAAGCGAG ATTAAAATCA CCAGGGnCAC 300
 15 CAAAATTTTT ATCGACGGCn TG 322

(2) INFORMATION FOR SEQ ID NO: 4372:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4372:

CCTAAGTCTA GTGCGTCTGC CAATTCCGCC ACACCCGCAA ATGGTGAGCC ATAGAGGATT 60
 30 CGAACCTCTG ACCCTCTGAT TAAAGTCAG ATGCTCTACC AACTGAGCnA ATGGCTCTTC 120
 CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA GTTTGCTCTA 180
 CCAATTGAGC TAGGCCGGCA ATATGTAAAG AATAAATGGT GGGAGAATGA CGGGTTcGnA 240
 35 ACGGCGGAAC CCTCTGCTTG TAAAGCAGAT GCTCTCCAGC TTGAGCTAAA TCTCCGATTT 300
 AAAACTGCTG GGCAAGTTCT ACTCTAG 327

(2) INFORMATION FOR SEQ ID NO: 4373:

40 (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4373:

50 CATTTTAATT TATTGTACAG AACGAAATGT GATGTTAGTA GATCATAGGG TTGATGATAA 60
 TATTAAAGCT GAAAACGTTA TATTTATTGG CCTTTTGTGT AAACATGGAC ATTGGCATGC 120
 AGTCATTTAT GACATTGCTC AAGACAAAAC TGCCGAACTC GAAATTGAAA ATATTATAGA 180

TCAATTTTAA AACCCCATCG ATTCCTAAAA AACAGCAGTA AGATGATTTT CAATTAGAAA 300
 ATATCTTGCT GCTGTTCTCT ATTTATACAA TACTTCGTAT TGAATGGCTC GCTTTCCCAG 360
 5 GGnGCCGCTC AGCCTGGGCC TCGACTGGCA ATGCTCCCTC 400

(2) INFORMATION FOR SEQ ID NO: 4374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4374:

TAATGGATTT TTTAGTGTG GTGTCGTTAT TGTCTTCTCA CCTTTTGTG CTTCTCTTGT 60
 20 TACTTTTTCT GTCCCTGGTG CTAAATCAGG ATTAAATTTA CGTTCTTTCT CGAATGGAAT 120
 CTCTTCTTTT TCTACAATCG AGTCTCCTTT TACAGGTCCA TATTTTGTTA CGCTATCGAC 180
 CCGTGGTCTA ACTACATCTC CTGTTTCTGG ATTCTTAATT CCTGGTTTAC CTGGGAACTT 240
 25 CCTCTTTCTC TCCTGTTGGT AACTTCGGGA TCAAATTCGT CTCGATGGAC CTGGTGTGTA 300
 nCGTTTCTGG GTCCGnAAGT CTGTnGAATT GCAG 334

(2) INFORMATION FOR SEQ ID NO: 4375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4375:

ATACATGCAA GTCGAGCGAA CGGACGAGAA GCTTGCTTnG TGAATGTTAG CGGCGGACGG 60
 GTGAGTAACA CTGGATAACC TACCTATAAG ACTGGGATAA CTTCGGGAAA CCGnAGCTAA 120
 45 TACCGGATAA TATTTTGAAC CGCATGGTnA AAGCTTGCAA AGACGGTCTT GCTGTCACTT 180
 ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAGGTAA CGGCTTACCA AGGCAACGAT 240
 GCATAGCCGA CCTGAGAGGG TGATCGGCCA CACTGGAAC T GAGACACGGT CCAGACTCCT 300
 50 ACGGG 305

(2) INFORMATION FOR SEQ ID NO: 4376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4376:

	GATAAAGTGA AAGAACTCGG ACGTGACACC TATTGCACGA TTCGTTGGTT TTAAGGCAGT	60
10	AGGCGTTGAC CCGAAAATTA TGGGTATTGG GCCTGGCATA TCGGATTCCT GAAGTATTGT	120
	CACTCAGCAA TCTATCTGTT GAAGACATTG ATTTGATCGA ATTGAACGAn CATTTGCTCT	180
	CAAACGATTG CATCTATTAA AGAAGTAGGT CTAGATATAT CACGTACGAA TGTGAATGnT	240
15	GGCGCTATTG CTTTAGGTCA TCCATTAGGT GCTACAGGCG CAATGTTAAC CGCGCGTTTA	300
	CTTAA	305

(2) INFORMATION FOR SEQ ID NO: 4377:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4377:

30	AATGTCTTCT ACCCCATCAC AGCTCAGCCT TGAACGAGTA CCGGGTTTGn CCTAATACTC	60
	AGACCTTGAC TGCTTAGACG TGACAATCCA ATACGACACG CTTCGCCTAT CCTACTGCGT	120
	CCCCCATCG ATTAAAACGA TTATAGGTGG TACAGGAAAT ATCAACCTGT TATCCATCGC	180
35	CTACGCCTGT CGGCCTCAGC TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG	240
	GAAACCTTAG TCAATCGGTG GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT	300
40	TCTCACTTCT AAGCGCTCCA CATG	324

(2) INFORMATION FOR SEQ ID NO: 4378:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4378:

50	CATCATGCTT AGAAAACGCT TAATTTAGGT TTTGACTTTT TAATCAGAGT ATATAAGCAA	60
55	AACTTATCAT ACAGGTAAGG TGTAATAAGT ATTTTTTATT AATTGAGAAT AATTATCAAT	120

TGGCACCAAA CTTTAATATT TTTTCAATG TCATTCTTTT GATGGGAGTG GGACAGAAAT 240
 GATATTTTCG CAAAATTIAT TTCGTCGTCC CACCCCAACT TGCATTGTCT GTAGAAATTG 300
 5 GGGAAATCCCA ATTCCTCCTT GGTGGGGGCC CATCCCCACC TTGCACATAA TGGnAGCnGG 360
 ACCTTTCCGC CGCTCCGGGG TGGGGGCCTC nACCCCAATC 400

(2) INFORMATION FOR SEQ ID NO: 4379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4379:

20 ATAAATATA TCACTTGAAA AATTTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA 60
 TTGTGACTGA GATGAACTTT TATGTCTTAG ACACTACAAC ACTATATTGG CAGTAGTTGA 120
 CTGCGGGGCC CCAACATAGA GCAAATTGGA TTCCCAATTT CTACAGACAA TGCAAGTTGG 180
 25 GGTGGGCCCC AACATGAAAG AAATACTTTT TCTTTAGAAA TTAGTATTTT TTATGCATGA 240
 GTGTACTCAT GTTGCGATTA TTTTThAGTA CACATTAGCT GTGGACTAAT GATAAAGGnn 300
 TCGCTACATA ATCCATCCAT TAGGTCGTTC CTTGATTCAT TCCCT 345

(2) INFORMATION FOR SEQ ID NO: 4380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4380:

CTAAAGCTGn CATATGCGGC TTGCCGATGA AGCCAACCCT GCTGCTGTTG GTACAAAATT 60
 45 GTCGCTTTCA ATTTCTGCAT ACCAATCGAT GCCAGCTCTA TTTCTGACAA TATCCATATA 120
 TTTTGAAATT TTCTCTAATT CTTTGCCACT AACCTTTTCA CCATTCAACC AAAATTGATC 180
 CTGTGTTAAC TGGTCGTAA AAGTGACTTT CGTTTCAGTG TAAAATTTT CTAATGTAAC 240
 50 AGATATGCTA TTAFTCATGG AAGATTAGTG CTTTCATCTT TTTACCCCAA TATTTTATAA 300
 GTGCAATATC GTAGTGCAGG CTTGCCACTT TAACACGCAT AACTCCTAAA TCTCAACCAG 360
 ATn 363

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4381:

ACCTGAATGA CTCAAACTTG ACTTTnCGAC AATTGACTGT nCATTTTGCA TAGTTGTATG	60
nCTCCATTnC GTAATTATTA GATTGTTCG CTTACGTCTA TTGAATCATA CAGCTTTATT	120
ATAGTTAGCG TATTTCACCC TTGCACATT AAACCATGTT TAATAATCAT TGAATCATT	180
TTAAGTAAAT TAAGGAATCT ATAATGTTTCG TTAAATAAAA CTGATCCCGT TGTGGCTTCA	240
CACCCGATAG ATAGGGATTT ACAGATAAAT TCAGGTCTCT TCCACGTCCA TATTGGGAC	300
CCATCGAAAA TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACAGTAGG	360
GCCGTTGTCA CTTAACTTCT GTTTTTCCGA TGACAGCTTC	400

(2) INFORMATION FOR SEQ ID NO: 4382:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4382:

GnACTACAAA GCAATGGGGT TTGCCAGTTT CTTTATTAC TGACGAATAC TGGCAATGAC	60
ATCAGATACA TGTGGCAnCA CCAATCCATT TCTTTTCACC ATTGATAACC CAAGTATCGC	120
CTTGGGTTGC AGGGACTGTT TCAAGACCTC CCGCAACGTC CGAACCGTGT TCTGGTTCAG	180
TTAAAGCAAA GCATGTTACG CnTTCATGTG AACTGTAATT TAGGTACATA TTTCGCAATT	240
TGTTCTTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG AACACCGAGT	300
AGGG	304

(2) INFORMATION FOR SEQ ID NO: 4383:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GTGCATTATT TTGGAGAATT AGCTCAGCTG GGAGAGCATC TGCCTTACAA GCAGAGGGTC 60
 GGCGGTTCTGA ACCCGTCATT CTCCACCATT TTGATTATTA AATTATATGA ATAAGCTGGA 120
 5 GGGGTAGCGA ATGGCTAAAC GCGGCGGACT GTAAATCCGC TCCTTCGGGT TCGGCAGTTC 180
 GAATCTGCCC CCCTCCACCA TCTATATATT GGGCTATAnC CAAGCGGTAA GGCAACGGAC 240
 10 TTTGACTCCG TCACTCGTTG GTTCGAATCC AnCTAGCCCA GCCATTAGAG nCATTAACTC 300
 AGTTGGTA 308

(2) INFORMATION FOR SEQ ID NO: 4384:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4384:

AATTTTGGCC AAAACACCCA TCCGCTGTAA CTTGAGAGTG TCATTGGCAT TTATTACACT 60
 25 ATCTCCAACCT CCTAGTGGA CAACCACATC TCGTCCTTGG GGTGCATGGA ATGTTCCGTC 120
 AGCCCTGTGA ATTATTTCTT GAACTCCACC ACCTGGGGCG TTTCCAGAAC CTCTATCATT 180
 30 TAATACAGCA AATGTCGGTT GCGTTAATGC TCCTGAATTA TCGGkAGCTA CACCCTTTCC 240
 TGCTAAAGTA CCAGTAGACA ATGTAGGTAT TGGCTTGATG AGATTTtTAT CAGTAATGGC 300
 TTTAGAnAT 309

(2) INFORMATION FOR SEQ ID NO: 4385:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4385:

AAAGGTGAAA AGCACCCCGG AAGGnAGGTG AAATAGAACC TGAAACCGTG TGCTTACAAG 60
 TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTGA GAATGAACCG GCGAGTTACG 120
 50 ATTTGATGCA AGGTTAAGCA GTAAATGTGG AGCCGTAGCA nAACAGGTCT GAATAGGGCG 180
 TTTAGTATTT GGTCTAGACC GAnAACCAGG TGATCTACCC TTGGTCAGGT TGAATTCAGT 240
 AACACTGAAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA ACTGAAGGTA 300

(2) INFORMATION FOR SEQ ID NO: 4386:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4386:

TAGAATCTTC ATCAATATGA TCTAACCAAT ATTGATAAAA CCTTGATGTG TTTCGTGTCA	60
ATGACATACC ATATCGACTA GGTACCTTTT TAGAATGTTG ATTAATCAnG GCAAATATCA	120
TGGCAAGGTC ATCTTCAAAA TGATTGATT CAAGTGAAG GCATATGACG TCTCATCACT	180
ATACCCTTTT TCCCATTCTG CAAATCCACC ATAAATACTA CGCGACGCGG AACCCGGACC	240
CATTCGCGGC AATCTCGGTh AATCCTTATC TGGACAGCTG GCATGTCTAG CGGCTGGATT	300
TACAAGCTGG CTGGCTAAAG CTGGCATATG CGCTTGCCGG TTGAAGCCCA ACCTGGCTGG	360
CTGGTGGGGn ACAAATTGGT CGCTTTTCAA TTTCnGGCAT	400

(2) INFORMATION FOR SEQ ID NO: 4387:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4387:

TCAATTTATG GGGCATTATG ACTTTATATA CCTAAAATAC TATTAAGAAG TCCTGAAAAA	60
TTACATTAG CAGTTGGATT GTTCAACTTT ATTAATGATA AGTATGCAAA TAATTCACA	120
GTGTTTGCAG CAGGGGCAAT TATGATTGCA GTACCTATAG CAATCGTATT CTTGTTCTTG	180
CAACGCTATT TAGTATCAGG TTTAACAACA GGTGCGACAA AAGGTTAGTT TGAAATTCnC	240
GnGTGGGGCA GAATTGATAA AGAACCACnA ATGACGATAA AGATTAAAAG GAGGACGTTA	300
TGGATGACGA	310

(2) INFORMATION FOR SEQ ID NO: 4388:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4388:

AACATCATGC TGATGTTGTT GAATATGAAG AAGATACAAA CCCAGGTGGT GGTGAGGTTA 60
 5 CTA CTGAGTC TAACCTAGTT GAATTTGACG AGATTCTACA AAAGGTATTG TAACTGGTGC 120
 TGTTAGCGAT nCATACAACA ATTGAAGATA CGAAAGAATA TACGACTGAA GTAATCTGAT 180
 10 TGA ACTAGTA GATGAACTAC CTGAGGAACA TGGTCAAGCG CAAGGACCCA TTCGAGGAAA 240
 TTA CTGGAAA ACATCATCAT ATTTCTCATC nGGTTTAGGn ACTGAAATGG TCACGGTAAT 300
 TTTGGCGTGG 310

(2) INFORMATION FOR SEQ ID NO: 4389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4389:

TTTACCATAT CATCCACTAT TTATTAAACC TAATAAAGAT GAATTAGAAG TGATGTTTAA 60
 25 TACAACAGTG AACTCAGACA CAGATGTTAT TAAATATGGT CGTTTGTTAG TTGATAAAGG 120
 TGCGCAATCT GTTATTGTCT CGCTTGGCnG TGGATGGTGC TATTTATATT GATAAnGAAA 180
 30 TCAGTATTAA AGCAGTTAAT CCACAAGGGA AAGTGGTTAA TACAGTTGGC TCTGGTGATA 240
 GTACAGTTGC AGGCATGGTG GCTGGGAATT GCTTCAGGTT TAACGnTTGA AAAGGCATTC 300
 35 CA 302

(2) INFORMATION FOR SEQ ID NO: 4390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4390:

AAAGAGTGCg TAATAGCTCA CTAGTCGAGT GACACTGCGC CGAAAATGTA CCGGGGCTAA 60
 50 ACATATTACC GAAGCTGTGG ATTGTCCTTT GGACAATGGT AGGAGAGCGT TCTAAGGGCG 120
 TTGAAGCATG ATCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG 180
 CGAAAGACGG GTGAGAATCC CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCCTC 240

TnCTTACCA CCTATAATCG nTTAATCGTG GGG

333

(2) INFORMATION FOR SEQ ID NO: 4391:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4391:

AGTGC GTTTG TGCACa nACT TGA CTGnAAC TTAGTGCCAT TGCAGCACCA GCAACCCATG	60
GCGCAATAAG CCCAATGCAG CTATAGGGAT ACCGnCAATA TTATAGCCGA ATGCCCAAAA	120
TAGATTTTGA CGAATATTAC GAATGGTTGC TTTACTTGCA TAAATGGCTT TAGGAATAAG	180
CATCAAGTCG CCACCAAGAA TAGTAATATC AGCTGCTTCA ATGGCAACTT CTGTACCTGT	240
ACCAATGGCG ATACCGATAT CAGCTTTAAC TAATGCAGGT GCATCATTTA CACCGTCACC	300
AACCAT	306

(2) INFORMATION FOR SEQ ID NO: 4392:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4392:

TACGGTATGC ATATCTTTTA AAACCTATTC TTTTGTATT AGGACATATA AATTCATCAT	60
TAAGTTCGTC ATATTTCCAA TTTTAAGTGT TGAAAATGTC ACTTTTAAAC TTTCTAGTTT	120
TATCTTTAAT AAACATGCCA TACGTAATAA GTGGCGTTTT ATTAAATCA TCTATAATAG	180
CCATATAGTT TTGCTCACTA CCATAACCTG CATCAGCTAC AATATACTCC GGTAATAAAC	240
CGAAGGGATT TTGAATCATT GTTAAAAATG GAATTAAAGT TCTAGTATCT GTTGGGTTTT	300
GAATAGGGTC ATGGGATAAA CCAAATGnGG AATTnGCCnC AATTnGTAAA TGGAA	355

(2) INFORMATION FOR SEQ ID NO: 4393:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 364 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4393:

5 CATTCCGTAA TAAAATTACG TGGTTACAAA TTATTCAGG TTTCTTCTTT GCATTGCGT 60
 CTTTAACATA TCTTATTTCA GCACAACCTA ATATGAATGG TTTAGCAACT GGATTTATTC 120
 TTTCTCAAAC ATCCGTTGTG CTTGCTACAT TAACTGGTAT TTATTCTTA AAACAACATA 180
 10 AAACGTCAAA AGAAATGGTT ATTACAATCA TCGGCTTAGT ACTCATTTTA GTAGCCGCTT 240
 CTGTTACAGT ATTTATAAAA TAAGGAGTGT AGATGTCATG AAAAAATCAG CGGTTTAAAT 300
 GGAACCTATT CCAAAGCCAT CGCGACCAAT GGGTCATTG GATTAnTAAC GATAATGGCG 360
 15 nnGG 364

(2) INFORMATION FOR SEQ ID NO: 4394:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

25 GATTAAAACG ATTATAGGTG GTACAGGAAT ATCAACCTGT TATCCATCGC CTACGCCTGT 60
 CGGCCTCAGC TTAGGACCCG ACTAACCCAG GAnCGGACGA GCCTTCCTCT GGAAACCTTA 120
 30 GTCAATCGGT GGACGGGATT CTCACCCGTC TTTGCTACT CACACGGCA TTCTCACTTC 180
 TAAGCGCTCC ACATGTCCTT ACGATCATGC TTCAACGCCC TTAGAAGCT CTCCTAnCAT 240
 35 TGTGCCAAAG GACATGCCAC AGCTTCGGTG AATATGTTTA GCCCCGGTAC ATTTTCGGCG 300
 CATGTnCACT CGACT 315

(2) INFORMATION FOR SEQ ID NO: 4395:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4395:

50 AGCCCCAAA TGGGTATTGA AATTGAATGG TGGGnCTGA AnTGGA CTG AACCACCGAC 60
 CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT AGGCCCATTA ATTTGAATGA 120
 ACAAACATTC AAAACTGAAT ACAATATGTC ACGTTATTCC GCATCTTCTG AAGAAGATGT 180

TACGACTTCA CCCCAATCAT TTGTCCCACC TTCGACGGCT AGCTCCTAAA AGGTTACTCC 300

ACCGGCTTCG GGTGTTACAA AC 322

(2) INFORMATION FOR SEQ ID NO: 4396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4396:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60

AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120

GTTTTAGACA TAAAAAAGA nACCTCACGG TCCAACTTG CCTGGCAACG TTCTACTCTA 180

GCGGAANTGA ATTGGCTACC ATCGnCGCTA AAGACCTTTC TTGACTTGTG ACAATCGCTT 240

GCTTCTTTCC TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT 300

CTT 303

(2) INFORMATION FOR SEQ ID NO: 4397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4397:

TAAGAATATA AATGATTTTG AAAGCATTTG AAAGCTACAA CATTCTATA AAATTTTCA 60

ATAACAATTG CGCCACTAAA ACTCAAAATT TCCACCACCA ACATCCAAAT TATCAACATC 120

GCAACATAAC CAAATGTTAT AATAAATCTA TTACACAAAG AGATAAATTA CTTATGCAAA 180

GGCGGAGGAA TCACATGTCT ATTACTGAAA AACACGTCA GCAACAAGCT GAATTACATA 240

AAAAATTATG GTCGATTGCG AATGATTTAA GAGGGACATG GATGCGAGTG AATTCCGTAA 300

TTACATTTTA GGCTTGATTT TCCTATCGn TCCTTATCTG GAAAAAnCCG ACCAGGATnT 360

GCAGATGCCT GGCCAGG 377

(2) INFORMATION FOR SEQ ID NO: 4398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4398:

	TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT TGAGCAGTGT TTTTATTATC	60
10	GCCAGTTAAC ATGGGCAACT TCAATGCCCA TATCATGGCA ATTGTTTTAT AGCATCTTTG	120
	GGCATGATnT TTGACAGTAT CTGCCACTGC GATGATACCA GTTAATGAAT AATTAACAGC	180
	AATGAGCATA nCAGTTTTAC CATCTCGTTC ATAATGTGTT AAATCATCAG AAATATGCTT	240
15	AAGCAACTAA TATCATTGTC AACCATTAAAT TTACCGTTAC CAACCAATAT ATGGTGATGA	300
	TCnATCCTTC CTC	313

(2) INFORMATION FOR SEQ ID NO: 4399:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4399:

30	TGGCTATGAT CATCCAAAAT ATGGTGAATC AATTGCTGCA GCCATTATAC TTCGCGAAGA	60
	TGAACCTCAT TACGCTGAAA TTTTAAATCA ACATATGCGA AGTCGTTTAG CAGGTTATAA	120
	AGTCCCAAGA ATGTATGTAC CAGTGACACA TATGCCGTTA AACAGTACGC AGAAACCAGA	180
35	TAAACTTGCG ATTCGACAAA TGATGAATGA CAAAGTCTCG CAAACACTTT AAAGGTGATA	240
	AAAATTTTTG ACATTTAGTG TAAGCGTTTA CAAATAAAGC GTGTTGTTTT TGAATTAAAT	300
	GCATTCACA TTAGTATTCA TATTATnTTT AGGAGGAATT TATATGACAT TTGAAAAGA	360
40	ACGGGCTTAA AACATTATTC CTGAGATGTA CTAGTATGCT	400

(2) INFORMATION FOR SEQ ID NO: 4400:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4400:

	CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT TTCGTCAGAT TCAAACGTTT	60
--	--	----

55

AAAAGAGACC TCgtCTCAAC TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTGGC 180
TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 240
5 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGCTTG CGCTCTTTTC TCGTTTCGTC 300
ArATTCAAAC GtTTTCacTT CGGCCAAGGC ATTTTCTTT GTGGTTACTT TTTAATTGG 360
ACGGTTTTAG GCATAAAAAA AAAGGGGACC CTGCGGGCTC nAAAGGGGG 409
10

(2) INFORMATION FOR SEQ ID NO: 4401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4401:

TCATGTAGAC TTTCAAGAAT CGACACATGA AAATTCAAAA CATCATGCTG ATGTTGTTGA 60
ATATGAAGAA GATACAAACC CAGGTGGTGG TCAGGTTACT ACTGAGTCTA ACCTAGTTGA 120
25 ATTTGACGAA GATTCTACAA AAGGTATTGT AACTGGTGCT GTTAGCGATC ATACAACAAT 180
TGAAGATACG AAAGAATATA CGACTGACAT nnATCTGATT GAACTAGTAG ATGAACTACC 240
TGGAAGAACA TGGTCCAAGC GCAAGGnCCA ATCCGAGGAA ATTGACTGGA AAACAATCCA 300
30 TCCATATTTC C 311

(2) INFORMATION FOR SEQ ID NO: 4402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4402:

TTAACGGATT ATTTGGCAAT TCGGTTAGTT GTCGAACAAT TGCTAGTTGG TGATGAGTTT 60
45 AAGTCAGTCG CTAAGATTG TGAAAGTAGA TCGGAAATT GGTTTAAGCA AACTGTTGCA 120
TCATGGTGTT ACTACAGTGA TATGCCTAGC GATGTATTAC TACAACATGG ACGTCAATGT 180
AAATTrCAA CGTTTATTCA TTTTGGCAGC AACTATGGAA TAAAAATGTA TTTAAAAATT 240
50 TATGGCTAAT TGCCTGGGGA AATGACATAC GAATCTCAGG TTAAACAGA AAATTAAAGC 300
AGGTCCATGT nAAGTGTTGG CGGGnCGCAT 330

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4403:

TGnTCACACA TAATTTGCGG CCATATGTTG TTGGCACTGG CCGTTTTGAT TATCTGGCAC 60
 TTTGGGCCCCA TATGTTGnCA AAATACGCGC CAATTGCTTC TTTATAAGTT GTTATTTTTT 120
 TACTTTTTTCC ATCGATAAGC CATACCTCTG GATGATACAT ATGATGCCCC ATCGCAGACC 180
 AATAGCGAAA TTCACCCGTT AAAGTTTCGA GCTCTGATAA TTGTATAGAC CATTGATGAT 240
 TTTGAGGTGG TACTTGATAT AAATTTTCIT CTCTAAAATA TTCATTTAAA ATGCGTTCGA 300
 TAGCCGCATA CGCTGCCATG TTGTATTAAT CnTTAATTG 340

(2) INFORMATION FOR SEQ ID NO: 4404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4404:

TTAACATATA TTTTGGGACC TTAGCTGGTG GTCTGGGCTG TTTCCCTnnA CGAACACGGA 60
 CCTTATCACC CATGTTCTGA CTCCCAAGTT AAATTAATTG GCATTCCGAG TTTGTCTGAA 120
 TTCGGTAACC CGAGAGGGGC CCCTCGTGCC AAACAGTGCT CTACCTCCAA TAATCATCAC 180
 TTGAGGCTAG CCCTGAAAGC TATTTCGGGA GAGAACCAGC TGATTTCCAG GTTCGATTGG 240
 AATTTCTCCG CTACCCTCAG TTCATCCGCT CACTTTTCCA ACGTnAATCG GTTCGGTGCC 300
 TGCCATT 307

(2) INFORMATION FOR SEQ ID NO: 4405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4405:

AnACTTGAGT GCAGAAGAGG AAAGTGGAAAT TCCATGTGTA GCGGTGAAAT GCGCAGAGAT 120
 ATGGAGGAAC ACCAGTGGGC GAAGGCGACT TTCTGGTCTG TAACTGACGC TGATGTGCGA 180
 5 AACGTGnGGG ATCAAACAGG ATTAGATACC CTGGTAGTCC ACGCCGTAAA CGATGAGTGC 240
 TAAGTGTTAG GGGGTTTCCG CCCCTTGAGT GCTGnCAGCT AAACGCATTA AGCACTCCGC 300
 CTGGGGGAGT GACGGACCGC AAG 323
 10

(2) INFORMATION FOR SEQ ID NO: 4406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4406:

AATTATGGGA TGCAATGGGA TACGAACGTG TTAAAACACG TATGGAAGAC GAACTTGGAG 60
 ACTTACCACA ATGGATTAGT GATTTAGATG GTGGCTTTTA TAAACAAGAT GAGACCATTG 120
 25 AATATGCAAC ACCTATTTCT CACTTCGTAA AAGATGAACT TTGGGATAAA GGTGATGCCA 180
 AACTTTCCGT AACTCATGAT GATCAACTGT TACTGAAATT ACAAAGTAAA AATAATGTCA 240
 TTACCGATGA ATTCAACGGT GCGTTAGTTG ATGCGATTGA TTTACTGGGA AATGACCCTT 300
 30 ACnChAGnAT GGGTA 315

(2) INFORMATION FOR SEQ ID NO: 4407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4407:

CACCACCTCC CTACCTACTC GCGCCCCATC ATAAAATAGG TGGACAGGAA TATCAACCTG 60
 45 TTATCCATCG CCTACCCTGT CGCCTCAGCT TAGGACCCGA CTAACCCAGA GCGGACGAGC 120
 CTTCCCTCTGG AAACCTTAnT CAATCGGTGG ACGGGATTCT CACCCGTCTT TCGCTACTCA 180
 CACCGGCATT CTCACCTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT 240
 50 AGAACGCTCT CCTACCATTG TCAAAGGAA TnCACAGCT TCGGTAATAT GTTTAGCCCC 300
 GGTACATTTT CGGCGCATGT CACTCGACTA nTG 333

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4408:

ATTTAATGAA GTGCTTGTTA ATGAACCAAG CGCTAAAGAT ACTGTTGAAA TTTTAAAGG	60
TATTCGCGAA AAATTCGAAG AACACCATCA AGTAAAATTA CCAGATGACG TATTAAAGC	120
ATGTGTTGAC TTATCAATTC AATATATTCC ACAACGATTA TTACCAGATA AAGCAATCGA	180
TGTGTTAGAT ATTACAGCAG CACATTTATC TCGCAAAGT CCCAGCTGTC GATAAAGGTT	240
GAAACTGAAA AACGGATTTC TGGATTnGA AAATGATAAA CGTAAAGCAG TAAGTGCTTG	300
AAGGGATTTT AAAAAAGCTG ACGGACCATT CCAAATTGG AATCCAAATC nntTACCAGG	360
TTAAATTGG GAAAATGGTT AATTGGTGGG ACC	393

(2) INFORMATION FOR SEQ ID NO: 4409:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4409:

GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC	60
TACTAAACTC GTTGCCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA	120
GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTA GGCATAAAAA AAAGAGACCT	180
TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG	240
AAGTnAATTG GGCTACCATC GTCGCTAAAG ACCTTTCCTG ACTTGTGGAC AATCGCTTGG	300
CnTCTnTCCT CTCCTTCGG	319

(2) INFORMATION FOR SEQ ID NO: 4410:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATTAAACAT TTCATTTTAA TCAATGAGAC TAAATACGC CTAACCTCGT TAACTTTTAA 60
 AATGTATTAA AATTCTAAAG TTTCTTTTGC TTTTTCnATG ATGTCATTTT TGTTTGGTAA 120
 5 CCAAACATTT TCAGCTTGAG TGAATGGATA AATTGTATCT GCCTGCCTGA ACTCTTCCAA 180
 TAGGTGCTTC TAATGAAAGG ATTGCACGTC ACTTAATTCA GCTAACAACT GCTGCACCAA 240
 CACCAGCTTG CnGTTGTGCT TCTTGACTAC AACTGACGA CCAGTTTTTC AACTGAGCAC 300
 10 AATTGTGCAC ATCGATTGGT GACAG 325

(2) INFORMATION FOR SEQ ID NO: 4411:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4411:

GAGTTGGACA ATGCCGAAGC GTGAGCAAAG TTTTACCAT GCATGGTTGC ATTTAGCGCA 60
 25 ACATGACCAT AGTTTTACTA AAGCACAGCG CCAAGTGATT AAAGGCTTAC CCAATGATCC 120
 TGAAATGACG ATAGAGTCAG TATTAECTCA TTTTCAATA GATCAGGAAG ACTAnCAAGC 180
 TTATGTTGAA GGACATCTTT TGGCGTTACC GGGTThGGCA nGTATGTTGT ATTACCGTTC 240
 30 ACCACAGCAT CACTTTGAAC CACCTTTGTT AACGGGTIAA TTGGCCATTC GGGTAAGTTG 300
 TCCGACCATT GCCAAGTGGG TGATGAGTTh AGGCCAGTCC GCAAAGATT GGGAAAGTAG 360
 TCCGAAAAT GGGTTAAGCC AACCTGTTGC CATCCAGGGG 400

35

(2) INFORMATION FOR SEQ ID NO: 4412:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4412:

GATATATGGC AGCTCAAAGG AATGGGTTTC AGTTGAAGTG AAATTATCAC AGTCACTAGA 60
 CCCGAGCACA TTATTTCAATC TCACTGACAA TGAGGCAGGA GATCGCTTTT ATATGCGTTT 120
 50 GAATGATAAT CGAACGTCAT ATTTTGGCTA CAAAGCAATT CAATTATTCA AAAATAATTC 180
 TAAAAATAAA CAATCTATTT TAAAGACTG GGGAAAATTA AACATAACCA TCACCATTTA 240

55

CCATAAATCA GATGATGAAT GGCGnGAGTT TGGCCTAAAn CATTGGAAT ACCCGGAGTT 360
TTAATTCCA 369

5 (2) INFORMATION FOR SEQ ID NO: 4413:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4413:

15 TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 60
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTGTTG CGCTCTTTTC TCGTTTCGTC 120
 20 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 180
 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCnACTCTA 240
 GCGGAAGTAA GTGGGCTACC ATCGTCGCTA AAGACCTTTC TTGGACTTGT GGACAAncGC 300
 25 TTGCGTCCTT ncCTC 315

(2) INFORMATION FOR SEQ ID NO: 4414:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4414:

GACCATCTCC TAAGGCTAAA TACTCTCTAG TGACCGATAG TGAACCACTA CCGTGAGGAA 60
 AGGTGAAAAG CACCCCGGAA GGAGGTGAAA TAGAACCTGC AAACCGTGTG CTTACAAGTA 120
 40 GTCAGAGCCC GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT 180
 TTGATGCAAG GTTAAGCAGT AAATGTGGAG CCGTAGCAGA ACAGGGTCTG GAATAGGGCG 240
 45 TTTAGTATTT GGTCGTAnCC GnAAACCAGG TGATCTACCC TTGGTCCAGT TGAAGTTCAG 300
 GTTnACACT 309

(2) INFORMATION FOR SEQ ID NO: 4415:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

{xi} SEQUENCE DESCRIPTION: SEQ ID NO: 4415:

5 TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 60
 TCTTTCCTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT 120
 CTCAAATGCG GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAAnTA 180
 10 AGTTCGGACT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 240
 TGACCTCCTT GGCTATAGTC ACCAGnACAT ATGAATGTGA AATTTATACA TTCAAAACTh 300

(2) INFORMATION FOR SEQ ID NO: 4416:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

{xi} SEQUENCE DESCRIPTION: SEQ ID NO: 4416:

25 AGAAAAATAA GCGAACTGnA ATAAATAAAG ATTCAATTAA CGCATCAGTA TTAGGATTCA 60
 CTCTAAAACG ATTAATAGTT TTATAAGAAG GTGTTTGATC TTGAGCTAAC CACATCATTC 120
 GAATACTGTC ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT TGAGTATATG 180
 30 CATATAAGAT GATTTTTAAC ATCATCTTTG GATGATAGGA TGTTGCGCCA CGATGATGTC 240
 TGAATTCATC GAATTTGCTA TCAGGTATCG TTTCAACAAT TTCATT 286

(2) INFORMATION FOR SEQ ID NO: 4417:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

{xi} SEQUENCE DESCRIPTION: SEQ ID NO: 4417:

45 TTTGATAAAA ATGGGCCATC GTCACGAGCT TCAACAATTC GTTTCGCAAC GTTTTCGCCA 60
 AGCCCAGCCT GATATATTAC ATGAGGAGCG GTGCAAATGT TGTTAGAAAT TAAAGATTTA 120
 GTGTATAAAG CGAGCGATAG AATCATACTA GATCATATCA GTCTAAAAGT AGATAAAGGC 180
 50 GAGAGTATTG CCATTATAGG TCCATCAGGT AGTGGTAAAA GTACATTTC AAGCAAATA 240
 TGTAATTTGT TTAGTCCAAC TAGTGGAGAA CTTTATTTTA AAGGTAAACC CTATAATGAT 300

55

GTTTGGTGGA ACGnATTGGA nGATAACCAT GGATAATTCC

400

(2) INFORMATION FOR SEQ ID NO: 4418:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4418:

GTATTTACAA TCAAACAAAG CAAAAGTATT CAGATGCCTC AGATAAAGCT TGGGCGCATT	60
CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA CGCATATAAA AGTGCAAAGG	120
GTTGGCTAAT AGATATGGCT AATAAATCGC GCTCGAAATG GGATAATATT TCTAGTACAG	180
CATGGTCGAA TGCAAAATCC GTTTGGnAAA GGAnCATCGA AATGGTTTAG TAACTCATAC	240
AAATCTTTAA AAGGTTGGAC TGGGGATATG TATTCAAGAG CCCACG	286

(2) INFORMATION FOR SEQ ID NO: 4419:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4419:

CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCCT CAACGCCCTT AGAACGCTCT	60
CCTACCATTG TCCAAAGGnA TGCnCACAGC TTCGGTAATA TGTTTAGCCC CGGTACATTT	120
TCGGCGCATG TCACTCGACT AGTGAGCTAT TACGCACTCT TTAAATGATG GCTGCTTCTA	180
AGCCAACATC CTAGTTGTCT GGGCAACGCC ACATCCTTnT CCACTTAACA TATATTTTGG	240
GACCTTAGCT GGGTGGTCTG GGCTGTTTCC CTTTCGAACA CGGACCTTGA TCACCCCATG	300

(2) INFORMATION FOR SEQ ID NO: 4420:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4420:

GGTGAGCGGA GCGAACTCnC GTTAAGGAAC TCGGCAAAAT GACCCCGTAA CTTCGGGAGA 120
 AGGGGTGCTC TTTAGGTTAA CGCCAGAAAG AGCCGCACTG AATAGGCCCA AGCGACTGTT 180
 5 TATCAAAAAC ACAGGTCTCT GCTAAACCGT AAGTGATGTA TAGGGGCTGA CGCCTGCCCCG 240
 GTGCTGGAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAACT ACGAATCGAA GCCCCAGTAA 300
 ACGGcGGCCG TAACTATAAC GGTCTAGACG ATCTGC 336

10 (2) INFORMATION FOR SEQ ID NO: 4421:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4421:

GGnCACCTC GTGCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG GCTAGCCCTA 60
 AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTTCGATT GGAATTTCTC CGCTACCCTC 120
 25 AGTTCATCCG CTCACTTTTT AACGTAATCG GTTCGGTCCT CCATTCAGTG TTACCTGAAC 180
 TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT AAACGCCCTA 240
 TTCAGACTCG CTTTCGCTAC GGCTCCACAT TTA CTGCTTA ACCTTGCATC AAATCGT 297

30 (2) INFORMATION FOR SEQ ID NO: 4422:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4422:

GTACATCGTC TAATAATAAG TTGACGATAT CTTGCAATGC ATCTTTATCT AAATGTAAGA 60
 ATTCAACGAT GCCGTTGAAG CGGTAAAGGA ATTCAGGGCG GAAGAATTTT TTCATTTTCT 120
 45 GCATAATATC TTTTCTTCA GCGTCATTGC CATTGCCAAA GCCAGCATTT GATGTACAAA 180
 TAATAATTGT ATTTTAAAG TTGATGACAT TACCTTGACC ATCAGTCAA TTACCATCAT 240
 CCATTACTTG TAATAACAAT GTTAAATTG TGGATTGCTT TTCGATTCA CAATAGAATG 300
 50 ACTGAGAnGG GATACGGCGA CTTTTCAGTA AACGGATTGA ATGGCATCAT AnCCACATAC 360
 CAGCGTGGAC CATCATTTTG GAACAGCGTG GGCACATATC 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4423:

AAGTTGAGTC GCATAGCTAG TATGAAACGT GGTGTGCGCA TGGGAACAT CAAGCTTTGA 60
 AGATGTGGTA CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT 120
 CCATTAAATG AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT 180
 AAAATTGCCT ATAAATTTTT AGCACATAAA ATAAGAnGnG CCAACCATTG TTAGACTATA 240
 ACAACGGTTG GCTCTTTAAT TGTAAAAAGA AAACCATACG CTATGGTAGT T 291

(2) INFORMATION FOR SEQ ID NO: 4424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4424:

AACTGCCACC ACCTGGGGnC GTTCCAGAA CCTCTATGCA TTTCAATCAC AGnCAAATGT 60
 GCGGTTGACG TTCAATGACT ACCTGCAATT CATCGGTCAG CTCACACCCT TTACCTGnCT 120
 AAAGTACCAG TAGACAATGT AGGTATTGGA CTGTCATGAG CATTTTTATn CAGTAATGGG 180
 CTTTAGATAT TTTATTAATA CCGGCCAATC ATGCTATTCA AACCGCCAAT AGCTTTATTA 240
 GCAACATTTT TACCTAAATC AGCCGCAGCT CTTCCCATGT CTTTACCAAT ATCTCTAATC 300
 CAATCATATG TTTTGCATA GCCATTTTCT AAAACCATTA AATACTGATT TAGCGTTAGA 360
 CCATGCCGAA CTGAAATTG CATCAAAACG ATCGTGGGCT 400

(2) INFORMATION FOR SEQ ID NO: 4425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4425:

AGATGATAAA AGCAACAGGT GGT TTTGCGA AAAGTGAAGT ATGGCGTCAA ATGATGTCAG 120
 ATATATTTGA CACAGAGTTA GTGGTTCCTG AAAGTTATGA AAGTTCATGC TTAGGTGCCT 180
 5 GCGTGCTCGG ACTTAAAGCT GTAGGTGACA TTGAAGATT TTCAATCGTT TCATCGATGG 240
 TCGGTGCCAC AAACAATCAT ACGCCGATTG AAGAAAATGC ACTGTTACCA AGAnTCGAAT 300
 10 CCATTnTTAT CATTAAAGCGT CTTAnCAGAG ATATGACAAT 340

(2) INFORMATION FOR SEQ ID NO: 4426:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4426:

CTGAAGATGA TAAAGATGCA GATGGTGGCG AGTTGCACGT AACAAATTACG GATCATGATG 60
 ATTTACACT TGATAACGGA TACTTCGAnG AATTATCATC AGACAGCGAT TCAGACTCAG 120
 25 ATAGTGACTC AGACAGCGAC TCAGACTCAG ACAGCGACTC AGACTCAGAC AGTGATTCAG 180
 ATTCAGACAG CGACTCAGAT TCAGATAGCG ACTCAGATTC GGACAGCGAT TCAGACTCAG 240
 30 ATAGCGACTC AGATTCAGAT AGCGATTCAG ACTCAGACAG CGACTCAGAT TC 292

(2) INFORMATION FOR SEQ ID NO: 4427:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4427:

AACAGTGCTC TACCTCCAAT AATCATCACT TGAGGCTAGC CCTAAAGCTA TTTCGGAGAG 60
 AACCAGCTAT TTCCAGGTTG GATTGGAATT TCTCCGCTAC CCTCAGTTCA TCCGCTCACT 120
 45 TTTCAACGTA ATCGGTTCGG TCCTCCATTC AGTGTTACCT GAACTTCAAC CTGACCAGGG 180
 TAGATCACCT GGTTTCGGGT CTACGACAAA TACTAAACGG CCCTATTCAG ACTCGGCTTT 240
 50 CGCTACGGTT CCCACATT TA CTGGCTAAAC CTTGCATCAA AATCGGTAAC TCGnCGGGTC 300
 ATTCTAn 307

(2) INFORMATION FOR SEQ ID NO: 4428:

(A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4428:

10 GACCATACAT CGTCATCGTT TGCACCGTCA AATACTGGTG ATGCAACGTG AATACCAAGA 60
 TTTTtagcag CCATACCTAA GTGTAGCTCT AATACTTGTC CGATGTTTAT ACGAGATGGT 120
 ACACCAAGAG GATTTAACAT GGATATCGAT CGGGACGTCC ATCTGGTGAA GTGAAGGCAT 180
 15 ATCTTCTTCA GGAACAATC TTGAGGAAAT GGACACCTTT GTTGACCATG TCGGACCACA 240
 CATGCTTATG CACCAACATG GAATTTTACG TTTTGGAAh GATGATTATT ACACGTnACT 300
 AATTGGTTTA CACCAGGTGG AnaATGTTAT CGTCGGCCTT GCTTCACGAT TGGA 354

20

(2) INFORMATION FOR SEQ ID NO: 4429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4429:

30

GTGnACTATC nGCTTGTCTA TGATAATATT ATTCTTTGTA CTGTTTTAAA AGATATTAGA 60
 CTAAAACCTAA AAACAGCAGT AAGATGATTT ATGATTAAAA CTATCTTACT GCTGTTCACT 120
 35 TTTTATAATA CTTCTGAATG TCTCATTAT ACTTCTAGTC ACAGATTTAA ATAATCAAAA 180
 GTGCACATTA TTAAATATC AATTTACAC TCAATGCGGC TCATCGCATT CATTTCTTGT 240
 CTAGCAACGT TCTACTCTAG CGGAACGTAA GTAGCTACCA TCTCGCTAAG GAACTTTCTT 300
 40 GACCTGGTGA CAACCGCTGC GnCTnTCTCT CTTCGGCTCT CGCTTACTCC ATTTAGCTCC 360
 ACTAAACTCG TCGGGCCCTT CCCGTTTCGC AGATCCAACG 400

40

(2) INFORMATION FOR SEQ ID NO: 4430:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4430:

55

ACCATTACACA CCTTGACAGC CACATAACAT AACTAAGTTT AAGATnGGGG GATAAATCGT 120
 ATCTGAGTTA AACCAATGGT TAATACCCGC ACCCATGATA ATCATTGAAC GCCCTTCAGT 180
 5 ATCGATAGCG TTTTGCGCAA ATTCTTTCGC TACTTGAATG ACAACACTTT GTTTTACGCC 240
 TGAAATGGCT TCTTGCCAAG CAGGTGTATA TTTTGATTCT GCATCGTCGT AA 292

(2) INFORMATION FOR SEQ ID NO: 4431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4431:

20 TGAGCCGnAC ATCGAGGTGC CAAACCTCCC CGTTGATGT GAACTCTTGG GGGAGATAAG 60
 CCTGTTATCC CCGGGGTAGC TTTTATCCGT TGAGCGATGG CCCTTCCATG CGGAACCACC 120
 GGATCACTAA GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCATC AAGCTCCCTT 180
 25 ATGCCTTTAC ACTCTATGAA TGATTTCCAA CCATTCTGAG GGAACCTTGA GCGCCTCCGT 240
 TACCTTTTAG GAGGCGACCG CCCAGTCAAA CTGCCCCGCT GACA 284

(2) INFORMATION FOR SEQ ID NO: 4432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4432:

40 TATCATTGTG GTACGATAAG GCATATGTTG TACCTATGnA TGGTGGAAGA GCCTTCAGTT 60
 GTCGCTGCAG CTAGTTATGG TGCAAAGCTA GTGAATCAGA CTGGCGGATT TAAAACGGTA 120
 TCTTCTGAAC GTATTATGAT AGGTCAAATC GTCTTTGATG GCGTTGACGn TACTGGAAAA 180
 45 TTATCAGCAG ACATTAAAGC TTTAGAAAAG CAAATTCATA AAATTGCGGn TGAGGCATAT 240
 CCTTCTATTA AGCGCGTGTG GTGGTTACCA CGTATAGCGA TTGATACATT CCTGGCCACC 300
 50 AGTTCTATCT TT 312

(2) INFORMATION FOR SEQ ID NO: 4433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4433:

	CGGTACTCGT TAAGGCTGAG CTGTGATGGG GAGAAGACAT TGAGTCTTCG AGTCGTTGAT	60
10	TTCACACTGC CGAGAAAAGC CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC	120
	AGGTAGTCAA GATGAGAATT CTAAGGTGAG CGAGCGAACT CTCGTTAAAG AACTCGGCAA	180
	AATGACCCCG TAACTTCGGG AAAAAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC	240
15	AGTGAATAAG CCAAGCGAC TGTTTTATCC AAAACACAGG TCTCTGCT	288

(2) INFORMATION FOR SEQ ID NO: 4434:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 336 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4434:

	GGACCGAACC GACTTACGTT GAAAAGTGAG CGGATGAACT GAGGGTAGCG GAGAAATTCC	60
30	AATCGAACCT GGAGATAGCT GGTCTCTCTn nAAATAGCTT TAGGGCTAGC CTCAAGTGAT	120
	GATTATTGGA GGTAGAGCAC TGTTTGGACG AGGGGCCCT CTCGGGTAC CAATTTCAGA	180
	CAAACCTCCA ATGCCAATTA AATTAACTT GGGAAATCAG AACATGGGTG ATnAAGTCCG	240
35	TGTTTCGAAA GGAAACAGCC CAGACCACCA GCCAAGTCCC AAAATATATG TTTAATGGGA	300
	AAAGGTGTGG CCTTTGCCCA GGACAACCAA GAAGTT	336

(2) INFORMATION FOR SEQ ID NO: 4435:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 304 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
45	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4435:

50	ATTGACGCCG CATTTTACG GAATGGGAAT AAAGCGACAC AAACCGTCAC GTCnGTGTTG	60
	GTGTCATGAC AAGGTAATGC GAGTGATCTG ATGTATGGCT TATCATGGCA ATCTGTTATG	120
	GnCTGACTGA TCGGACGATG TATCATTCGC CAATTCGTTT ACTTGTCGTT ATTCAGGCAC	180

55

AATCATTGGC TGC GTTTTAA TGAGCGTAAT GAGGAAGGGG CGTTTAAAAA GTTGGATTTA 300
ACGA 304

(2) INFORMATION FOR SEQ ID NO: 4436:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4436:

AATATACTCC GGTAATAAC CGAAGAGTTT TGAATCATTG TTAAAAATGG AATTAnAGTT 60
CTAGTATCTG TTGGGTTTTG AAATAGGTCA TAGGATAAAA CAAATnGAGA ATTTGTCGCT 120
ATTGTAAAT TGTATCCTGG CTTAAGTTGG CCATTTTTCA TATGGTCTTC CTTCAATTCTC 180
ATAAAAGTTG CATCATGGAT CAGTTTTAGA AAAGCTATTT CTATCTTTAA GAATCGATT 240
TTGTTCTTCA TATTTATTTT TTCTTTCGGA ATAATCATCA AATTTATnTT TGGAACCTCT 300
TAATC 305

(2) INFORMATION FOR SEQ ID NO: 4437:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4437:

ATCGTTTAAA TCAGTTAGTA AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAAATA 60
TTATAGAAAA CATCAAAGGA TGTTAAGAAA TACAATTTAT TACCCAGCAT TTAATAATGG 120
TGCTATAGAA GGAATTAATA ATAAGATAAA ATTAATCAAG TGAATTTCTT TTGGTTACAG 180
AAATTTCAAC AACTTTAAAG CACGTATAAT GATGATTTTC AGCTTGTACA AGGGGGAnAA 240
AAGGAnGnCA ACCAAGCCCA ATAATGGACT GGCCGCCTAA TATTAAAAAC TCTAAAGGTT 300
GTATTTTAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA CCCGTTAAC 359

(2) INFORMATION FOR SEQ ID NO: 4438:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4438:

5 ACTTACAGTT ATTTTAACTT GGnCAGAATC CATCATCCAT AAGTTCGAAA TGTTGTAAAA 60
 CATAAACCTT GnAAACGGCA ACATTTTTGG GTCCTTCTCC ATCATTTTAT TTAAAAGCGC 120
 ATTATGATCA ATATCATGCC CAATTAACCT TCCAGCAATT TCCATAGTAT GTTCTGAGGT 180
 10 ATTGTTAAAA AGGAATCGCC CAGTATCACC GACGATACCA AGATATAAAA CGCTCGCGAT 240
 ATCTTTATTA ACAATTGCTT CATCATTAAT ATGTGAGATT AAATCG 286

(2) INFORMATION FOR SEQ ID NO: 4439:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4439:

TCGCTTGACT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAnCTCT ACTAAACTCG 60
 25 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTCT 120
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 240
 30 GCTACCATCG ACGCTAAGAA CCTtCTTGA CTTGTGACAA aTCGCTTGCT TCTTCCTCn 300
 TCTTCGGTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCTCTTT TCTCGTTTCG 360
 35 TCAGATTCAA CAGTTTTCAT TCGCCAAGCC ATTT 394

(2) INFORMATION FOR SEQ ID NO: 4440:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4440:

TAATAGGTTT GAGGTGGAAG CATGGTGACA TTGGCAGCTG ACGAATACTA ATCGATCGAA 60
 GACTTAATCA AAATAAATGT TTTGCGACAA TGCAACTTTT ACTTACTATC TAGTTTTGAA 120
 50 TGTATAAATT ACATTCATAT GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTTCCTATG 180

55

TAGAACGTTG CCAGGCAAAA AATGGATGCG ATGACCGCAT TGAGACCGCA GcNtn

295

(2) INFORMATION FOR SEQ ID NO: 4441:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4441:

TTTCATAAAA AGATTTCAAA CGCGTTCATC AAnCCTCGTC GCAGGTCTTT CGAACACTAG 60
 CGATTATTTC tTATGAATTC AAGCTTATTT AAAACTCTTT ATTCaCTCGG TTTTGCTTGG 120
 TAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA CAATTTCTTT TTAGTCAAGC 180
 GCTCGCATAC TGCTTTATTT TCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 240
 TAAATAAACA TTCAAACTG AATACAATAT GTCACGTTAT TCCgCATCTT CTGAAGAAGA 300
 TGTTCGGAAT ATATCCTTAG AAAGGAGGTG ATCCnGCCGn ACCTT 345

(2) INFORMATION FOR SEQ ID NO: 4442:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

AATCATTGTC AAAACTACGT TCTGGTAAAC AAGGACAACC CGTTTGAACC ATTGGCCCAC 60
 ACCATTTGAT AGGCAGnCAT GTGCGCAATG GACATCCACA TAGTTGCGTA ATGTTTCATA 120
 CGTCATTGCT CAAATCATTG ATGACTAGCG CAACATGATT ACCTTGTCGT GnGCACCTTC 180
 ATTAAAGnAA CTTATGATAG ATTTATTTCC CGGGACATTA AGCATTGCA TCGTTAACAT 240
 GCGTATTGCA CCCAATTTAG AAGTTCCTCC GTGCCGTTTG GTATATCACA AATTTGTAGT 300
 GTATCTTGGA TGC 313

(2) INFORMATION FOR SEQ ID NO: 4443:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4443:

AGCATGGTGT TTCTCAGATT GTCGGATGTA TAAATGTGTA TGTTATGTTT TAATTTTTTCC 60
 5 CAGTCTTTAA AAATAGATTG TTTATTTTTA GAATTATTTT TGAATAATTG AATTGCTTTG 120
 TAGCCAAAT ATGACGTTTC ATTATCATTC AAACGCATAT AAAGCGTATC TnCTGCCTCA 180
 TTGTCAGTGA GATGAAATAA TGTGCTCGGG GTCTAGTGAC TGTGGATAAT TTCACCTCAA 240
 10 CTGAAACCCC ATTCCCTTTG AGCTGCCCAT ATATCTCTTT GGACAATATC GGTCCCTCTA 300
 ATACGGnCCG TAGnCCATTC CATTTCAATT CTTTTC 336

(2) INFORMATION FOR SEQ ID NO: 4444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4444:

CAGACTGGGA TATTTATAAA ACGTTGGCAA AAGCATTTTC AGAAATGGCA AAAGACTATT 60
 25 TACCTGGAAC GTTTAAAGAT GTTGTGACAA CTCCACTTAG TCATGATACA AAGCAAGAAA 120
 TTTCAACACC ATACGGCGTA GTGAAAGATT GGTGGAAGGG TGAAATTGAA GCGGTACCTG 180
 30 GACGTACAAT GCCTAACTTT GCAATTGTAG AACGCGACTA CACTAAAATT TACGACAAAT 240
 ATGTCACGCT TGGGCCTGTA CTTGAAAAAA GGGGAAATTT GGAGCACCTG GGGGTAAGTT 300
 TCCGTGTCCA GTTGAACCAT TATGGAGGAn TThAAAAAGT ATGTTAAGGG ACCTGGGAGT 360
 35 TGAATACCCA ATGGATnGAT TCCCGTGAAG AGCCGAATCC 400

(2) INFORMATION FOR SEQ ID NO: 4445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4445:

TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA GCTCGCGTAC 60
 50 CGCTTGTAAT GGGCGAACAG CnATCGCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 120
 GCCGACATCG AGGTGCCAAA CCTCCCCGTC GATGTGAACT CTTGGGGGAG ATAAGCCTGT 180

CACTAAGTCC GTGCTTTTCCA CCCTGACTAC GGA CTGTGThA GGTCTGCGGC ATTCAAGCTT 300

CCCTTGATGG CCTTTGACAC TGCTTATGGA ATGnATTTG 339

5 (2) INFORMATION FOR SEQ ID NO: 4446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4446:

15 CAATTTTAAG TGTGAAAAT GTCAC TTTTA AACTTTCTAG TTTTATCTTT AATAAACATG 60

CCATnCGTAA TAAGTGGCGT TTTATTAAAA TCATCTATAA TAGCCATATA GTTTTGCTCA 120

20 CTACCATAAC CTGCATCAGC TACAATATAC TCCGGTAAAT AACCGAAGGA TnTTTGGAAT 180

CATTGT TAAA AATGGAATTG AAAGTTCTAG TATCTGTTGG GTTTTGAAAT AGGTCATAGG 240

ATAAACAGG GTGAGAATTT GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAT 300

25 TTTTnCATAG GTCTTCCT 318

(2) INFORMATION FOR SEQ ID NO: 4447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4447:

TTTTGAAATT CTCTATGTTG GGGCCCCGAC TATAATTGAA AAATGCTTGT TACAAGTGCA 60

40 TTTTATTTC A GTCAACTACT AACAAATATAA CATTGTGGAG CCCAGAnCTT TGATTAATGT 120

ATATGAAAAT CAAAGTAATG CTTATGTATG ATTATTTCAA ATATTTTACA TACATGAACT 180

TTTCCAATGT ACGATACTAT TATTATAAAG CGCTCGCTAA GATTTTACGA TGATTAGAGG 240

45 GTAAAAAATG AACGATCAAT GGTnTAACCA TTTAATTGG 279

(2) INFORMATION FOR SEQ ID NO: 4448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4448:

5 GACACCGGCA TTCTCACTTT CTAAGCGCTC CACATGTCCT TACGATCATG CTTCAACGCC 60
 CTTAGAACGC TCTCCTACCA TTGTCCAAAG GACAATCCAC AGCTTCGGTA ATATGTTTAG 120
 CCCCAGTACA TTTTCGGCGC AGTGTCACTC GACTAGTGAG CTATTACGCA CTCTTTAAAT 180
 10 GATGGCTGCT TCTAAGCCAA CATCCTAGTT GTCTGGGGCA ACGnCACATC CTTTTCCTACT 240
 TAACATATAT TTTGGGACCT TTAGCTGGTG GTCTnGGGCT GTTTTCTGnA TTGAACACGG 300
 GA 302

(2) INFORMATION FOR SEQ ID NO: 4449:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4449:

25 CGTTGGTATA TAGAGGGCAA CCGTCACCTG ATAAAATGTG GACACAGTTT TTACAAGAGG 60
 TTAAGGAAAT GAGTTTGGAG GCATACGAGC ATCAAGAATA CCCATTGAA TGTTTAGTAA 120
 ATGACTTAGA TCAATCACAT GATGCCTCAC GGAATCCATT ATTTGATGTC ATGTTAGTAC 180
 30 TACAAAACAA TGAnACGAAA TCATGCTCAT TTTGGGCATA GTAAATTTAA CACACATTCA 240
 ACCCAAATC AGTGACGGGC GGAAATTTGG ATTTnTCCTT TTCCATCATT GGAAGAAGGA 300
 35 TCGCGGATGA CCTAATAnCA ATCCAATTAT CGGGGTATAA ATACCGGATT TTATAACCA 359

(2) INFORMATION FOR SEQ ID NO: 4450:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4450:

45 GATGACAAAA TTTGCTTGAA AACCGAAATG GATGGTCATC ATTGACTGnA TCAAGGTACA 60
 TCATTCTTTG GTGCTTATGC ATTTAGACAT TATACAAAA CAATACTTT ATAGGGCAAC 120
 50 CTTATGGGGT TCTATCGGCT ATACATTACC TGCAACATTA GGTTCACAAT TAGCAGACAA 180
 AGATCGTCGn TAACTTATTA TTAATTGGTG ATGGCTCATT GCCAACTAAC TGTTCAGCT 240

GCTATACGGT AGAACGACTT ATTCCC

326

(2) INFORMATION FOR SEQ ID NO: 4451:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4451:

GAAAACATCA AAGGATGTTA AGAAATACAA TTTATTACCC AGCATTTAAT AATGGTGCTA 60
 TAGAAGGAAT TAATAATAAG ATAAAATTAA TCAAGTGAAT TTCTTTTGGT TACAGAAATT 120
 TCAACAACCTT TAAAGCACGT ATAATGATGA TTTTCAGCTT GTACAAAGGA GAAAAAAGA 180
 AGACAACCAA GCCCAATAAT GGA CTGGCCG CCTAATAATA AAAACTCTAA AAGTTGTATT 240
 TTAAAAATAG GTCTTTAAAT TATATACCCC CCCCATTTGG GTGGAGAACC GGTA AACCAT 300
 GCCTAGGTGC CTAACCTCCn ATAATGGnAC CCCTCCTTAC CATTTGGGCC ATGGGGCCAA 360
 TAAAGCGGGG GGCAATTGGG G 381

(2) INFORMATION FOR SEQ ID NO: 4452:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4452:

TTAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG TTATTAATCT TGTGAGTGTT 60
 CTTTCGAACA CTAGCGATTA TTTCTTATGA ATTCAAGCTT ATTTAAACT CTTTATTCAC 120
 TCGGTTTTGC TTGGTAAAT CTATATTTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 180
 CTTTTTAGTC AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAATAT TTGAATGTTA 240
 AATAAACATT CAAACTGAA TACAATATGT CACATn 276

(2) INFORMATION FOR SEQ ID NO: 4453:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4453:

GGCGAAACCG CGTAGCGTTT TTAAAGTCTG ATGTGAAAGC CCACGGTCAA CCGGGAGGGT 60
 5 CATTGGAAAC TGGAAACTT GAGTGCAGAA GAGGAAAGTG GAATTCCATG TGTAGCGGTG 120
 AAATGCGCAG AGATATGGAG GAACACCACT GAGCGAAGCG ACTTCTGGT CTGTAAGTGA 180
 CGCTGATGTG CGAAACGTGG GGGATCAAAC AGGATTAGAT ACCCTGGTGA GTCCACGCCG 240
 10 TAAACGATGA nTGCTAAATG TTAGGGGGTT TCCGCCCCCTT AGTGGCTGCC AGCTAnACGC 300
 ATTGAAGCAC TGCCGCCTGG GGAGTGACGA CCGCAAnTTG A 341

(2) INFORMATION FOR SEQ ID NO: 4454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4454:

ACnCTCCCCA AAGTCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA GTGnCCAAGG 60
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTTAT AAGTCAAACG 120
 CTCACATACG GCTTCGTTTT CATTATTTTA AATGCTCATT TACATAAGTA AACTCTGCTT 180
 30 TAAAATAATT TAACTCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT TTAAACGCGT 240
 TATTAATCTT GTGAGTGTTT TTTTGAACAC TAGCGATTAT G 281

(2) INFORMATION FOR SEQ ID NO: 4455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4455:

ATGTCTTCAC TTATACTTCT AGTCACAGAT TTAAATAATC AAAAGTGCAC ATTATTAAAA 60
 TATCAATTTT AACTCAATG CGGCTCATCG CATTCAATTC TTGTCTAGCA ACGTTCTACT 120
 50 CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 180
 GCTTGCTCTT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTGTTG 240
 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCnGT 279

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4456:

```

10  ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT      60
    CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT      120
    AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT      180
15  ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TnTCGTCAGA TTCAAACGTT      240
    nTCACTTCGC CAAGCCATTT TTCTTGTGTT TACTT                                275
  
```

(2) INFORMATION FOR SEQ ID NO: 4457:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4457:

```

30  ATCCGATTCA CAAAGCACAT CATCATATAC AAGTCAGTCA ACAAGCCAAA GTGAATCCAC      60
    ATCGACATCA ACGTCACTAA GCGATTCAAC AAGTATATCT AAAAGTACGA GTCAATCAGG      120
    TTCGGTAAGC ACATCAGCGT CATTAAAGTG TTCAGAGAGT GAATCTGATT CACAAAGTAT      180
35  CTCAACAAGT GCAAGTGAGT CAACATCAGA AAGTGCGTCA ACATCACTCA GTGACTCAAC      240
    AAGTACAAGT AACTCAGGAT CAGCAAGTAC GTCAACATCG CTCAGTAACT CAGCAAGCGC      300
40  AnTGGAATCC GATTTGTCGT CAACATCTTT AAGTGGATTC AACATCTGCG TCnATGCCAA      360
    AGnnGTGAAT CCGATTCA CAAGCACATCA GCATCCTTAA                                400
  
```

(2) INFORMATION FOR SEQ ID NO: 4458:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4458:

AGTCGCTGTC TGAATCTGAA TCACTGTCTG AATCCGAATC GCTATCTGAT TCTGAGTCGC 120
 TATCTGAACC TGAGTCGCTG TCTGAGCCTG AGTCACTGTC TGAATCCGAA TCCGGATCCG 180
 5 GGTCTGGGGn TGGTTCCGGT TCTGGGTCTG GGACTTGGTT CTGGATCTGG CGTTGGTTCT 240
 GGGTCTGGGG TCTGGACTGG TTCTGGGGTC AAACGGCGGC CCTGGAGTGG GGTCTTTCGG 300
 AATnAACGGC GGAATCACCA TCAAGCAACT TnCAACAACC ATAACGAAAA A 351

10 (2) INFORMATION FOR SEQ ID NO: 4459:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 271 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4459:

ATCCTGCAGT TGATCAGTAT GGTGATATTA ATTTAGTTAA TACGAACGCG TCATCTACAA 60
 GTGAAATCAT TTACGATTTA ATCTCACATT TTAATGATGA AGCAATTGTT AATAAAGATA 120
 25 TCGCGAGCGT TTTATATCTT GGTATCGTCG GTGATACTGG GCGATTCCTT TTnACAATA 180
 CCTCAGAACA TACTATGGAA ATTGCTGGAA AGTTAATTGG GCATGATATT GATCATAATG 240
 CGCTTTTAAA TAAATGATG GAGAAGGnCC C 271

30 (2) INFORMATION FOR SEQ ID NO: 4460:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4460:

ACTGTGGATT AATATTATGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTCGACTAC 60
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 120
 45 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAA ACTAGATAGT AAGTAAAAGT 180
 GATTTTGCTT CGCAnAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 240
 GCCACATGTC ACCATGCTTC CACCTCGAAC CTATnAACCT CAG 283

50 (2) INFORMATION FOR SEQ ID NO: 4461:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 base pairs
 55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4461:

CTTCTACAAG TCCTGAATAT ACTTATGAAT CTCTTCTTTC GTGTATGCAA ACTGACGTTG 60
TAATTTAAAT AACGTCTCAT CTTTCCATTG CGAATCTTGA TATTGTATAT TTTCAAAATC 120
AAAGTCAACT TTATGGTTAT CAATCCACGC TTTATATGGT AATTCTCCAG CAATCGCACC 180
TTTTAAATCA TTATTTTCAA TGACTTTATT CTGTAAAAT CAACAAnCAT AACTTTCCnG 240
GATTCAATTG ACCTTTAAAA GCAACATTAC TTCC 274

(2) INFORMATION FOR SEQ ID NO: 4462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4462:

GGCTGCTAAA AATCTTGGA TTCACGTTGC ATCACCAGTA TTTGACGGTG CAAACGATGA 60
CGATGTATGG TCAACAATTG AAGAAGCTGG TATGGCTCGT GATGGTAAAA CTGTACTTTA 120
TGATGGACGT ACAGGTGAAC CATTGATAA CCGTATTTCA GTAGGTGTAA TGTACATGTT 180
GAAACTTGCG CACATGGTTG ATGATAAATT ACATGCGCGT TCAACAGGAC CATATTCACT 240
TGnTACACAA CAACCACTTG GCGGTnAAGC G 271

(2) INFORMATION FOR SEQ ID NO: 4463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4463:

GCGGCTCATC GCATTCATTT CTTGTCTAGC AACGTTCTAC TCTAGCGGAA CGTAATTAGC 60
TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 120
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGCTTG CGCTCTTTTC TCGTTTCGTC 180
AGATTCAAAC GTTTTCACCT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTAnTTTGAC 240

55

(2) INFORMATION FOR SEQ ID NO: 4464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4464:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60
 TTCCTTGTCTG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTGCGGC ACTGTCTCAA 120
 CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG GACAGGACGG 180
 GAAAGACCCC GTGGGAGCTT TTA CTGGTTA GCCTGGATAT TGGAAATTCG GGCACACTTG 240
 GTTACAGGAT AGGTAAGGAG CCTTTTGAA ACGTTGAGCG CTACTTTAnG TTGGGAGGCG 300
 CTGGTnGGGA TACTTACCCT AACTGTGTTT GGCTTTTCTn AACCGGCACC ACTTATCCTG 360
 G 361

(2) INFORMATION FOR SEQ ID NO: 4465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4465:

CTGTATGTAC ACCACCAATC GGTTTAGGTT TAGCAACGTT TGTTCAAAAG TATAAATTCA 60
 ATCATTCCGA AAGAGAAATG GGTAAGGCTT CCTTCACTAT GGGACTATTT GGTATTACTG 120
 AAGGTGCTAT TCCTTTTCGA GCCCAAGATC CATTGCGCAT TATACCTGCA AACATCATTG 180
 GTGCAATGAT TGCATCAGTC ATTGCAGCCA TTGGTGGTGT CGGCGATAGA GTCGCACATG 240
 GnGGTCCCAA TCGTGGCTGT ATTAGGTGGG TTTTGT TTTTnTTTT TT 292

(2) INFORMATION FOR SEQ ID NO: 4466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GCAAACAAAA CAGTATTAGT AGATTATGAA AAATATGGTA AGTTTTATAA CTTATCTATT 60
 AAAGGTACAA TTGACCAAAT CGATAAAACA AATAATACGT ATCGTCAGAC AATTTATGTC 120
 5 AATCCAAGTG GAGATAACGT TATTGCGCCG GTTTTAACAG GTAATTTAAA ACCAAATACG 180
 GATAGTAATG CATTAAAGA TCAGCAAAAT ACAAGTATTA AAGTATATAA AAGTAGATAA 240
 TGCCnCTGAT TTATCTGAAA GTTACTTTGT GGAATCCCGG AAACCTTGAG GGTGGCCCCCT 300
 10 AATAnTGG 308

(2) INFORMATION FOR SEQ ID NO: 4467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4467:

AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCATAATAA TTACAGTATA TCGGAAGAC 60
 25 AGGATTTCGAA CCTGnGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120
 CCCGTATAAT TAAAGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180
 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATAGTG CCGAGGACCG 240
 30 GAATCGAACC GGTACGTGAT CACTCACCGC A 271

(2) INFORMATION FOR SEQ ID NO: 4468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4468:

TGTGTTAGGT ATTACATCAT CACATTTATC TCGTCAAAG TCCAGCTGTC GATAAAGTTG 60
 45 TAAACTGTAA AAACGCAATT TCTGAATTAG AAAATGATAA ACGTAAAGCA GTAAGTGCTG 120
 AAGAnTATAA AAAAGCTGAC GACATTCAAA ATGAAATCAA ATCATTACAA GATAAATTAG 180
 AAAATAGTAA TGGTGAACAT ACTGCTGTTG CTACAGTTCA TGATATTTCA GATACTATTC 240
 50 AACGATTAAC TGGTATTCCA GTTTCTCAAA TnGATGATAA CGnTATTGAA CGTTTAAAAA 300
 ATATTT 306

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

```

10  GGGTTTATTAA CAGCATTCTT ATCAGCATT TTGTTTATAA CTTCTGTGTG      60
    AAGCGCAATA TTACAATTAA AATGCCGAAA GAAGTACCGC CGAATATTTC ACAAGTATTT      120
    AAGGACTTAA TTCCATTTTC AGCGGTAATC ATCATTCTTT ATGCATTAGA TTTAGTCATT      180
15  CGCAACAGCT TTAAATCAAA TGTCGCGGAA GGTATTTTAA AATTATTCGA ACCATTATTT      240
    ACAGCAGCAG ATGGATGGGT TGGTGGTCAC CATTTAACnT TGGGnGCnTT TGCATTAATC      300
20  CTGGGTTTGT AGGGTAATCC ATGGGTCCG                                329
  
```

(2) INFORMATION FOR SEQ ID NO: 4470:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4470:

```

    AACTGGGTGA TAAGGTCCTG TTCGAAAGGA AACAGCCAG ACCACCAGCT AAGGTCCCAA      60
    AATATATGTT AAGTGGA AAA GGATGTGGCG TTGCCAGAC AACTAGGATG TTGGCTTAGA      120
35  AGCAGCCATC ATTTAAAGAG TCGGTAATAG CTCCTAGTC GAGTGACACT GCGCCGAAAA      180
    TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTGGACAAT GGTAGGAGAG      240
40  CTTCTAAGGA CTTGAAGCTG ATCGTAAGAC TGTGGAGCGn TAGAATGAGA TGCCGTGTGA      300
    TAGnAAAGAC GGTGAGATCC CTCCACCGTT GACTAAGTTC CAGAGGAAGC TCTCCGTCGG      360
    GTTATCCGGT CCTAAGnGAG GCCGACAGCT AGGCATGGnT                        400
  
```

(2) INFORMATION FOR SEQ ID NO: 4471:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TCATTTTTAG AAATATTATC TTTTCCACAA ATCATTGAT ATAAAGTGCG ATCATTGCCC 60
 GCGAGTGCTG CCATTGACAC TAGCTGTTGC GTATCATTTT TGGCTAGCAC TTCGGGATAC 120
 5 TTTCTTAGCT GAACAGTTAG ATGACCTAAT TGATCTTTGA AAATATCATT ATCTTGACCC 180
 ATATATGACC ACCAAGCTGT TTCATCACAA ACCATGACAT ACTTAGCTAG TGCTTCATCT 240
 TTTTCTATAA GCTGACGTAA TAATTGTCTG CTTGTCTCTC GTTTTnCATG TACCGCGAGG 300
 10 CGTAAnCTTA AAGGGCCCCAA GGnCG 325

(2) INFORMATION FOR SEQ ID NO: 4472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4472:

CCCGTCTTTC GCTACTCACA CCGGCATTCT CACTTCTAAG CGTCCACAT GTCCTTACGA 60
 25 TCATGCTTCA ACGCCCTTAG AACGCTCTCC TACCATTGTC CAAAGGACAA TCCACAGCTT 120
 CGGTAATATG TTTAGCCCGG TACATTTTCG GGGGCGAGTG CACTCGACTA GTGAGCTATT 180
 ACGCACTCTT TAAATGATGG GCTGCTTCTA AGnCAACATC CTAGTTGGTC TGGGGCAACG 240
 30 CCACATCCTT TTTCCACTTT AACAnATATT TTGGGA 276

(2) INFORMATION FOR SEQ ID NO: 4473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4473:

AATTTnCCAA AAAATTCAAA TGGCTCATTT ACCAAAAGGT AAACCTCCGC CTTTAAnTTT 60
 45 CTTaATGCAT kGTCTAACAA cCGCTTTCTT TAAAGaAATA GATTGTCAAG CGCTCGCATA 120
 AGCAATATCA CTTTAACCAA AAAATATTTG AATGTTAAAT AAACATTCAA AACTGAATAC 180
 AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG 240
 50 AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTtGTTA CGACTTCACC CCAATnCAT 300
 TGTCCACCT TCGACGGGCT AGCTCCGAAA AGG 333

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4474:

TATAAAATAG CAACGTTATT CCAATTATCT TAATGGTTAT CTTATCCTCA ACTAAATTGG 60
 AGGAATCACT ATGACAATTA ATAAAGTAAC CGTTCTTGGC GCAGGCACAA TGGGCGCTCA 120
 ACTGGCAGCA CTTTTGTGA ATGCTGGACT TAAAGTAAaA CTATTAGATA TTGTAGTGGA 180
 CAAAAACGAT CCAATCTCA TTGCGAAAAA ATCTTACGGT TAAATTACAG GTAAGAAACG 240
 GCCGCTACTA TTCGnCTTAA ATCTAGCGGT CATTTACCAT ATGGTATTTT GATGTGCTTG 300
 GTAAATGTGT GCTGTTTGAT ATCGA 325

(2) INFORMATION FOR SEQ ID NO: 4475:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4475:

TAACTGCGGC AACATTTGCT TGTTTTGGTT ATGGTTGGCA CATTGATGTC GGCATTCATA 60
 CAATACATCT AGTATTATCT GGTATTTTGG ATCGTTATCC AAAGTTAAAT AATGATTATT 120
 GGACATTGGG GTGAGTTTAT CCCATTCTTC TTAGAAACGT ATGGATGAAG CTTATTCGCT 180
 GACATTTnAC CACCCTGTAA GCTATACTTT AAAAATAAAT TTTAATCACA CCGAGTGGCA 240
 TGTTAACGAG CCACAGTTTG ATTTAGTCAA GAAGnAGAGG TATTGTAGAn TCTTATGCGC 300
 TGATATCC 308

(2) INFORMATION FOR SEQ ID NO: 4476:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4476:

CCTACCTATC CTGTACAAGC TGTGCCGAAT TnCAATATCA GGCTACAGTA AAGCTCCACG 120
 GGGTCTTTCC GTTCTGTGCG CGGGTAACCT GCATCTTCAC AGGTACTATG ATTTCAACCGA 180
 5 GTCTCTCGTT GAGACAGTGC CCAAATCGTT ACGCCTTTTCG TCGGGGTCGG AACTTACnCG 240
 ACAAGGAATT TCGCTACCTT TAGGACCGTT ATAGTTACGG 280

(2) INFORMATION FOR SEQ ID NO: 4477:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4477:

20 GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG 60
 CTTACTCATT TAGCTCTACT AAACGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 120
 25 GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA 180
 TAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA 240
 ATTGGGCTAC CATCGnCGCT AAAGACCTTT CTGACTTG 279

(2) INFORMATION FOR SEQ ID NO: 4478:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4478:

40 GAGGATCCCG GAATGTTGAA CCCATCACTG ATTCTGGTTC ATAATTATCC ATCATCCATA 60
 ACGTTAAATC TAAAGCGTGT GTACCGATAT CGATTAATGG TCCTCCACCT TGAGCTTCTT 120
 45 CGTCTAGAAA GACACCCCAT GTTGGnACTG CTCGACGACG AATGGCATGT GCCTTTCCGA 180
 AGTAAATGTC TCCTAAGTCG CCACGTTGCG CTGCTTGATG TAAAAATTGA CTATCTGCTC 240
 GGAnACGATT TTGATAACCT ATTGTTAATT TT 272

(2) INFORMATION FOR SEQ ID NO: 4479:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4479:

5 GAAATTGGGA ATCCAATTTT nCTTTGTTGG GGGCCATCCC CAACTTGCAC ATTATTGTAA 60
 GCTGACTTTT CGTCnCTTAC TGTGTTGGGG CCCTCACCCC AACTCGCATT GCCTGGTAGA 120
 ATTTCTTTTC GAAATTCTCT GTGTTGGGGC CCCTGACTAG AATTGAAAAA AGCTTGTTAC 180
 10 AAGCGCATTT TCGTTCAGTC AACTACTGCC AATATAACTT CGTAGAGCAT AGAATATTGA 240
 TTTATGTCCC AGCCTGAGTT AATTT 265

(2) INFORMATION FOR SEQ ID NO: 4480:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4480:

25 ACATAGAAAT GCCACTTTTA CAAACAAATG AATATTCGTC TTTTACATC ATTACGCATA 60
 ATAAAAGAAG CTAAGCAACA TGTAACCGT TGTCACCTAA CTTCTTGTTT TTCCGATGAC 120
 AGCTTCTATT TAGAGAATGT CATGATTATT TTATATTCAC TTCAATGTTA TCAATATTAG 180
 30 TGCCATCTAT GACGCTGCGC ATACGATGCT CTGGCAGTTT TTTGGTGGTA ATTCAAACGT 240
 ATATTCCCAC CGTTTTTCATT TAATAACGTT GTCCnGGACC CATGTACCGT AAGATATGTT 300
 TTCATAGTGG TTCCAATTAA ACCAnTCTTC AGGAACCTCn TAG 343

35 (2) INFORMATION FOR SEQ ID NO: 4481:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4481:

ACTGCGGCAA TAGCAGCAGC ACCACAAACG GCCTGTGTCC GGACACCTAG GTAATAATGC 60
 GCATGTTTTT GTCACCATGC CAACAGTTTG TTGACAAAGA GCATCATTAC AATACTGGAA 120
 50 AATAACGACA CCTACATCGA TGGCTAATAG TTTACTACCT TGACCGATAA TATCGAATAT 180
 ATTGAGTTTA AGTCCATATA GGATGATTGC AAATCTTAAAT AAATATTTAG ATGAAAACGT 240

55

(2) INFORMATION FOR SEQ ID NO: 4482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4482:

GAGGCATCCC CGGGCCTTCC TTCCCAACAG TCGCTTCAAA GTTTGGTGGT AAACCTGnTA 60
 CATCAAATTA TCGGTGCTAC TGtnAGGTAC GTGTAATCTT CGCTATTTTA TTAGCCGTAT 120
 CACATCAAGT GGCTTCCCTA CTGGAACCAA TTTGCTATTC GCCTTATTAT CAGGTGCAGG 180
 ATGGGGATTG GGACAAATCA TTACATTTAA AGCGTTCGAA TTAGTCGGCT CATCTCGTGG 240
 CCATGCCAGT CACAACAGCA TTCCAATTAT TAGGCGCATC TTTATGGGG 289

(2) INFORMATION FOR SEQ ID NO: 4483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4483:

AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC ATCGCATTCA 60
 TTTCTTGCTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT CCTCGCTAAG 120
 AACCTTTCTT GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT 180
 CATTTAGCTC TACTAAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTnC 240
 ACTTCGCCAA GnCATTITTTT TTTG 264

(2) INFORMATION FOR SEQ ID NO: 4484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4484:

CTGTACCACC TATAATCGTT TTAATCGATT GGGGGACGCA TAGGATAGGC GAnGTGGCGA 60

TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA 180
 NAAGCCTCTA GATAGAAAAA GGTGCCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240
 AATTCTAAGG TGAGCGAGCG A 261

(2) INFORMATION FOR SEQ ID NO: 4485:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4485:

ATGCAGCTAT TATTTTTGAC AGATTCCATA TCGTTCAACA TTAAATAGA GAACTTAATA 60
 AGTATCGTGT ACAAGTTATG AATGAATACC GTAATAAAAA AGGACCTGAT TATACAATTT 120
 TTAAGAATAA CTGGAAAGTC CTATTGATGG ATACTAGTAA AACCATATTT AGTAAATACA 180
 GATGGANTAA ATCTTTTAAG GCTTATAAAC GCTCATCTGA CATTGTAGAN GTCATGCTTT 240
 CAAAAGACGA TATACTACGA C 261

(2) INFORMATION FOR SEQ ID NO: 4486:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4486:

AGCAACATGA TGCACTTCTC GTGTCTCACC AGATTTAGCG ACTAACTTG TAGACATACG 60
 TAAATCTGCT TTAATAAGTA ATTAATGCAC ATGACTTATT GCGAGTAACA TCGGCATTGC 120
 AAAGCCATTG CTATCAACTA ATCCACTATC ATCTAACACT AGANTTTGAG CGCCTTGCTT 180
 TACAGCATTG ACTGCTTCTC GGCCTAATGC TTCTAACGCA TCTTCCAAAT CCCCTTCATA 240
 TACCGTTGAT AAATAAGTTA 260

(2) INFORMATION FOR SEQ ID NO: 4487:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4487:

5 ATGAGGTGCA TAGGGATAAA ACAGnnAGCA GCAATTTGTC GCTATTTGTA AATTGTATCC 60
 TGGCTTAAGT TGGCCATTTT TCATATGGTC TTCCTTCATT CTCATAAAAG TTGCATCATG 120
 ATCAGTTTTA GAAAAGCTAT TTCTATCTTT AAGAATCGAT TTTGTTCTT CATATTTATT 180
 10 TTTTCTTTTCG GAATAATCAT CAAATTTATT TTTGAACTTC TTAATCTTAG TTCTTTTTTA 240
 CGGGTCTGTT TTCCAATTG AGTACTATCC TCGTCCCCA ATAGAATGAA TTAAACCTT 300
 CCGATTTCCT TTAAnC 316

(2) INFORMATION FOR SEQ ID NO: 4488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4488:

25 CACTTTTACT GCTAAAACGT CAATTGTTGA TGAGTCGTGT TTTATCTCAA GATGTGTTAC 60
 TCAAAAAGTT ATAGAAGAAG CTACTAAAGT TAAAACAGAG ATTGATACTG CCAGAAGATA 120
 30 ACTGTATCTC TCCATCTACT GTAAGTCCGT ATTAGAACTA AAGCGGCTAA TTCATTACGA 180
 ATTAAACCTT TTAATTGTTT GCCAGACACA TCGCTATGGA TGAATTTAAA GCGTnAAAAT 240
 GTACTGGATC ATGAGTTCAT TTTTATAGnT ATGTACnCAT GTGTATAGTA TTTAGAAATA 300
 35 GACTCAA 307

(2) INFORMATION FOR SEQ ID NO: 4489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4489:

50 TTGGCAAATG TCATATAACT AGTAACATGA TCATCGACAT CAAATTTAGT ATGATCAAAT 60
 GTTCCCCAAT CATTAAATTG ATTCGGTTGT TTGCTCAATT GATTATATGT TTTTCCTAGC 120
 ACTTCATGCG GCACCATATC TTTACCTAGT AGCCCCACAA AGATAAGTCT AACAAGTGGC 180
 55 ACCATAATCG ATAAACTACC GCCACCTGCA CGCTTATGGT AAAACACCCA GCCAGCACTT 240

TAGCAGTATG CCACnCCGGn GACGATATGG TAGCGACGTA AnAA

344

(2) INFORMATION FOR SEQ ID NO: 4490:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

15	CCCAACCGGC ACATTGTTGT AAGCTGACTA TATGTCACCTT CnTGTGTTGG GGCCCCCTGTC	60
	TTCGACTGGC ACTGCTCCCT CAGGAGTCTC GCCATTAATA CTACGTATTA ACATGTAATT	120
	TTACTTTTAA ATACTTTTAA AAAATAAGAC ACTTTGGTCC AACTTAAGCC AGGGATACAA	180
20	TTTACAAATA GCGACAAATT CTCAATTTGT nTTATCCTAT GGACCTATTT CAAAACCCAA	240
	CAGGTACTnA GTAACTTTGA ATTCCATTTT TTAACAATGG ATTGCAAAAT GACCTTACGG	300
	TTCATTTGAC CGG	313

(2) INFORMATION FOR SEQ ID NO: 4491:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4491:

35	AGGTCTGACT CTAGAGGATC CCCGATGAGT TTAAAGAAAA ATATCAAACA CCTGAATTAT	60
	ATTTTAAAGC TTGGCAAGGT TTTTACCACG AGGTTCCACAA TGAGCCAGAA CGTGATGAAG	120
40	TAATGCGTTA TATTCTGACT TTCTTAAATA ACAGCGTCAA TACAATGGGC TTTATTGTTG	180
	AAGATGACGA AATTGTAGAA ATTTAATATT CTAAAAAGGT TGGGACATAA ATCCCTAAAA	240
45	AACAGCAGTA AGATAATTTT CCATTAGAAA ATATCTTACT GCTGTGChCh A	291

(2) INFORMATION FOR SEQ ID NO: 4492:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

GCCGTCTCAG CCTTGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAATACT 60
 ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACTTAAAAAA ATAAAACACT TTGCCCAACT 120
 5 TACACTACCA ATAGAAACTG CTGTTAGAAT TCCTCAAAAT GATATTTTCGC GATATGTTAA 180
 TGAAATTGTT AAAAAGATAG CTGATAGCGA GATTTCGATGG AATTCAGACA TCATCGTGGG 240
 CGCAACATCC TATCATCTAA AAATGATGTT AAAAATCACC TGCATATTGC ATATACTGCA 300
 10 ATCTGGAATT TTCTGGGCCG TGAGAATGAG AAAAATnGAC nTCATGAACA GTGATTGCGA 360
 ATGGATGTGG GTTAAGCTnC AAGATTCAAA CACCTTGcNT 400

(2) INFORMATION FOR SEQ ID NO: 4493:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4493:

25 TGATCCAGAG ATTTCCGAAT GGGGAAACCC AGCATGAGTT ATGTCATGTT ATCGATATGT 60
 GAATACATAG CATATCAGAA GGCACACCCG GTAGAACTGA AACATCTTAG TACCCGGAGG 120
 AAGAGAAAGA AAATTCGnTT CCCTTAGTAG CGGCGAGCGA AACGGGAAGA GCCCAAACCA 180
 30 ACAAGCTTGC TTGTTGGGGT TGTAGGACAC TCTATACCGA GTTACAAAGG AnGACATTAG 240
 ACGAATCATC TGAAAGGTG AATCA 265

(2) INFORMATION FOR SEQ ID NO: 4494:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4494:

45 CATTACTAAA AAAGATAATC AAGGTATGAT TTCACGCGAT GTTTCAGAAT ACATGATTAC 60
 TAAGGAAGAG ATTTCCCTTGA AAGAGCTTGA TTTTAAATG AGAAAACAAC TTATTGAAAA 120
 ACATAATCTT TACGGTAACA TGGGTTTCAGG AACAATCGTT ATTAAAATGA AAAACGGTGG 180
 50 GAAATATACG TTTGAATTAC ACAAAAAACT GCAnGAGCAT CGTATGGGCA GACGTCATAG 240
 ATGGGCCCTA TATTGATACC ATTGGAGGTG AATnTAAATA ACCATGCACT CTC 293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4495:

ACTTACAAAG TTCTGTGAAC CAAGTACCAT CAACTGCTGG TATGACGCAA CAAAGTATTG 60
 ATAACTATAA TGCGAAGAAG CGTGAAGCAG AAACTGAAAT AACTGCAGCT CAACGTGTTA 120
 TTGACAATGG CGATGCAACT GCACAACAAA TTTCAGATGA AAAACATCGT GTGCGATAAC 180
 GCATTTAACA GCATTNAAAC CAAGCGAAAC ATGANTTTAA CTGCAGATTA CACATGCCTT 240
 AGGAGCAAGC AGTGCA 256

(2) INFORMATION FOR SEQ ID NO: 4496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4496:

GTCATCAGAA ACCCTTGTC CACAAGGCTT GTATTTTTTA TACTTATTTT TTAAATTAAA 60
 TTCATCATT TCTAATTTAA AACAAATATAC TAAACGTTTC ATAATTATCG CCTGTACAAT 120
 ACGCACAAAA ACATGTCTTG AAACGCCTTT CATTACTCTA AATATACCAA TATACTTTTT 180
 ATATCGTTTC GATTCTGAGT ATTTTCAGACG ATTTTCTGCA TAAAAATAAA CGTGTTCCTCA 240
 GGCAATATAT TGCA 254

(2) INFORMATION FOR SEQ ID NO: 4497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4497:

AATCGGCTGT CTGATTCTGA ATCGCTATCT GAGTCCGAAT CGATATCTGA ATCCGAGTCG 60
 CTATCCGAGT CTGAGTCGCT ATCTGAATCC GAGTCACTGT CGGAGTCGGA ATCACTATCT 120

GAGTCACTGT CGGAATCTGA ATCGCTATCT GAATCCGAAG TCACTGGTCG GGAATCTGAG 240
TCACTGTnGG AATCTGAATC GCTATCTGA 269

(2) INFORMATION FOR SEQ ID NO: 4498:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4498:

CACCCCGGCA CTATAAAAT GGAGCAGAAG ACGGGATTTCG AACCCGCGAC CCCAACCTTG 60
GCAAGGTTGT ATTCTACCGC TGAAGTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC 120
CCACGCCGTA AGCTTAGhAT ACCTCAAGTC TAGTGCGTCT GCCAATTCCG CCACACCCGC 180
AAATGGTGAG CCATAGAGGA TTCGAACCTC TGACCCTCTG ATTAAAAGTC AGATGCTCTA 240
CCAAGTGAGC TAAATGGCTC TThCAGGTGC CGG 273

(2) INFORMATION FOR SEQ ID NO: 4499:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4499:

GTAGTAAAC GCATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT CACGGCAATT 60
TAGGGATTAA TATCAAGAAT GACGCTATTG CATCGAATGG TTATATCACA CCAGGTGTTT 120
TTGAATATTA AAAGGAGAAT CGATTTGAAG TGCnnCATAA GACAATACCG ACTTATCAAA 180
TCAACGAAGG AGACAACTA GCTCAATTGG TTATCGTGCC TATATGGACA CCTGAACTAA 240
AGCAAGTGGG GGAATTCGAA GTTGTTCaNa CGTGGAGAAA AGGCTCGGAG AGCGGGTGAA 300
AGCATCTTAG TCGA 314

(2) INFORMATION FOR SEQ ID NO: 4500:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4500:

ATTGTAAGGC TATCATGTCA AAGATTATAA CAATAAATCT GGTGAGATT TGGTGGCGGG 60
 5 GCGATGGAAG CTATCTATTT GACCATCCAT TTGGCAAAGG TTTGGGAGTT ACACAGGTGG 120
 ACTTAACTTT AATGGCGGTC GTCACATATGG TATCGACTTT GGTATGCCTA CAGGAACGAA 180
 CCATTTATGC TGTTAAAAGG CGGTATAGCT GATAAAGTAT GGnCTGATTA CGGTGGCGGT 240
 10 AATTCTATAC AAATTAGGAC CGGTGCTAAC GAATGGAnCT GGTATATGCA TTTATCTAnG 300
 CATT 304

(2) INFORMATION FOR SEQ ID NO: 4501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4501:

TTCCTTCATT CTCATAAAG TTGCATCATG ATCAGATCAG TTTTAGAAAA ACTATTTCTA 60
 25 TCTTTAAGAA TCGATTTTTG TTCTTCATAT TTATTTTTTC TTTCGGnATA ATCATCAAAT 120
 TTCTTTTTGA ACTTCTTAAT CTCAGTTATT TTTTACGGG TCTGTTTTCT AATTTGAGCA 180
 30 CAATCTTCGT TCTCAATAAG AATGATTTAA ATCTnCGATT TCTTTATCTA AATGGACTAC 240
 CAATTAAATC TAT 253

(2) INFORMATION FOR SEQ ID NO: 4502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4502:

AGTTCGGTCC CTATCCGTCG TGGGCGTAGG AAATTTTnGA GGAGCTGTCC TTAGTACGAG 60
 45 AGGACCGGGA TGGACATACC TCTGGTGATC CAGTTGTCGT GCCAAnGCAT AGCTGGGTAG 120
 CTATGTGTGG ACGGGATAAG TGCTGAAGAT GCTTAAGCAT GAAGCCCCC CAAGATGAGA 180
 50 TTTCCCAACT TCGGTTATAA GATCCCTCAA AGATGATGAG GTTAATAGGT TCGAGGTGGA 240
 AGCATGGTGA CATGTGG 257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4503:

ATACGTTTAA TACACAAAA ACTGCAAAGC ATCGATGGCA GACGTCATAG ATGGCACTAA 60
 TATTGATAAC ATTGAAGTGA ATATAnAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA 120
 TCGGAAAAAC AAGAAGTTAA GTGACAAGnT TTACATGTTG CTTAGCTTCT TTTATTATGC 180
 GTAATGATGT AAAAAGACGA ATATTCATTT GTTTGTAAAA GTGGCATTTC TATGTCTTAA 240
 AAGTGACGAA ACTTCAAATG TGCCAAGTGT 270

(2) INFORMATION FOR SEQ ID NO: 4504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4504:

TACCTTGACC GAAGTTCTTA CCTACATCAC CTAAATTAAT GACATGTCCA CCAGTCATAT 60
 ACTCTAATCC ATGGTCGCCG ATACCTTCAA CGACAACATC TACACCACTA TTTCTAATAC 120
 AGAATCTTTC TCCTGCACTA CCGTTAATAA ATGCCTTACC ACTTGTCGCA CCATAGAATG 180
 AGACGTTACC AGCAATAATT TCATTTTGTC GTTCTTCAAA AGGTGCTTTG ACAATGACCG 240
 TACCACcGn T 251

(2) INFORMATION FOR SEQ ID NO: 4505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4505:

AGAAGTTAAG CTCCTTAGCG TCGATGGTAG TCGAACTTAC GTTCCCGCTA GAGTAGAACG 60
 TTGCCAGGCA AATGACAAAT CGGAGAATTA GCTCAGCTGG GAGAGCATCT GCCTTACAAG 120

TAGCTCAATT GGTAGAnCAC TGACTTGTA TCACTAGGTT GGGGGGTCAG TCCTCTGGCC 240
GGCACCATCT TTTGnCCATA 260

(2) INFORMATION FOR SEQ ID NO: 4506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4506:

TTCTTTAGTA GATACTAAGG CGTTATTAGA CGCATTAGAC AATGGTGTGA TTAAAGGTGC 60
AGCACTTGAT ACGTATGAAT TTGAACGCAA ACTTTTCCCA AGTGATCAAA GGGGCAAAAC 120
ACTGAACGAT CCATTGTTAG AATCGTTGAT TGACAGGGAA GATGTCATAT TAACACCACA 180
TATTGCGTTT TATACTGAAG CTGCAGTTAA AAATCTATTG TCGTGCATTA GGTGCAACAT 240
TAGGTGTATT GCAGCTTGGG GAACTTnGnT ACGGGTAAAT TTAAAATCGG CTGTGGGTAT 300
TTTGGnTTTT GGG 313

(2) INFORMATION FOR SEQ ID NO: 4507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4507:

GnCAATACGG CCAATTCCTA AGATTGCTAC TTCTGGGTGG ATTGATAACT GGAGTGAACC 60
ATTGTCCACC AGCTGnAACC GATATTACTG ATTGTGCATG TAGCACCTTT CATTTTCATCG 120
GCTGTTAATT TACCATCACG TGGCTTTAAC AGCTAATTCA TTAATTTTCAT CTGAAATTTG 180
GGAAAATAGA CTTACGGATC AGCATGTTTA ACAACAGGTA CTAATAATCC TCTATCAGTG 240
TCTGCTGCAA TT 252

(2) INFORMATION FOR SEQ ID NO: 4508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4508:

CATCGAACCA GATGTACTCG CACTTGTGTA GTCTGATGTT GAATCACTAA CACTATCAGA 60
 5 TAATGACGTT GAATCACTCA TACTTGTGTA TGTACTTGTC GAAAGCGACA TACTTTGTGA 120
 ATCACTAGTA CTTGTACGCA TCGAAGTACT AGTTGAAGCT GATGTACTAC GAGAGTCACT 180
 TGTGATGTT GATGTACTTG CTGATCCTGA TGCACCTGTA CTTCTTGATG TGCTTTGTGA 240
 10 ATCGGATTTT GCTCGTGCnT GGTACTnG 268

(2) INFORMATION FOR SEQ ID NO: 4509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4509:

CGAGAGTGCG TTAATTCGGT TACTGCTATC ACgTAAGGGG CGGAAACCCC CTAACACTTA 60
 25 GCACTCATCG TTTACGGCGT rGACTACCAG GGTATCTAAT CCTGTTTGAT CCCCACGCTT 120
 TCGCACATCA GCGTCAGTTA CAGACCAGAA AGTCGCCTTC GCCACTGGTG TTCCTCCATA 180
 TCTCTGCGCA TkTCACCGCT ACACATGGAA TTCCACTTTC CTCTGCTGGC ACTCAAGTTT 240
 30 TCCAGTGTCC AATGACCCTC CACGGTTGAG CCGTGGGCTT nCACATCACA CTTAnA 296

(2) INFORMATION FOR SEQ ID NO: 4510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4510:

TTACTACTTA CTGAGTGACC TGTACCTGCT TTCGGAGTAA TTGTGATTGA TGAATTTGGT 60
 45 TTTATAGTAT TGGCATTGAA CGTCACTTTA CCAGTTTGTG CATCTAACGT TACATAGTCA 120
 GGCTTATTCG CAATTGTCCA TTGnTTATTT TGACCACGAA CAACATTAAT TGTCTTACTA 180
 TGTGCTGCA CCATTACCCA CTTnTTCAGT GTAAGCAATA TCCATTGCTT GAGTTGGGAT 240
 50 TAATTAAATG GTCCTGA 257

(2) INFORMATION FOR SEQ ID NO: 4511:

(A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4511:

10 AAAATCACAT CAGCCTGCAT TAACGACGTC GTTAATTTAT ATACATCTCC TGTAATATCT 60
 AGATAATTCT TTCCAACGCT AAATTCTAAT TCAAGTTCTC GTAAATCCAT CAACTCTATT 120
 TGATGTCCCT CATTGATGAC TTCTAGTTCA TTTTAAAT CATCCATAGC AATTCTCGTT 180
 15 TTAGAACCTA CTGTGGAACC TGACAATAAT ACAATATTCA nGAnGACGCC CCTCCTATT 240
 TGATAAATGC 250

20

(2) INFORMATION FOR SEQ ID NO: 4512:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4512:

30 AGCTGGnTTC GAACCAACGA GTGACGGAGT nAAAGTCCGT TGCCTTACCG CTTGGCTATA 60
 GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCTGAAGT CCGAACCCGA AGAGCGGATT 120
 TACAGTCCGC CGCGTTTAGC CACTTCGCTA CCCCTCCAGC TTATTCATAT AATTTAATAA 180
 35 TCAAAATGGT GGAAGAATGA CGGGTTCGAA ACCGCCGACC CTCTGCTTGT AAGGCAGATG 240
 CTCTCCCCAG CTG 253

40

(2) INFORMATION FOR SEQ ID NO: 4513:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4513:

50 GnCGACCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA CGTTAACATG 60
 nAAGTTACGT TCTTTTATAA AAAGATTTAA ACGCGTTATT AATCTGTGC AGTGTTCCTT 120
 55 CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG 180

GTGGAGACTA GC

252

(2) INFORMATION FOR SEQ ID NO: 4514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4514:

GTCATTGAAT ATGGAACCTT TAGAATTACA AGGCGCTAAA TTACGATACC ACCAAGTCGG	60
ACAAGGACCC GTGCTCATCT TTATTCCTGG TGCAAACGGT ACCGGAGACA TTTTCTGCC	120
TCTTGCAGAA CAGTTAAAG ACCATTTTAC TGTTGTAGCC GTTGATCGTC GTGATTATGG	180
AGAAAGCGAG TTAAGTGAAC CACTCCCTGA TTCCGCTTCA AACCTGACA GTGATTATCG	240
TGTC	244

(2) INFORMATION FOR SEQ ID NO: 4515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4515:

TATTAGGCAA ATCCGGTACT CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT	60
TCGAGTCGTT GATTTACAC TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCCGTAC	120
CGCAAACCGA CACAGGTAGT CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA	180
AGGAACTCGG CAAAATGACC CCGTAACTTC GGGAGAAGGG GTGCTCTTTA GGGTTAACGC	240
CCA	243

(2) INFORMATION FOR SEQ ID NO: 4516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4516:

GATTGTCCTT TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG 120
 ACATGTGGAG CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC 180
 5 CCGTCCACCG ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT 240
 CCCTAACCT GAGGCCGCAA nnGTAGG 267

(2) INFORMATION FOR SEQ ID NO: 4517:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4517:

20 TTGAATCTGA CGAAACGAGA AAAGAGCGCA ACGAGTTTAG TAGAGCTAAA TGAGTAAGCG 60
 AGAGCCGAAG AGAGGAAAGA AGCAAGCGAT TGTCACAAGT CAAGAAAGGT CTTTAGCGAC 120
 GATGGTAGCC AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAAAAA ATGGGATGCG 180
 25 ATGAGCCGCA TTGGAGACCG CAGTCCTnTn TnTTTTTTTA TGGCCTTAAA ACGTCAAAAT 240
 TAAAAAGTTA AACACAAAGA AAATGGGCTT TGGCGAGTGG AAACGTTTTG AATCTGGACG 300
 GAACGAGAAA GAGCGCACG 319

(2) INFORMATION FOR SEQ ID NO: 4518:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4518:

GGTATAATAG ATGACTATGT ACTATTTCCG GTACATCCTT GGCAATATCA GCATATTCTG 60
 CCGAACGTCT TTGCGAAAGA GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT 120
 45 GGAGATTATC TGTCGTCTTC AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC 180
 CATGTCAAAG TACCATTTCG AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GACTACGGTT 240
 ACATGAAAAA CGGGGAACA 259

(2) INFORMATION FOR SEQ ID NO: 4519:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4519:

	ATAGGGTGTT GCTGAATAGG GCGTTTAGTA TTTGGTCGTA CCGnnAACCA GGTGATCTAC	60
10	CCTTGGTCAG GTTGAAGTTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	120
	AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGG AGATAGCTGG	180
	TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGA TTATTGGAGG TAGAGCACTG	240
15	TTTGGACGAG GGG	253

(2) INFORMATION FOR SEQ ID NO: 4520:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 245 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4520:

	AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT	60
30	TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT	120
	CTCAACTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCnACC ATCGTCGCTA	180
	AAGACCTTTC TTGACTnGTG ACAATCGCTT GCTTCTGTCC TCTCCTTCGG CTCTCGCTTA	240
35	CTCAT	245

(2) INFORMATION FOR SEQ ID NO: 4521:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 251 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4521:

	GGGCCTAAGT GGACTCGAAC CACCGACCTC ACGCTTATCA GGC GTGCGCT CTAACCAGCT	60
50	GAGCTATAGG CCCATTAAAT TGAATGAACA AACATTCAAA ACTGAATACA ATATGTCACG	120
	TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG	180
	CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TnCCCACCTT	240

55

(2) INFORMATION FOR SEQ ID NO: 4522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4522:

```

nATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGT TGATGGCGTG      60
CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA      120
GCCGTAGCGA AACGATGTCT GAATAGGGCG TTTAGTATTT GGTCGTAGAC CGAAACCTGG      180
TGATCTACCC TTGGTCAnGT TGAAGTTCAG GTAACACTGA ATGGAGGACC GAACCGACTT      240
ACGTTTGAA                                     249
  
```

(2) INFORMATION FOR SEQ ID NO: 4523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4523:

```

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG      60
GGATGGACAT ACCTCTGGTG TACCAATTGT CGTGCCAAng CATAGCTGGG TAGCTATGTG      120
TGGACGGGAT AAGTGCTGAA GATCTnaAGC ATGAAGCCCC CCTCAAGATG AGATTTCCCA      180
CTTCGGTTAT AAGATCCCTC AAAGATGATG AGGTTAATAG GTTCGAGGTG GAAGCATGGT      240
GACAGTGG                                     248
  
```

(2) INFORMATION FOR SEQ ID NO: 4524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4524:

```

AACGTTAAGA TCCCTATTAA ATTATCTTAG GAATCATCAT GGGCATTATAT GATGTCTTAA      60
  
```

AAATTAGTAA TCTGAATCTG CTTCTAAACC TTGTCATAAT TTGA_nCGGCT GTGGCTCG_nA 180
 CCAATACGGG TCGGACCTGC TT_nAACCATT TTATTGGAAA TCTTCTAAAT TACGGACGGC 240
 5 ACCCGGATGC TTTTACTTCT ATATCAGCAC CTACTGTATC TTTCATTAAT TTAACGGCTT 300
 CTGCAGTCGG ACCGGCAACT GCAAAA 326

(2) INFORMATION FOR SEQ ID NO: 4525:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4525:

20 AAGAGCACCC TTCTCCGAGT TACGGGGTCA TTTGCCGGTT CCTTAACGAG AGTCGCTCGT 60
 CACCTTAGAT TCTCATCTTG ACTACCTGTG CGGTTTGCGG TA_nGGCACCT ATTTTCTATC 120
 TAGAGGTTTT CTCGGCATGT GAAATCAACG ACTCGAGACA CAATGTCTTC TCCCATCACA 180
 25 GTCAGCCTTA ACGAGTACCG GATTTCCTTA ATACTCAGCC TACTGCTTAG nGGCATCCAT 240
 CGCAGTT_nGC TATCCACTGG TCCCCCTCGA TTAAACGATT ATAGGTGGTA CAGATATCAA 300
 C 301

30 (2) INFORMATION FOR SEQ ID NO: 4526:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4526:

40 TGATATTATG AGCTGTGTTT TTAGCTTTAG AACCGAAGTC CCCTGCTTTT TTACCAAGAT 60
 TTTCAGTAAC TTGT_nCCATC CATTTTTTCT TTTTCGTACC ACCATGGAAT TTTGGCAAAA 120
 45 CACCCATCCG CTGTAACTTC AGAGTGTCAT TGGCATTTAT TACACTATCT CCAACTCCTA 180
 GTGGAACAAC CACATCTCGT CCTTGGGGTG CATGGAATGT nCCGTCAGCC CTGTGAATTA 240
 T 241

50 (2) INFORMATION FOR SEQ ID NO: 4527:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4527:

	CGATCACACT CTTCCGTCGT CATCGCCATT GGCTTTTCAC ACAATACATG GACACCATGG	60
10	TGTCAATGCT TCTATAGAAA GATCAGCATG GAATTTATTA GGTGTACAAA TGACCACCGC	120
	ATCAACAAGT TTAAACAGCT CGCTAGGTGT CTCAACTGCA TGAGGTATAT TGAAAGCGCT	180
	TCGCAACCAT nCAATCATCT GGCAGTGTTA TTGAATATCT TGTGACTGGC AACTTAATGA	240
15	GnACTGTGTC TTTTGGAGTT TCCAGnCAAT GCCGGGAATT ATGGACGGGT CTTGGTGGCA	300
	ATACCACCCA ACACCT	316

(2) INFORMATION FOR SEQ ID NO: 4528:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4528:

30	GTCCCAAGGG TTGGGCTGTT CGCCCATTAA AGCGGTACCG ACGACTGGGT TCAGAACGTC	60
	GTGAGACAGT TCGGTCCCTA TCCGTCGTGG GCGTAGAAAT TTGAGAGGAG CTGTCCTTAG	120
	TACGAGGAGG AnCGGGATGG ACATACCTCT GGTGnACCAG TTGTCGTGCC AACGGCATAG	180
35	CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAAGCAT CTAAGCATGA AGCCCCCTC	240
	AAGATGAGAT T	251

(2) INFORMATION FOR SEQ ID NO: 4529:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4529:

50	AGTACGTGAC GTTCACTACT CTCCTATGG CCGTATGTGT CCAATTGAAA CACCTGAGGG	60
	ACCAAACATT GGATTGATTA ACTCAATTATC AAGTTATGCA CGTGTAATG AATTCGGCTT	120
	TATTGAAACA CCATATCGTA AAGTTGATTT AGGATACACA TGCTATCACT GATCAAATGA	180

55

ATGGTCGTTC AGGTGATGAG TGTATGCGTT CGGGnACnAT CAGTATGCAA GAAAAGGTTT 300
 GTGACGCGAC AGTGTCnA 318

5 (2) INFORMATION FOR SEQ ID NO: 4530:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4530:

15 TAGCTGTGTG ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC 60
 GGCCTGACAT ACAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAGTT 120
 20 GAGCAAAGAn GATGTTCTnC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC 180
 CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA 240

(2) INFORMATION FOR SEQ ID NO: 4531:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4531:

CGGCTCTTCT GGGACGTTAA CCCTAAAGTG CACCCCTTCT CCCGAATTAC GGGGTCATTT 60
 35 TGCCGAGTTC CTTAACGAGA TTCGACTCGn TCACCTTAGA ATTCTCATCT TGACTACCTG 120
 TGATCGGTTT GCGGTTAGGG GCACCTATTT TCTATCTAGA GGCTTTTCTC GGCAGTGTGA 180
 40 AATCAACGAC TCGAAGACAC AATGTCTTCT CCCCATCACA GcncAGCCTT AACGAGTACC 240
 GGATTTGCCT AATA 254

(2) INFORMATION FOR SEQ ID NO: 4532:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4532:

55

TGAATAAACC GAATGTGGCT AAAGTCGTTA ACGCAAATA TGACGTCATC TATAACGGAC 120
 ATACTTTTGC AACATCTTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180
 5 CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

(2) INFORMATION FOR SEQ ID NO: 4533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60
 20 CATTGTACTA CTGGnCACTT TAGACAGGnC AAGGGTGTAG CTACCGATAA TTCAGGAGCA 120
 TTAACGCAAC CGACATTTGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180
 GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGA 240
 25 TGTGGTTGTT CCACTAGGAG TTGGAA 266

(2) INFORMATION FOR SEQ ID NO: 4534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTCAATT TTAAACGTA TTATTTTCATT 60
 40 GAGCAGAAAG AAAATTATGG CACCAACTT TAATATTTTT TTCAATGTCA TTCTTTTGAn 120
 GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTT GTCGTCCCAC CCCAACTTGG 180
 CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240
 45 CATTATTGTA AGCTGACTTT TCGT 264

(2) INFORMATION FOR SEQ ID NO: 4535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

5 GCGAATGGAT AACAGTTGAT ATTCCTGTAC CACCTGATAA ATCGTTTTAA TCGATGGGGG 60
 GACGCATAGG nATAGGCGAC TGCCGATTGG ATTGCACTCT AAGCAGTAAG GCTGAGTATT 120
 AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA 180
 GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC 240
 10 AAACCGACAC 250

(2) INFORMATION FOR SEQ ID NO: 4536:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 60
 25 AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA TTCGAACTAC 120
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAnATAGT AAGTA 235

30

(2) INFORMATION FOR SEQ ID NO: 4537:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

TGCATCTTCA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60
 TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120
 45 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAG CTAACCACTC 180
 CTCCTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT 234

50

(2) INFORMATION FOR SEQ ID NO: 4538:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

5 ACCCTCTGCT TGThAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC 60
 CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGACTACC ATCGACGCTA AGGAGCTTAA 120
 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 180
 10 TGTAATTTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACCATT 240
 TA 242

(2) INFORMATION FOR SEQ ID NO: 4539:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

25 TCATTAACAC CATCACCATA AATAAACCT TCCATATCTG TTCCTGTGCC AATAAGCCA 60
 TATTGCGTTT GgNtGTCTGT GCCAGTGCAA GATTTC AAC GATAATTTCT AGGCGTCAC 120
 GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTGnTTT 180
 30 ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT 234

(2) INFORMATION FOR SEQ ID NO: 4540:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AAcnGTTGAA TCTGACGAAA CGAGAAAAGA 60
 45 GCGCAACGAG TTTAGTAGAG CTAAATGAGT AAGCGAGACC GAAGAGAGGA AAGAAGCnAG 120
 CGATTGTCAC AAGTCAAGAA AGGTTCTTAG CGAGGATGGT AGCTAACTTA CGTTCCGCTA 180
 GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT 240
 50 AT 242

(2) INFORMATION FOR SEQ ID NO: 4541:

55

(A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

10 GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA GTCAAACGCT CACATACGGC 60
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120
 ACTCAATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180
 15 GnAGTGTCTTCT TTCGAACATA GGCGATTATn TCTTATGAAT TCAAGCTTAT TTAAAACTCT 240

(2) INFORMATION FOR SEQ ID NO: 4542:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCAN TTAGCTAATA TGCAAGCACA 60
 30 TGGTGAATAT GACGAGGTTG CAACTTCAAC GGCGAGGnTG ATGAATGCCT TACGTTTGCG 120
 TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGGTAAT GGCATACTGA GCTGACGATT 180
 ATGATATTGT CACGTTTTCT TCTCTGTATG CAGAAGCGAT TTACACGTAC GAGGTACACA 240
 35 TG 242

(2) INFORMATION FOR SEQ ID NO: 4543:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA 60
 50 ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTACTGAT 120
 TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCCGGCAAT ATGTAAGATT AAATGGTGGA 180
 GAnTGACGGG TTCGAACCGC CGACCCTCTG CTTGTAAGGC AGATGCTCTn CCAGCTGAG 239

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC AACTGAGCTA 60
 ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA 120
 GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG 180
 GTTCGAACCG nCGACCCTCT GCTTGTAAGG CAGATGCTCT nCCAGCTGAG CTAAATTCT 239

(2) INFORMATION FOR SEQ ID NO: 4545:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

AATTCATGCT TTCAAAGAC GATATACTAC GACACTCCTA CGAACTTGTC CAAGGATTAC 60
 GAAAAGACCT AAGGTTATGT AATTGGCCTA AATTTATTAA TCGTTTAAAT TCAGTTAGTA 120
 AAAAGTCTGT GAGTAAGGT GTATGGAAAG TGGTTAnATA TTATAGAAAA CATCAAAGGA 180
 TGTTAAGAAA TACnATTTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA 233

(2) INFORMATION FOR SEQ ID NO: 4546:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

ACTTTGTTGT CTTCCATCAA CTTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC 60
 CACTATTACT CTTTCCACCT AATTGGTTCA TGGCTTGTGC TAnTTTTTCA TGTGCTTCCG 120
 CTGAAATCGA TCCATAACTC ATCGCCCCTG TATTAAAGCG TTTGACAATG TCACTTACCG 180
 GTTCAACTTG GncGATGTCA ATCGGTGTAC ATGCTTTAAA TTCAAGTAAA TGTCTAATGT 240

(2) INFORMATION FOR SEQ ID NO: 4547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATTA CTGAAAACAA TCATCATATT TCTCATTCTG GTTTAGGAAC TGAAAATGGT 60
 CACGGTAATT ATGGCGTGAT TGAAGAAATC GAAGAAAATA GCCACGTGGA TATTAAGAGT 120
 GAATTAGGTT ACGAAGGTGG CCAAATAGC GGTAATCCAG TGCATTTGAG GAAGACACAG 180
 AAGAAGTTTA AACCGAAATA TGnAACCAAG GTGGGCATTA TCGTTGGTTA TCGATTTTCG 240
 ATAGTGTACC TCAAATTTCA TGGGTCCAAA TTAATGGTTA ACCCATCCAT TCGAnGnAGG 300

(2) INFORMATION FOR SEQ ID NO: 4548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT CACCAGACAT ATGAATGTAA ATTATACATT CAAACTAGA TAGTAAGTCA 60
 AAGTGATTTT GCTTCGCAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 120
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGGA 180
 TCTTGATAAA CCGnAAGTTG GGGAAATCTC ATCTTTACGG GGGGGCTTCA TGCTTAGGAT 240
 GGCTTTnCAG CACTTTATGC CCGGTnCCAC ACATTAGGCT TACCCAGCCT ATGCCCGTTT 300
 GGCACG 306

(2) INFORMATION FOR SEQ ID NO: 4549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:

CTTCTACTTT TGTACCATCA ATAAGATTTT GCTTTAAACA TTGACTATGA AACTGGATAA 120
 ATAAAGATTC AATTAACGCA TCAGTATTAG GATTCACCTCT AATACGATTA ATAGTTTTAT 180
 5 AAGAAGGTGn TTGATTTTGA GCTAACCACA TCATTGCAAT ACTGTCATGn AG 232

(2) INFORMATION FOR SEQ ID NO: 4550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTCAG AACGTCGTAT GnAGTTCGGA TCCCTATCCG TCGTGGGCGT AGGAAATTTG 60
 20 AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG TACCAGTTGT 120
 CGTGCCAAng CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AACATTCTTA 180
 AGCATGAAGC CCCCTCAAG ATGAGATTTT CCAACTTCGG TTATAAGATC CCTCAAAGAT 240
 25 GATGAAGTTA ATAAGTTC 258

(2) INFORMATION FOR SEQ ID NO: 4551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT GCGAGTTGGG GTGAGGGCCC ACACAGAAGC TGACGAAAAG TCATGACAAT 60
 40 AATGTGCAAG TTGGGGATGG GCCCACAAAG AGAAATTGGA TTCCCAATTT TACAGACAAT 120
 GCAAGTTGGG TGGGACGACG AAATAAATTT GCGAAAATAT CATTTCTGTh CCCTCCCTCA 180
 AAAGATGACA TTGAAAAAAT ATTAAAGTTG GTGCCATATT TTCTTCTGCT CATGAATATA 240
 45 CGTTAAAATT GATTGATCAT CGCGAATTGA TATTATTCTC ATTATAAAAA TACTTATTAC 300
 ACTTACCGTA TGATAGTTTG nTATATACTC TGATAAAGTC AAACCTAATA GCGTTTCTAG 360
 CTGTGnGTGT TTCATAATTA TATACATTAT CAGGCTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

	ATAGGAAACT GCCAATTGGA CGGTTGCCGC ATTCAAACCC AGCACGATTA CGGCGAATTG	60
10	CACGTGAAnC ATTTCTACAG CTTGATCTTG ACCTATGATT TTA CTCTTA AACGATTAGA	120
	AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTGG AGAACTGGG AATACCATTG	180
	AATCGTTGnA ATAGTATCTG GAAATATCAT GGAAGTGTAG CAACAGCAGT GTGTTGCACC	240
15	ATTrACTGAT TTTGCTAATT TATCTTGGTG AATGGATTG GATTTCATT TTGGAATGTG	300
	CGTGCAGCTT TT	312

(2) INFORMATION FOR SEQ ID NO: 4553:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

30	AGCAGCGATC AAAAATAATC CGCAATACGC TGGCAAATA CCAATACCAA ACCATAGAAC	60
	AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAATC AATTGAAATA GCGGTTGAT	120
	AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA	180
35	TGCGACAACA AAGnCCGCTA CAAATCTCCA TGAATAATT GCTAAATGTG GnGAATTCT	240
	CCAGTAACAA TGGA	254

(2) INFORMATION FOR SEQ ID NO: 4554:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4554:

50	GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCn	60
	AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTCGC	120
	TGTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC	180

55

CTGGGGCTTG G

251

(2) INFORMATION FOR SEQ ID NO: 4555:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTACTGAAAA 60

ACAACGTCAG CAACAAGCTG AATTACATAA AAAATTATGG TCGATTGCGA ATGATTTAAG 120

AGGGAACATG GATGCGAGTG AATCCGTAA TTACATTTTA GGCTTGATTT CTATCGCTTC 180

CTATCTGAAA AAGCCCAACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTCC 240

AGAAGCATGG C 251

(2) INFORMATION FOR SEQ ID NO: 4556:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

AGCTACCCCG GGGATAACAG GCTTATCTCC CCCAAGAnTT CGCATCGACG GGGAGGTTTG 60

GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT 120

TCGCCCATT AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA 180

TCCGTCGTGG GCCTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGTTGGAC 240

ATA 243

(2) INFORMATION FOR SEQ ID NO: 4557:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTGTCT TTAATAAAT TTAACTCATT 120
 GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG TTATTAATCT TGTGAGTGTT 180
 5 CTTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTG 235

(2) INFORMATION FOR SEQ ID NO: 4558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTTAAGCA CTAAATCCGC TTAATAACGG CTTTCTATCG CGCGCAACAT CTCGTTTGAC 60
 20 TGCTTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTTCT TACCTCGTGC ACACCAAGTA 120
 ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTTAACGG ACAATCGAAT AACCAAnCTC 180
 ACGTGTGTTGA TCACCCAATT TAATGATTTT ACGCTTGTGC AATAATnATT TTCGAGACGA 240
 25 GAGGATCGGA TAAAACGAT CCCCTCCTCG TATGG 275

(2) INFORMATION FOR SEQ ID NO: 4559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATCGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT TCCGATGACT 60
 40 CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTTG GATGAATCCA 120
 GAAGCACCAT TTGTTGGTAC AGGTATGGAA CACGTTGCAG CACGTGTATT CTGnGTGCGG 180
 CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG AAAT 234

(2) INFORMATION FOR SEQ ID NO: 4560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60
 TTCTACTCTA GCGGAANTAA nTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA 120
 5 CAATCGCTTG CTTCTTTCCT CTCCTTCGGC TCTCGCTTAC TCATTAGCT CTAATAA 180
 CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AG 232

(2) INFORMATION FOR SEQ ID NO: 4561:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

TCAAAGGACG CATACCATTA CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT 60
 TCACTCCCCT TCCGGGGTGC TTTTnACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA 120
 CTAGAGAGTA TTAGCCTTA GGAGATGGTC CTCCCAGATT CCGACGGAAT TTCACGTGCT 180
 25 CCGTCGTACT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT 240
 CTTTGATTCA TCTTGTC 257

(2) INFORMATION FOR SEQ ID NO: 4562:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAAGTGC TGATTCAGTT 60
 GCCACAATTA CCATACCAAT TTTCTTTTTG TCTTCGTCTG TnATAATGTC CTTAGCAGCG 120
 TTAGCTCCGA TTGAAACGAT GTCTTGTTT ACAGGACTAA CAGCCATTTT AGTTTGACCA 180
 45 ATTCCAATTA AAAATTTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG 240

(2) INFORMATION FOR SEQ ID NO: 4563:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

5 CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 60
 TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTAA 120
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGCTCAT TTACATAAGT 180
 nGACTCTGCT TTAAATAAT TTAATCATT GTCTGCTAAA CGTTT 225

(2) INFORMATION FOR SEQ ID NO: 4564:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

20 TGTTAATTGG nGAATTGGGA TACTGGTTAT ATTCAGCTGC ACCGCAAGCA ACTTCTATTG 60
 ATGGCCTAAC TGCCTTTTTA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG 120
 25 GCTTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAAATTACG GTGGTTACAA 180
 AATTATTICA GGTTCCTTC TTTTGCAATT GGGTGCTTTA ACCATATCTT nTT 233

(2) INFORMATION FOR SEQ ID NO: 4565:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

40 AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAGATTC AGATAGCGAT TCAGACTCAG 60
 ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG 120
 ATTCAGACTC AGACAGCGAC TCAGATTCAG ATnGCGATTC GGAntCAGAC AGCGATTTCAG 180
 45 ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAGATTC AGATA 225

(2) INFORMATION FOR SEQ ID NO: 4566:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

CCAAGTGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 60
 5 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 120
 TGGAGAnTGA CGGGTTTCGAA CCGCCGAnCC TCTGCTTG TG AAGGCAGATG CTCTCCCAGC 180
 10 TGAGCTAATT CTCCGATT TA AACTGGCCT GGGCAACGTT CTACTCTAGC GGGAACT 237

(2) INFORMATION FOR SEQ ID NO: 4567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTTT 60
 GCCAAAATTC CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC 120
 25 TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AAGCTAAAAC ACAGCTCATA ATATCAAAAA 180
 GGTGCAGAGG AAATGGTTGA nngGCAGCGG ATAAATCAAG ATGGTGCAGT TGGTTAGCGT 240
 30 TAAATCGCGA TGTGTGGGTT AnTACACATC CGGGAAGTAG TAATAAGTAT GTCAGTTTAA 300

(2) INFORMATION FOR SEQ ID NO: 4568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

ATCCCGTGGA GGTTCAAGTC CTCTCGGCCG CATCAAAATT CTTAATTTAA ATAAGCGGGT 60
 GTAGTTTAAT GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTTGA TTCCCATCAC 120
 45 CCGCTCCATA GATAATTTTA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 180
 TCCAAAAACG TAACTATAAG TTACAAACAT TnATTTTAGT ATTTGATGGA GCCTnAATCC 240
 50 AAACATTCCA 250

(2) INFORMATION FOR SEQ ID NO: 4569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

GATCCCCTAG CTTTACGTC AACTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT 60
 10 ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT 120
 AAACCAGTTG TTCCTGAACA ACCTGGTGAG CCTGGTGAAA TTGAACCAAT TCCAGAGGnT 180
 TCAGATTCTG ACCCAGGTTC AGATTCTGGG CAGCGnTTCT AATTCAGATA GCGGT 235

15 (2) INFORMATION FOR SEQ ID NO: 4570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

25 AATCTATTTT TTCTATTGTT AAATCGCTAT CTCCATCTTC TTTTATCTCT GGTATTATTT 60
 TTTCTTCAAC TAAGTCACGA TATAATGTTT TTGAATTTTC GTTCAATTTT GATTCGTGAT 120
 30 TTTGAATACT TTTCTTCCAC ACAAATGTAT ACCTATTGGC ATTAGCnTCT ACTTTTGTAC 180
 CAnCAATAAG ATTTTGCTTT AAACATTGAC TATGAAACTG GGA 223

(2) INFORMATION FOR SEQ ID NO: 4571:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

CATGATATTT TGAACCGCAT GGTAAAGTT GCAAAGACGG TCTTGCTGTC ACTTATAGAT 60
 45 GGATCCGCGC TGCATTAGCT AGTTCGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG 120
 CCGACCTTAG AGGGTGATCG GCCACACTGG nACTAAGACA CCGTCCAGAC TCCTACGGGA 180
 50 GGCAGCAGTA GGGAATTTTC CGCAATGGGC GAAAGCTGTA CGGCGCAACG TCGTGTnAG 240
 TGCTGCAGGT TCTTCGGATC GTAAAAT 267

(2) INFORMATION FOR SEQ ID NO: 4572:

55

(A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

10 AATnCAACTT TTACTIONACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG 60
 ACTATAGCAA GgnGGTCACA CCGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG 120
 TCGATGGTAG TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAT AATATTAATC 180
 15 CACAGTAGCT CAGTGGTAGA GCTATCGGCT GTTAACCGAT C 221

(2) INFORMATION FOR SEQ ID NO: 4573:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA 60
 30 TTCGGTGCAh TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT 120
 ATACCTGATG CGTATTGCTG TGTGCTAGTA CnAGAGGGG AATTGCTTGA TCAACACAAG 180
 GATGTAGCGC AAGATTTGTA CAAGGTTATA AAAAGTCTGG CTTTAAAATG 230

35

(2) INFORMATION FOR SEQ ID NO: 4574:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

45 TCACATATCG ATAACATGAC ATAACTCATG CTGGGTTTCC CCATTCGGAA ATCTCTGGAT 60
 CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 120
 50 TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACTTAAT CnATGTTTCC ACCATTTTTA 180
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA 230

(2) INFORMATION FOR SEQ ID NO: 4575:

55

(A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

10 CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGACACAG AGAAATTAGC TCCTCAATTT 60
 CTACAGACAA TGCAAGTTGG CGGGGCCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA 120
 ATAGTGTGCA AGTTGGGGTG GGACGACGAA ATAAATTTTG CGAAAATATC ATTTCTGTCC 180
 15 CACTCCCAAA AAGACCGCAG TAGGATAATT CCATTTGGAA ATACCTTACT GCCnGTTTTT 240
 AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT 300
 CCTTAAATT 309

20

(2) INFORMATION FOR SEQ ID NO: 4576:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

30 TGATTCTAGG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGGTAA 60
 ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAA TAATGGTGGG CCTAAGTGGA 120
 35 CTCGAACCAC CGACCTCAG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC 180
 ATTTTTTTGA ATGTTAAATA AACATCnAAA CTGGnATACC ATATGTCACG GTAATCCGCA 240

40

(2) INFORMATION FOR SEQ ID NO: 4577:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

50 CTTCTGTGTA AAATTTGATG CACAATGGTC ATCATTTTTA TCTTTCCAAT AAGTACTGTC 60
 TGGGTAAAAA TnTATTAATT GGGTGGTTCG TGAAATGCAA TCTTTTTAAC GACTTCAGGG 120
 TAATCTTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA 180

55

(2) INFORMATION FOR SEQ ID NO: 4578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4578:

TAGGCATACC	AAAGTCGATA	CCATAGTGAC	GACCGCCATT	AAAGTTAAGT	CCACCTGTGT	60
AACTCCCAAA	CCTTTGCCAA	ATTGGATGGT	CAAATAGATA	GCTTCCATCG	CCTCCGCCAC	120
CAAAATCTTC	AAACCACGAT	TTACTTTGnC	TACTAATTC	TTTTTGAGCA	ATGAGTACGC	180
GCCTTAGCAA	TTTAnGTAG	CGTAGTCCGC	TCCAAAATAA	TATTAACTG	ACATACTTAT	240
TACnAGTTCC	CTGGATGTGT	ACATAATCCA	CACATCGCGA	TTTATCGCTA	ACAGAGCACA	300
CTTGATTACG	CGCGCTCAAC	ATTC				324

(2) INFORMATION FOR SEQ ID NO: 4579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

AATGTAAAAA	CTGATTTCTA	TTAATTATTT	GATAGAAATC	ACTTTTTTGT	ATTTTATAAT	60
GTACAGCTCG	TTGCATTCAT	ATAGCTTGAA	GTCACGTTTA	AAACCATATC	TATCATTATG	120
GTATGCATAT	CGTTTAAAC	CTATTCTTTT	GTTAnTAGGA	CATATAAATT	CATCATTAAAT	180
TCGTCATATT	TCCAATTTTG	AGTGThAAAA	ATGTCACTTT	TAAACTTTC		229

(2) INFORMATION FOR SEQ ID NO: 4580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

CGGGGACTCn	AACCCGTGTT	GACCGCCGTG	GAAAGGGCGG	TGTCTTAACC	GCTTGnACCA	60
------------	------------	------------	------------	------------	------------	----

CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA 180
 CGTAAGTTTCG ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACA 239

(2) INFORMATION FOR SEQ ID NO: 4581:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

CCGnACGAAT TTACACGTGT TCCGTCGTAC TCAGGATCCA CTCAGAGAG ACAACATTTT 60
 CGACTACAGG ATTATTACCT TCTTTGATTC ATCTTTCCAG ATGATTCGTC TAATGTCGTC 120
 CTTTGTAAC TCGTATAGAG TGTCCTACAA CCCCACAAG CAAGCTTGTT GTnTTGGGCT 180
 CTTCCCGTTT CGCTCGCCGC TACTAAGGGA ATCGAATTTT CTTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

TTAGTAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60
 AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTTAA TAATGGTGCT ATAGAAGGAA 120
 TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG TTACAGAAAT TTCAnCAnCT 180
 TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60

ATTTTGAAT CATTGTTAAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTTGGAAA 180
 TAGGTCATAG GGTnAAAACn TTTTGTAGAA TTTGTCGCTA TTTGTTAAAT TGTATCCCGG 240
 5 CTTGAAGTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTCGTA GCTTCGCAGA 60
 nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120
 ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnG GCCTATTCAA TGGGGGCTCT 180
 TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

(2) INFORMATION FOR SEQ ID NO: 4585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ATAGCGATTA 60
 TTTCTTATGA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGC TTGGTAAAT 120
 CTATATTTAC TTACTTATCT AGTTTTCAAT GTACAATTnC TTTTGTAGTCA AGCGCTCGCA 180
 TACTGCTnTA TTTTCAAAAA ATCAAATGCT CATTTACA 218

(2) INFORMATION FOR SEQ ID NO: 4586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:

GGAATTCCAC TTTCTCTTC TGA CTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120
 GAnCCGGGGC TTTTCACATC AGACTTAAAA AACC GCCTAC GCGCGCTTGT ACGCCCAATA 180
 5 ATTCCGGATA ACGCTTGCCA CCTACGTATT TACCGCGGGC TGCTGGCAGG TATTnAGCCG 240
 T 241

(2) INFORMATION FOR SEQ ID NO: 4587:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

20 CAGCCACCTG TTGCCACCAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60
 TGAAGTGAAT AAGAAATCAA TCATTTGCTC TTCTGT TAA TCATGTGTTT TTTCTAATTT 120
 AAAAAGTGCA CCGGGAATGG TACCCGAGGA ACCAGCTGTT GCGGTTGCAC AAATAATACC 180
 25 CATCGCAGCA TTGACTTCAT TGTTGCAAGG CACnTTGAC TGCGGCAATC ATTCATATCC 240
 GACnAAGCAG ATG 253

(2) INFORMATION FOR SEQ ID NO: 4588:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

40 ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG 60
 AGAAACTGGC TTACGATGGC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG 120
 CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTTTAGCA ATGTTGGTGC 180
 45 GGACGTACCA GTAGAAAAGG CTTTGGAAGC AGTTGAAT 218

(2) INFORMATION FOR SEQ ID NO: 4589:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

GCCATGGCTC CACAGGTAGG ACTCGAACCT ACGACCGATC GGTAAACAGC CGATAGCTCT 60
 5 ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA 120
 AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT 180
 10 GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA 216

(2) INFORMATION FOR SEQ ID NO: 4590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

AGATTTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC 60
 ATCnATTCA TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT 120
 25 CCTCGGCTAA GAACCTTTCT TGA CTGTGTA CAATCGGCTT GCTTCTTTCC TCTCCTTCGG 180
 CTCTCGCTAC TCAATTTAGC TCTACTAAAC TCGGTTGCGG CTC TTTTCTn GTTT 234

(2) INFORMATION FOR SEQ ID NO: 4591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

AATTGACTGA CTCGTTTTTA CCGCGTGTTT AATATTGTTA TACATATATT CTAATTGCAC 60
 ATTTAAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTTCG CAAAATTTAT 120
 TTCGTCGTCC CACCCCAACT TGCACATTA TTGTAACCTG ACTTTCCGCC AGCTTCTATG 180
 45 TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG 216

(2) INFORMATION FOR SEQ ID NO: 4592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

ATTCCGGATA ACGCTTGCCA CCTACGTATT ACCGCGGCTG CTGGCACGTn TTAGCCGTGG 60
 5 CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CACATATGTT CTTCCTAAT 120
 AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGnTGCTCC GTCAGGCTTT 180
 CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG 216

(2) INFORMATION FOR SEQ ID NO: 4593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA 60
 AGCTTTGATC CAGAGATTTC CGAATGGGGA AACCCAGCAT GAGTTATGTC ATGTTATCGA 120
 25 TATGTGAATA CATAGCATAT CAGAnGGCAC ACCCGGAGAA CTGAAACATC TTAGTACCCn 180
 GTGGAAGAGA AAGAAAATTC GATTCCCTTA GTAGCGGCGA GCAGAACG 228

(2) INFORMATION FOR SEQ ID NO: 4594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA 60
 TTTCATCATT AGAAGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT 120
 45 TAATCGAAGG TGTTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAAA 180
 TTATCGGTTT AGGTGCCACA GnAAGTGGAT TCCAGGTTAG CCAAAGGGGT TAATCTGGAT 240
 TAATTTTTTT Tn 252

(2) INFORMATION FOR SEQ ID NO: 4595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

5 ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA 60
 GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCG TTAATGGGTG 120
 10 ATGGCGTGCC TTTTGTAGAA TGAACCGGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA 180
 AATGTGGAGC CGTAGCAGAA GCACGGTTCT GGAATAGGGG CGTTTtagTT ATTTTGGGTG 240
 GTTACCCGGG AGnAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

25 CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCACTAG GATCTGCCGG TGCCGCACGT 60
 CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTTCAGCAA TTGCAACTAG CTCTGGTTTA 120
 30 TTTGAAGAAT GACGAACATC TTCTTGAATT TCCTTTAAAG TAGATGTCCT CCTGAACCAT 180
 TnCATTTGTTT AGTTGGGTAC ATTAATGCnG TATTATCGAC ACTACATCA 229

(2) INFORMATION FOR SEQ ID NO: 4597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

45 GCTCACCTTA GAATTCTCAT CTTGCACTCA CCTGGTGGTC GGTTTGGCGG GTAGGGTCAC 60
 CTATTTTCTA TCTAGCAGGC TTTTCTCGGC AGTGTGAAAT CAACGACTCG AAGnCACAAAT 120
 GGTCTTCTCC CCATCACAGC TCAGCCTTAA CGAGTACCGG ATTTGCCTAA TACTCAGCCT 180
 50 TACTGCTTAG ACGTGCAATC CAATCGCAGC CTTGCGCTAT CCTACTGnGG TCCCCCATC 240
 GATTAA 246

(2) INFORMATION FOR SEQ ID NO: 4598:

- (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

10 AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG 60
 TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTTAAACT TAGCAACATA ACTACTAGAA 120
 CAATTAGCCC TGCAACGTCA AATTTATGTG TATTGGTAAT TTCTGATTTC GTTTCAGGCG 180
 15 TCCCTTTGAT GAGTAGCATT GAAAGTACGG nAACGATGnG TTG 223

(2) INFORMATION FOR SEQ ID NO: 4599:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTCAG ATAATCCCGC ACGCAATGCA ATCGTTCGTG 60
 30 CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC AACAATGACA TCTTCAATCA 120
 TATTCTTATT GAATTTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA 180
 CATCATCAGG TCTTTCGTGG AATAATGCGC CTGCTTTGG 219

35

(2) INFORMATION FOR SEQ ID NO: 4600:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

45 AAGGTTAAGA GGAGTGGTTA GCTTCTGCGA ATACCGAATC GAAKCCCCAG TAAACGGCGG 60
 CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCTTGTC GGGTAAGTTC CGACCCGCAC 120
 50 GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACGAGAGACT CGGTGAAAAT CATAGTACCT 180
 GTGAAGATGC AGGTTACCCG CGGACAGG 208

(2) INFORMATION FOR SEQ ID NO: 4601:

55

(A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

10 AGTGCCAGTG ATTAAGTCA TTTTCAATA GATCAGGGAA GACTACCAAG CTTATGTTGA 60
 AGGACATCTT TTGGCGTTAC CGGTTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT 120
 CACTTGAACA ACATTTGTTA ACGGATTATT TGGCAATTCG TTATTGTCGA ACAnTGCnAG 180
 15 TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG 240
 TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC 286

(2) INFORMATION FOR SEQ ID NO: 4602:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

30 ATATGGCTAT GGTATTCACA TATCGATHAA CATGGACATA ACTCATGCTG GGTTTCCCCA 60
 TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT 120
 AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA 180
 35 TGGTTCACC CATTITTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG 240
 nTTAAACGGG GTATTAATCT TGTG 264

(2) INFORMATION FOR SEQ ID NO: 4603:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

50 GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC 60
 GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAAAGTAA GTGCGATTAA 120
 ACAAGTTGCT TCTGGGCGTT TTGGTGTAnC TAGTGATTAT TTACAACATG CCAAAGAATT 180

55

TATCCn

246

(2) INFORMATION FOR SEQ ID NO: 4604:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

ATTA ACTAAC ATGGGCATCT ACGATGGAAA CAGACGTGGT ATCCTCGCTA TTATCCAGCT 60
 AnCGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTTAA ATTTTGGAAG GGTGTATGGA 120
 CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA 180
 GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn 240
 TTTGATGG 248

(2) INFORMATION FOR SEQ ID NO: 4605:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

CAAGTTTTCC AGTTTCCAAT GACCCTCCAC GGTGAGCCG GGACTTnTCA CATCAGACTT 60
 AAAAAACCGC CTACGCGCGC TTACGCCCA ATAATTCCGG ATAACGCTTG CCACCTACGT 120
 ATTACCGCGG CTGCTGGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT 180
 GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTTG TTTTGTTTTn 240
 TGGGTT 246

(2) INFORMATION FOR SEQ ID NO: 4606:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG 120
 ATGTTTTTCA TCTGAAATTT GTTGTGCAGT TGCATCGCCA TTGTCAATAA CACGTTGAGC 180
 5 TGCAGTTATT TCAGTTTCTG CTTACGCTn CT 212

(2) INFORMATION FOR SEQ ID NO: 4607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAAT 60
 20 GACCCCGTAA CTTCTGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCAGAAG AGCCGCATGA 120
 ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGAntGTAT 180
 AGGGGCTGAC GCCTGCCCCG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC 240
 25 GGAATCGAAG CCCAGTAAA CGGCGG 266

(2) INFORMATION FOR SEQ ID NO: 4608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

TTCAGTACGT AAATACGCAC GTGAAAAGG TGTTAnATTA AAGCAGTTTC TGGATCTGGT 60
 40 AAAAATGGTC GTATTACAAA AGAAGATGTA GATGCATACT TAAATGGTGG TGCACCAACA 120
 GCTTCAAATG AATCAGCTGC TTCACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA 180
 CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG 215

(2) INFORMATION FOR SEQ ID NO: 4609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GGGTTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTGTG CGATTTTTTA AATCGAATCG 60
 CTCGAAATAG GCACGCAAGA ATCTTGTAGT TCTATTTTCT AAAATATCTA TAACATCATG 120
 5 GTATCATTAT CTATAAAAT GAAACTCATT GATCCAGTTA CATTTTTAAAC GCTTTTAAAT 180
 TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTChGA ATnGATTAGC 240
 10 C 241

(2) INFORMATION FOR SEQ ID NO: 4610:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 215 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

ATTCATTTCT TGTCTAGCAA CGTTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG 60
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 120
 25 TTAATCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 180
 TTTCAnTTG CCAAGCCATT TTTCTTTGGT GnTTA 215

(2) INFORMATION FOR SEQ ID NO: 4611:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA 60
 TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTGTGATA AATATGGCGT GCGTTTGGCA 120
 ATAGCATTAA TGCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA 180
 45 TGCAGTACCG TGTTTGTGTA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT 240
 TAAATTATCT TGTGATTCAG GTAAATCCAT CTTGTTAGCT ACTACGATTT GAGGTCTATC 300
 TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG 360
 50 GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4612:

55

(A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

10 AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA 60
 TGATAAGTAT GCAAATAATT TCACAGTGTT TGCAGCAGGG GCAATTATGA TTGCAGTACC 120
 TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTAGTA TCAGGTTTAA CAACAGGTGC 180
 15 CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCTAATG 240
 ACCGTTAAGG TtnAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4613:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

30 GACTTCGTTT CAGTGTA AAA TTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG 60
 ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC 120
 TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC 180
 35 AGCTTTTTTC TACAGCTTTT ACAATATTnn 210

(2) INFORMATION FOR SEQ ID NO: 4614:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGCCGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG 60
 50 AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT 120
 ATCTGAATCT GAATCGCTAT CCGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA 180
 GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA 235

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTAAATTTA 60
 TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTTCG ATGCTTTAAT TCAGTTAGAA 120
 GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGA CTGTATG 180
 TCnTTGGATA GAGTTACAAA CTTATTTTG 209

(2) INFORMATION FOR SEQ ID NO: 4616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA 60
 TGTGCGAaAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT 120
 GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC 180
 CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT 222

(2) INFORMATION FOR SEQ ID NO: 4617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTTCAATTC TGCGATTTCT 60
 TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA 120
 ATGTATCAAC ATATCGCGGT ATGTTTAAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG 180
 TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCTT ATATGGGGCT ATAATACGTT 240

(2) INFORMATION FOR SEQ ID NO: 4618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTh GAGGCTGGGA CATAAATCCC TAAATTTCan 60
 CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT 120
 CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT 180
 GCTCCCTCAG GGGTCTCGCC ATTTAATACT ACGTAT 216

(2) INFORMATION FOR SEQ ID NO: 4619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA 60
 GCGATTnGTC GTCCTAAAC AGGTACATAT GCGCTATCTG ACCTAGTCGG TTTAGATATT 120
 GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA 180
 TGGTCAAAAT TTGTAAATAC GTTGTTTTGA CAATGGGCGC ACCTCGGACC GTAAAACG 238

(2) INFORMATION FOR SEQ ID NO: 4620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCAATT ACGTTTTGGC TGACACGnAC GTATATCGCC TGCCCAAGCA 60
 GATGCAGCCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC 120
 CATTTTTCCT GGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCTTG nCATCAATTG 180

TTGACCAGC

249

(2) INFORMATION FOR SEQ ID NO: 4621:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG 60
 TAAATTTAAT CCTGATTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG 120
 TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA 180
 AGGTGAATCG AAGAGAAATC ACAAAGTCCG TnTGGnTTA CAGGTACGGC AGAACGATAC 240
 ACAGTCTCGG GCGATTGTCG AGTCCAC 267

(2) INFORMATION FOR SEQ ID NO: 4622:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

CAAAAGGTAG TTAAATTAG GAGTGGGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT 60
 TAAAAGGAnG ACGTTATGAT GACGATTAAA GTTGGATCAT TGGGTGTGGT GGTATTCCAA 120
 TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC 180
 GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C 231

(2) INFORMATION FOR SEQ ID NO: 4623:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

CGAAACCGGC CCGACCCGGA CnACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCGGGAA 60

CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA 180
 CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA 240
 5 AGCCTTCTAA ACCAGTGGAA CAAGGTAAAG TAGTAACACC TGTTATTGAA ATCAATGAAA 300
 A 301

(2) INFORMATION FOR SEQ ID NO: 4624:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:

20 CGAGGTGCTG CAGAAGGTGT CATTCGTCGT TATTTAATTG AAGAAAAGAA CTACTTAGAA 60
 GCTGTGATTG GTTGGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA 120
 GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT 180
 25 TTTGAAAAAG GGGnAAATCA TAATCATtng GCGATGCCCA AG 222

(2) INFORMATION FOR SEQ ID NO: 4625:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:

35 TGGAAAGTGA ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGGATC 60
 40 CTGAGTACGA CGGAGCACGT GAAATTCCGT CGGAATCTGG GAGGACCATC TCCTAAGGCT 120
 AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC 180
 CCGGAAGGGG AAGTGAAATT AGGAACCCTG AAAACCCGTG TGCTTTACCA AAGTTAnGTT 240
 45 CAAGAGGCCC CGTTTAAATT GGGGTnnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA 300
 A 301

(2) INFORMATION FOR SEQ ID NO: 4626:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

5 GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT TTACAAATAG 60
 CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA 120
 10 CATTAATCCC ATTTTTCATCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG 180
 TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC nAT 223

(2) INFORMATION FOR SEQ ID NO: 4627:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

TTGTTGGGGC CCCGCCnGCG nCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG 60
 25 GGGCCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTC AGTCAATTAC 120
 TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTTATT TCCCAGCCTA TTCTTTTCAT 180
 30 AAAAAAAGA CGGATTAATT ATCCGCTTTT TCCTTATATC T 221

(2) INFORMATION FOR SEQ ID NO: 4628:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA 60
 45 GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC 120
 GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTAAATCTG TATGTGTGAA 180
 TCCACCACAT GTTAAATATG CAGCAGAG 208

(2) INFORMATION FOR SEQ ID NO: 4629:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

5 ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG 60
 TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTCTGAC GCACTAACTA AAGTTCGTGC 120
 ACACAACTAA GATTGATCAG CTAAAGCTTA CTTCAAAATA AAGAGATATA GCCATTAGTA 180
 10 ACGTTAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA 240
 TTGATACTnT ATCGAGAGCG TGAGnGAACT GAATACTGCG CTCACGGTAT TACATGCGTG 300
 CACTG 305

(2) INFORMATION FOR SEQ ID NO: 4630:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

25 TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGTGTGACT 60
 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAACTAG ATAGTAAGTA 120
 30 AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT 180
 CAGCTCCACA TGTCACCATG CTTCCAnCTn GAA 213

(2) INFORMATION FOR SEQ ID NO: 4631:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

45 GAnGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA 60
 TGGCGTGCCT TTTGTAGAAT GAACCGGCGA GTTACGATTT GATGCAAGGT TAAGCACTAA 120
 ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG 180
 50 GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA 213

(2) INFORMATION FOR SEQ ID NO: 4632:

(A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

10 GCTTTTAAAT CAAATGATAG CGGAAGGGnA TTTTAAAATT ATTCGAACCA TTATTACAG 60
 CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCATTA TTCTGGTTTG 120
 TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA 180
 15 TCGAAGCGAA CTTCAAGTTG CTTCA 205

(2) INFORMATION FOR SEQ ID NO: 4633:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA 60
 30 CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnt ACTTTTTCTn TAGAAATTAG 120
 TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG 180
 CTAATGTGTT AAGAACTACT ACAT 204

35

(2) INFORMATION FOR SEQ ID NO: 4634:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

45 GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TG TAGGTAAG 60
 AACGTTnGGG CAAGGTATGA GTGGTGGTAT TGCCTTACGT TAGCCCGTCT GATGTAGAAG 120
 50 CTTTTGTTGA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAAA CACCAAGAAG 180
 AAAAAGCATT CATTAAGCAA ATGCTGGAAG AnCCATGTGT CACACA 226

(2) INFORMATION FOR SEQ ID NO: 4635:

55

(A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

10	CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC	60
	GAAGAGTTGT TGAATCATTG TTA AAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTTG	120
	AAATAGGTCA TAGGATAnAA CnGTACGGAG AATTGTGCGC TATTTGTAAA TTGTATCCTG	180
15	GCTTAAGTTG GCCATTTTTC ATATGGTC	208

2) INFORMATION FOR SEQ ID NO: 4635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

TTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTTAGGAC ATAAAAAAAA GTAGACCTTG	60
GGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA	120
GTAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC	180
TTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG	228

T

30

C

C

T

35

2) INFORMATION FOR SEQ ID NO: 4637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

ATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTATA GATGGATCCG CGCTGCATTA	60
CTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCTT GAGAGGGTGA	120
CGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC	180
TCCGCAATT GCGGAAAGCT GTACGGGCAA CG	212

45

C

G

50

T

T

2) INFORMATION FOR SEQ ID NO: 4638:

55

(

(A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4638:

10 ATnTnATTAA ATAGAGAACA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG 60
 TTTTTTAGGG ATTTATGTCC CAGCCATTTT TGTATTCATA TTAAATTTTC GATAATTTTT 120
 CAGGAAGCAT TTAAATTTTA CTAATGAAGC CATATTTTAA GATTAACCAA AATTAATATT 180
 15 TACATTTTCCT AACCATTTTT ATGTAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA 240
 GGTTAGGATA AAGAGG 256

(2) INFORMATION FOR SEQ ID NO: 4639:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

30 AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTTCTGTC CCACTCCCCT 60
 GAGAAGTTTA AAATTTTATA TGTGGCTTG TTATGTAAAG GGAATTAACA TGGTTGTCTT 120
 GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATTCCG TAAAATGCTA 180
 35 AATCTAACCA TCTATTAAAT TTAAAAACC 209

(2) INFORMATION FOR SEQ ID NO: 4640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGCTTAC 60
 50 AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT 120
 ACGATTTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG 180
 GTGCGTTTAG TATTTGGTCG TAGCCCGCAG AACCAGGGTG ATCT 224

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACnCA GATTTTAAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA 60
 AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC 120
 CGCTGAAC TA CTTCTGCATA TGC GG GTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTAnG 180
 ATCCTAAGTC TAGTGC GTCT GCCAA 205

(2) INFORMATION FOR SEQ ID NO: 4642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGTTG GGGTGGCTGG ACACGGCACC 60
 CTGAGGGAAG GGCACCCGTC ATCAAAAATT CTATTATAG AATTTTACAG TAATGTGACA 120
 GACGGGCAAA GCGAACCATT CAATACGAAG TATTGTATAA ATAGAGAACA GCAGTAAGAT 180
 ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTIAGG GATTTATGTn CCCAG 235

(2) INFORMATION FOR SEQ ID NO: 4643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA 60
 CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA 120
 GTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC 180
 ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC 240

(2) INFORMATION FOR SEQ ID NO: 4644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

CAGCAGGCCA CCAAAATTGT GGTCCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG 60
 TTCCTAACAT TTACACCCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA 120
 ATTTATTTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCTTCTT 180
 GTTGGGGGCC CGCGGGCAAG GTnACTAGAA TGAAAAAAGC CTGTTACAAG CGATTTTCGG 240
 TTCAGTCCAC TACTGGCAAT ATAAGTTGTA GAGCTAGGAC ATTGG 285

(2) INFORMATION FOR SEQ ID NO: 4645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG 60
 CGCTTGThTG GGGGTTCAAC TGGAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn 120
 TACGAACGTG TTAACACAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG 180
 ATTTAGATGG TGGCTTTTGA TAAACA 206

(2) INFORMATION FOR SEQ ID NO: 4646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

ACAGTTACCG ATACAAGTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA 60
 CTTACGGATC ATGATGATTT CAACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA 120

CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTcGGA TA

222

(2) INFORMATION FOR SEQ ID NO: 4647:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

GTACTATTCG TGTGTGACAA TGTTCTTCCA GCATTGCTT AATGAATGCT TTTTCTTCGT 60
 TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA 120
 GncGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA 180
 CCGAAATTAA TGACAGTCCA 200

(2) INFORMATION FOR SEQ ID NO: 4648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4648:

CCACCATTAA TTAAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC 60
 ACGCAGGAnG TCAGCGGTTT GATCCCGCTA GTCTCCACCA TTATTTGTAC ATTGAAAAC 120
 AGATAAGTAA GTAAAATATA GATTTTACCA AGCAAAACCG AGTGAATAnA GAGTTTTTAA 180
 TAAGCTTGGA ATTCATTAAG A 201

(2) INFORMATION FOR SEQ ID NO: 4649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGGAATAA ATCTTTTAAG GCTTATAAAC GCTCATCTGn CATTGTAGCA 60
 ATTCATGCTT TCAAAAGACG ATATACTACG AACTCCTAC GAACTTGTC AAGGATTACG 120

AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGThAAAT

218

(2) INFORMATION FOR SEQ ID NO: 4650:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

GTGGCGGTGC GACTGTCAGA AGCACGTTAA ATTAATGAAA GATACAGTAG GTGCTGATGT 60
 AGAAGTAAAA GCCATCAGGT GGCCTACGTA ATTTAGAAGA TTTCAATAAA ATGGTTGAAG 120
 CAAGTGGCAG ACGTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG 180
 ATTCnGATTA CTAATATnTA TG 202

(2) INFORMATION FOR SEQ ID NO: 4651:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:

AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAAACTGGnA TAACTTCnGG 60
 AAACCGGAGC TAATACCGGA TAATATTTTA AACC GCATGG TTCAAAAGTA AAAGACGGTC 120
 TTGCTGTCAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGGTAAGGT AACGGCTTAC 180
 CAAGGCAACG ATGCATAGCC GACCTGAGA 209

(2) INFORMATION FOR SEQ ID NO: 4652:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:

TGAAGATGCA GGTTACCCGC GACAGGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG 60
 ATATTGAAAT TCGGCACAGC TTGTACAGGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT 120

CCACTTATCG TGGTTGGAGA CA

202

(2) INFORMATION FOR SEQ ID NO: 4653:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA 60
 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGCTCT 120
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG 180
 AACCGGTACG TGATCACTCA ACnGn 205

(2) INFORMATION FOR SEQ ID NO: 4654:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACG TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC 60
 ATTAAGTGGT GAAGTAACAC CATTATCAGA AGTGCCTGAT CAAGTGTTC ACGAAAAAAT 120
 GATGGTGACG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT 180
 AAAGTACCAA TGATTTCCCA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn 240
 CTATTAATCC ACACGGGTTA GAnG 264

(2) INFORMATION FOR SEQ ID NO: 4655:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 211 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GCTTGATGCG CCACCACAAG 60

AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGtnACGCG 180

AAATCAGTTT GCTCTTGGCT GCAGTAAATC G 211

5 (2) INFORMATION FOR SEQ ID NO: 4656:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC ATCTTTCTTT 60

GTGTTTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTTGCGG TCTCAATGCG 120

20 GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTCGACT 180

ACCATCGACG CTAAGGnGCT TAACTGnTGG GT 212

(2) INFORMATION FOR SEQ ID NO: 4657:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

35 TGGGTTCGAA nTCCACTTAG GACCCACCAT TAACTTAATA CCTATTTGGG GGCTTAGCTC 60

AGCTGGGnAG AGCGCCTGCT TTGCACGCAG AGGTCAGCGG TTCGATCCCG CTATCTCCAC 120

CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAATA TAGATTTTAC CAAGCAAAAC 180

40 CGAGTGAATA AAGAGTTTTA 200

(2) INFORMATION FOR SEQ ID NO: 4658:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTGGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT 60

55

CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG 180
 AAAAn 185

(2) INFORMATION FOR SEQ ID NO: 4659:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAAGC ACTCCGCCTG 60
 GGGAGTACGA CCGCAAGTGT ATAACTCAAA GGAATTGACG GGGACCCnCA CAAGGTTGGA 120
 GCATGTGGTT TAATTCGAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC 180
 AACTCTAGAG ATAGAGCCTT CCCCTTCG 208

(2) INFORMATION FOR SEQ ID NO: 4660:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAGA TTAAAGTCA 60
 CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA 120
 GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTCTA TTATTTATTT 180
 GATAGAAATC ACTTTTTTGAT ATGTATTTnT ATGTACAGCT CGTTGAGCnC TATTTTCCTT 240
 ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC 300
 GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTTGAnT GGTTTTCGTT 360
 CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTTC TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT 60
 5 CCAATTCTCC TnATGTTGGG GCCCCGCAGT TCAACTACTG CCAATATAGT GTTGTAGTGT 120
 CTAAGACATA AAAGTTCATC TCAGTCACAA TTACTIONTATA GCCTATCCAT CATCTTTTCT 180
 ACATGAAATT TTTCCAAGTG ATATATTTT 209

(2) INFORMATION FOR SEQ ID NO: 4662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA 60
 AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC 120
 25 CCAGGTAAAG ATATTGCTGA TGACTATAAA CCTCAGCACT TAAACCAAGG TCTGTTATCA 180
 CGCACCTGGT GTTTCATAC CAGGAAGTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG 240
 GCCTAA 246

(2) INFORMATION FOR SEQ ID NO: 4663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT 60
 TTAAGGAAGC GATTCACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG 120
 45 CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAATCTA 180
 AAGCAGGCGT AGATTATCAA AGnTTTTGGT ATGCAACCAG CACACT 226

(2) INFORMATION FOR SEQ ID NO: 4664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

5 TTCCGTCTCG GCACCAATTTT AGCGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60
 CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTITT AAATTAATTG AATAACGGGA 120
 GTAGCTCAGC TTGGTAGAGC ACTTGGTTTG GGACAAGGGC GCAGGTTCGA ATCCTGTCTC 180
 10 CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTCTT nCAC 234

(2) INFORMATION FOR SEQ ID NO: 4665:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGGAATGAT TCAACAACTT 60
 25 CTAAACGTTT AATTnACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAACCT CATCGCGTAC 120
 AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180
 CATTTTTGCA CGAATT 196

(2) INFORMATION FOR SEQ ID NO: 4666:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTTCT 60
 TAGATTGTGG TTTTITAGTT GGTGCCATGC TTAAACCTTT TCATTGATTT CAATAACAGG 120
 45 TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAn 180
 GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTG GATTTC 226

(2) INFORMATION FOR SEQ ID NO: 4667:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

5 GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAnAA CCGGTGATCT ACCCTTGGTC 60
 AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAAC CGACTTACGT TGAAAAGTGA 120
 GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC 180
 10 CGAAATA 187

(2) INFORMATION FOR SEQ ID NO: 4668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTTCT 60
 25 GAAAATGCTT TTGCCAACGT TTTATAAATA TCCAGTCTG AACGCGATTG CCATAACGGA 120
 TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGn 180
 30 TT 182

(2) INFORMATION FOR SEQ ID NO: 4669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

AGTTACGTTA AAAGATGAAA ACGACAAAGT TTAAAAACA GTTACAACAG ATGAnAATGG 60
 TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTCG AGACACCATC 120
 45 AGGTTATACA CCAACTTCAG TAACCTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180
 TT 182

(2) INFORMATION FOR SEQ ID NO: 4670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

5 GGGGCAAAGT CATTnCATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG 60
 CACCTTTTAA AGTATTACGT AATGTTGTGT TCGTTTACA TCTTACCCAA AGTGCTAATG 120
 10 CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGCACCTG 180
 ATTGG 185

(2) INFORMATION FOR SEQ ID NO: 4671:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA 60
 25 GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA 120
 GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG 180
 30 CATTGAGACC GCAAGGnTnT 200

(2) INFORMATION FOR SEQ ID NO: 4672:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

CCCCGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC 60
 45 ATCCTGGGCT GTAGTCGGTC CCAAGGGTTG GGCTGTTTCGC CATTAAAGCG nACGnTGCTG 120
 GGTTTCAGACG CGTGAGCAGT CGGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC 180
 TGTCTTAGT ACCGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTCG TGCCACGCAT 240
 50 AGTGGGTAGT ATGTGTGGAC G 261

(2) INFORMATION FOR SEQ ID NO: 4673:

(i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

10

ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG 60
AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA 120
ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG 180
CGTT 184

15

(2) INFORMATION FOR SEQ ID NO: 4674:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

30

CCCAGTCAAA CTGCCCCGCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTTGAGAAA 60
GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT 120
CAAAGGCTCC TACCTATCCT GTGACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA 180
AAGCTCCACG GGGTTCTTTC CGT 203

35

(2) INFORMATION FOR SEQ ID NO: 4675:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

50

nnGTTTGTAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA 60
AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TACAGTATAT CGGGAAGACA 120
GGATTGGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC 180
TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTA 229

(2) INFORMATION FOR SEQ ID NO: 4676:

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATT	TTACCTCAAT ATGCTTGTCA	60
TCAGTGGCTT	TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC	120
TTACAAATTT AGTGTGChGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT		178

(2) INFORMATION FOR SEQ ID NO: 4677:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG	60
TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA	120
TGGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA	180
AAATCCCAAT CGAACCCTGG GAGATAAGCT TGGGnTCTCC TCCCGAAAAT AAGCCTTTTA	240
GGGGCTTAAG CCTCCAAAGT GGATGATTTA ATTTGGAAGG TAAAn	286

(2) INFORMATION FOR SEQ ID NO: 4678:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATT	TGGAGCGGAA GATAGGTTTA	60
CACCTATACC TCGTTCCGGA AGGAnTGTTT	TAAAAGTGAA CTAATCCCGC AATATTAAAT	120
ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG	AGGATGTATT CTAAGAGTGA	180
AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATACn		229

(2) INFORMATION FOR SEQ ID NO: 4679:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACCTT 60
CGCCAAGCCA TCTTTCTTTG TGTTCGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG 120
ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACCTTTTGG CCTGGCAACG TTC 173

(2) INFORMATION FOR SEQ ID NO: 4680:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA 60
TTAACTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT 120
AATGnATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT 180
CCC 183

(2) INFORMATION FOR SEQ ID NO: 4681:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG 60
AGATGGTCCT CCCAGATTCC GACGAATTTT ACGTGTTCG TCGTACTCAG GATCCACTCA 120
AGAGAGACAA CATTTCGAC TACAGGATTA nTACCTTCTT TGATTCATCT TTCCAGATGA 180
TTCGTCTAAT GTCGTCCTTT GTA 203

50

(2) INFORMATION FOR SEQ ID NO: 4682:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

GGGTCACACC TGTTCCCATG CCGAACACAG AAGTTAAGCT CCTTAGCGTG CGATGGTAGT 60
 5 CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCAAA AAGTGGGATG CGATGGAGCC 120
 GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC 180
 10 ACAAAGA 187

(2) INFORMATION FOR SEQ ID NO: 4683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG 60
 TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG 120
 25 CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CGGTGCAGTT 180
 TTAAATT 187

(2) INFORMATION FOR SEQ ID NO: 4684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA 60
 AACCGTTATT AATCTTGTA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA 120
 45 AGCTTATTTA AAACCTCTTA TTAAGTCGGT TTTGTAAAT CTATATTT 168

(2) INFORMATION FOR SEQ ID NO: 4685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGA CCAAGGGGTC GCAGGTTCTGA 60
 ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG 120
 AGCGCCTGCT TThCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT 168

(2) INFORMATION FOR SEQ ID NO: 4686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT 60
 TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTGA GTCAAGCGCT CGCATACTGC 120
 nTTATTTTCA AAAAATCAAA TGCTCATTTA CAAAAGTAAA CTCCGCTTTT AATT 174

(2) INFORMATION FOR SEQ ID NO: 4687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

TGTTGTTGAA TATGAAGAAG ATACAAACCC AGGTGGTGGT CAGGTTACTA CTGAGTCTAA 60
 CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA 120
 TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA 166

(2) INFORMATION FOR SEQ ID NO: 4688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT TCCCCTTCGG 60

GCAACGAGCG CAACCCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG 180
 GTGACAAAC 189

(2) INFORMATION FOR SEQ ID NO: 4689:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGCGTCA CCCCTATACA TCACCTTACG 60
 GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTAC TGCGGCTCTT 120
 CTGGGCGTTA ACCCTAAGAn ACCCTTCTCC CGAAGTACGG GGGCATTTTG CGAGTCCTAA 180
 CGAGGTCGTC GTCACCTAGA TTCTCATCTT GATACTGTGT GGTGCG 227

(2) INFORMATION FOR SEQ ID NO: 4690:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC 60
 GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCCAA AATGCTTGGA TTATGTGCAA 120
 TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGTGG GGTG 174

(2) INFORMATION FOR SEQ ID NO: 4691:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTTA AAAAAAGGGA AGGGAAAAAnA AAAAGGGAAA AAAATTTAAC CCAAGGGTTT 60
 TTAAAGGGGG CCCAATTTTT CCCAAAAAA AAACCCTTTG GGTAAATTT TTTTAAAAA 120

GTTAAATTTT TTTAAAAAGG GTTCCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTTT 240
 TTAAGGGAAT TTAATAAATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAAA 300
 5 AAAATTAATT AAAAaACCCA TTTTTTTTTT TTAATTTTTT AACCCAAAGG GGGTAATTG 360
 GCC 363

(2) INFORMATION FOR SEQ ID NO: 4692:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

20 TAGTGTCAAT TTTATTGATA TTTGCAATTA AACTGAAATT TAATTTTTCG GATGTATTTT 60
 nTTTACTTAA AGTAAAATAG AACACGATTT TGATGTCTGG GAATAGTGGA AATGATAAAA 120
 ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTCAGCTAAT TGTTACTTAA 180
 25 AAATAGGAAT ACATGAGTAA AACTCAATGG 210

(2) INFORMATION FOR SEQ ID NO: 4693:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA AGTATTTTCT TCCAAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT 60
 40 CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTCATCATC TTTAGGATCT 120
 TATAACCAAT TGGAAATCTC ATCTTGAGGn nGCTTCATCT TAGATGCTTT CACACTTATC 180
 CCTCCACACA TAGCTACCCA GCTATCCGT 209

(2) INFORMATION FOR SEQ ID NO: 4694:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 50 (D) TOPOLOGY: linear

GCACATTAAC CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG 60
 CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA 120
 5 GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT 180
 ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG 222

(2) INFORMATION FOR SEQ ID NO: 4695:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

20 TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120
 TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTCG 159

25 (2) INFORMATION FOR SEQ ID NO: 4696:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

AATATGGTAG TTTTAACTT ATCTATTAAAG GTACAATTGA CCAAATCGAT AAAACAAATA 60
 ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTAFT GCGCCGGTTT 120
 40 TAACAGGTAA TTTAAACCA AATACGGATA GTAnTGCATT A 161

(2) INFORMATION FOR SEQ ID NO: 4697:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

CCAAACTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT 60

ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA

170

(2) INFORMATION FOR SEQ ID NO: 4698:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA 60
 TTGGGCGTAA ACGCGCGTAG GnGTTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA 120
 GGGTCATTGG AAACCTGAAA CTTGAGTCAG AAGAGGAAGT G 161

(2) INFORMATION FOR SEQ ID NO: 4699:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA 60
 TGACATACCA TATCGACTAG GTACCTTTTT AGAATGTTGA TTAATCACAA CAAATATCAT 120
 GGGCAAGGTC ATCTTGCAAA ATGGATTGGA TTCAAGTGGG AGGGnCGATG ATGGACGTGC 180
 TGCATGCACT GATGACCCTT TTTGCCCATC CTGGCAAATC CCACCATGAA ATGACTGACG 240
 CGGACGCh 248

(2) INFORMATION FOR SEQ ID NO: 4700:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4700:

CCCCACGAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT 60
 GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 120

(2) INFORMATION FOR SEQ ID NO: 4701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG TGAGATTTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT 60
 AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTCCTTGCA GGCATATGCA CCGAAAGCTT 120
 AATGATTCAT CATACTGGAG ATGCGAATGA CTATGTTGGG TAAAGGATTT ATCTGGT 177

(2) INFORMATION FOR SEQ ID NO: 4702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 60
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTT ACACTGCCGA 120
 GAAAAGnCTC TAGATAGAAA ATAGGTGCCC GTACCG 156

(2) INFORMATION FOR SEQ ID NO: 4703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG ATGGTTATTC TGTGAAGTA ATTGACTTAC GTACTGTTCA ACCAATCGAT 60
 GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTnGTCAG CAAGACGCAC 120
 AACGTCAAGC TGGTGTGGT GCAGCAGTTG TAGCTGAATT AAGTGA 166

(2) INFORMATION FOR SEQ ID NO: 4704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG 60
10 ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT 120
GGCAACGTTT TACTCTAGCG GAACGTAAGT TCG 153

(2) INFORMATION FOR SEQ ID NO: 4705:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG 60
25 AATGCCAATT AATTAACTT GGGAACTCAG ACACATGGGT GATAAGGTCC GTATTGAAA 120
nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAAATATA TGT 163

30

(2) INFORMATION FOR SEQ ID NO: 4706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

TAAGGTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG 60
40 CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTTG ATTGGCTGCA GTCGCGATGG 120
45 TTTGTAATCC TGATGAGCAG TAGCGATTCA TGTTTGACCh GTACCCGTCA GATATCCGCA 180
GCAATGCAAT GTTGTGCAAG TTT 203

(2) INFORMATION FOR SEQ ID NO: 4707:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTCAGGAGGCTCGT CCGCTCTGGG 60
 5 TTAGTCGGGT CCTAAGCTGA GCGCAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG 120
 TACCACCTAT AATCGTTTTA ATCGATGGGG GGC 153

(2) INFORMATION FOR SEQ ID NO: 4708:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

20 nCTATAATGA ATAAATAATT TAGAAATATG CTTCCGATTG TTCGATGCTT TAATTCAGTT 60
 AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG 120
 TATGTCTTTG GATAGAGTTA CAAACTTATT 150

(2) INFORMATION FOR SEQ ID NO: 4709:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

35 AAAATTCGGG TTCTCAAATC ATCGGAACAT AACAAAACAA CCTAAGCAAC ATGTAGGCCG 60
 TTGTCACTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTAT TnAGAGAATG TCATGATTAT 120
 40 TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA 156

(2) INFORMATION FOR SEQ ID NO: 4710:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

50 GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC 60

TCGTTAAGGC TGAGCTGTGA TGGGGAGAA

149

(2) INFORMATION FOR SEQ ID NO: 4711:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT 60

TGGCTTTTCT TTTGCATAAT TGACAATGGC TTCTGCCAAT GGGTGTTTCAG AATCTTTTTC 120

AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG 160

(2) INFORMATION FOR SEQ ID NO: 4712:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

ATAGTGAACC AGTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA 60

CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTTG 120

TAGAATGAAC CGGCGAGTTA CGATTTGATG C 151

(2) INFORMATION FOR SEQ ID NO: 4713:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC 60

CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GCGGAGAAAT TCCAATCGAA 120

CCTGGGAGAT AGCTGGTTCT CTCCG 145

(2) INFORMATION FOR SEQ ID NO: 4714:

(A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

10 TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA 60
 TAGCGATGTA CCTATAATAA TGGAGGAATA CCCAAGTCCG GCTGAAGGGA TCGGTCTTGA 120
 AAACCGACAG GCCTTAACGG GCCGCGGGGG T 151

15 (2) INFORMATION FOR SEQ ID NO: 4715:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

25 TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 60
 GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACG TGTAATTTTA CTTTGnAATA 120
 30 CTTTAAAAAA ATAAGACACT TTGCCAACTT G 151

(2) INFORMATION FOR SEQ ID NO: 4716:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

40 GCTGTCATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT 60
 45 TATTATGCGT AATGATGTAA AAAGACGAAT ATTCATTGT TTGTAAAAGT GGCATTCTTA 120
 TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC 152

(2) INFORMATION FOR SEQ ID NO: 4717:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGGANT AAATCTTTTA AGGCTTATAA 60
 5 ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAAGAC GATATACTAC GACTCCTA 120
 CGAACTTGTC CAAGGATTAC GAAA 144

(2) INFORMATION FOR SEQ ID NO: 4718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGCAGTC 60
 20 AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA 120
 CTTAACCCAA CATCTCACGA CACGA 145

(2) INFORMATION FOR SEQ ID NO: 4719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60
 CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACGTGA ATGGTGTCGT 120
 40 ACACnATGCC ATTTAAAAAT AGCATACCGG CAAAGC 156

(2) INFORMATION FOR SEQ ID NO: 4720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC 60

TAACTCGGAT CAAATTCGTC TCGATGACCT GG

152

(2) INFORMATION FOR SEQ ID NO: 4721:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT 60
 TTAATTAGCT TAAACGCGnGC AATCCCTGTG TTACTAGGGC GGATAACATT GGTACCACGG 120
 TTACAGCTAT CTTAGCTAGT TTAGCC 146

(2) INFORMATION FOR SEQ ID NO: 4722:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

CCACACCAAT ATTTTGCGCT AAGTAnATCG CATTAAACGT TTGTCTTCCG CCATTGAGC 60
 CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC 120
 TAACATTACC CAGCCATACA GCCATACCAG GGCCAC 156

(2) INFORMATION FOR SEQ ID NO: 4723:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCACCTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn 60
 GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG 120
 AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A 161

(2) INFORMATION FOR SEQ ID NO: 4724:

(A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

10 CAGAAAGCTC ACGGGGCTTT CGTCTGTCGC GGGTAACCTG CATCTTCACA GGTACTATGA 60
 TTTACCCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA 120
 ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTTAT AGTTA 165

15 (2) INFORMATION FOR SEQ ID NO: 4725:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

25 GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCC CTCAAGATGA nATTTCCCAA 60
 CTTGCGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT 120
 30 GACATGTGGA GCTGGACGAA TACTAATCG 149

(2) INFORMATION FOR SEQ ID NO: 4726:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4726:

40 TTGAATTTTT GAAAAAAAAA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA 60
 45 ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATTT 120
 GCAGATAAAA TTGTCATCAG TGGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT 180
 CAGCATGCCG GTGTTCTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA 240
 50 GAnCGGTAAA GTAGACAnCG GTAGTATACT GAAAT 275

(2) INFORMATION FOR SEQ ID NO: 4727:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTGT 60
AACTCTATCC AAAGACATAC AGTCAATACA AACATTACG TATCTTTACA ACAGTAATCA 120
TGCATTCTAT GATGCTTCTA ACTGAATnA 149

(2) INFORMATION FOR SEQ ID NO: 4728:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA 60
TGACAATTAA TAAAGAACCG TTCTTGCGCG AGCACAATGG GCGCTCACTG GCAGACTTTT 120
GTGATGCTGA CTTAAAGTAA ACTATTAGAT ATTGnGTG 158

30

(2) INFORMATION FOR SEQ ID NO: 4729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTCTG ATCTGGACCA TATTTTTTTA 60
TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTT GAnCGCACGT 120
GCCCTCCCAT ACCTCGGG 138

45

(2) INFORMATION FOR SEQ ID NO: 4730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTCGG ATTTGTCTGA ATTCGTAACC 60
 GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT 120
 5 AAAGTATTTC GGAGAGAACC AGCTATTTCC AGTTCGATTG GAATTTCTCC GCTACCCTCA 180
 GTTCATC 187

(2) INFORMATION FOR SEQ ID NO: 4731:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

20 CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA 60
 AGCTGGGTTC AGAACGTCGT GAGACAGTTC GGTTCCCTAT CCGTCGTGGG CGTAGGAAAT 120
 25 TTnAGAGGAG CTGTCCT 137

(2) INFORMATION FOR SEQ ID NO: 4732:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

35 TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120
 40 TCTTCAACTA AGTCACG 137

(2) INFORMATION FOR SEQ ID NO: 4733:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

50 TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60
 55

TCTTCAACTA AGTCACG

137

(2) INFORMATION FOR SEQ ID NO: 4734:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

AAAACATAAA TACAAAAATA TAGCTATTAC TATAAAAAAC AGCAGTAAGC ATATTTCCAA 60
 ATTGCAAATT ATCCTACTGC TGTTCTTTTT GGGCAGTGGG nACAGCAAAT GATATTTTCG 120
 ACAAAATTTA TTTCGTCGTC CCACCCCAAC TTG 153

(2) INFORMATION FOR SEQ ID NO: 4735:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCATC CCCAACTGTC ACATnATTGC 60
 AAGCTGACTT TTCGTCACCTT GCTTTGTTGG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG 120
 TACTTTGATT GATGTCCAAG TT 142

(2) INFORMATION FOR SEQ ID NO: 4736:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

ATGTTATTCA AAGTAAATTG CTTTGCTGA TTTTGACAGAC TGATAAATCG CTTCAAGAAT 60
 TTTTGTAACCT ACCATTGCTT GTTCCGTTT CACAACTGGT TCAGTATCAT TTACAACnGC 120
 ATCAATCCAA GCTTTTG 137

(2) INFORMATION FOR SEQ ID NO: 4737:

- (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

10 GGTCTTTAG TATTTGGTCG TACACCGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA 60
 AGTTCAGGTA ACACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAAT GAGCGGATGA 120
 ACTGAGGGTA GCGGAGAAAT TCCA 144

15 (2) INFORMATION FOR SEQ ID NO: 4738:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

25 GGGTAGCTAT GTGTGGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60
 TGAGATTTC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTCGAGGTG 120
 30 GAACATGGTG ACATGThATC TGCTTTTCTA ATCATAC 157

(2) INFORMATION FOR SEQ ID NO: 4739:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

40 GCTTTATGTC TAAAACGTCA AAATAAAAAG CAAACACAAA GAAAAATGGC TTGGCGAAGT 60
 45 GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAnATG 120
 AGTAAGTGAG AGCCGAAGAG AGGGA 145

(2) INFORMATION FOR SEQ ID NO: 4740:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTCGGTCT 60
 5 CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG 120
 TTTCACCTCG CCAAGCCATT TTTCTTGTTGTT TATTTTATT TGACGTTTAG ACATAAAAAA 180
 GAGACCCACG TTCAACTTGC CnGCACGTTT TACTCTGCGG AnTAGTGGCT ACCA 234

(2) INFORMATION FOR SEQ ID NO: 4741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GGCGCATTAC CAGAGTTGCA 60
 TGGTCAAAAT ATATTGTTGT CATTGAAGA TGGACGTGTA CAAAATGCG TGTTACGTGA 120
 25 TCATGATACT GTCAn 135

(2) INFORMATION FOR SEQ ID NO: 4742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA 60
 AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GAnAGCTGGT 120
 TCTCTCCGAA ATAGCTTTAG GGCTA 145

(2) INFORMATION FOR SEQ ID NO: 4743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

TGATTATCAT GGGTGC GGGT ATTAACCATT GGT TTA ACTC AGATACGATT TATnGTGCAA 120
TCTTAAACTT AGTTATGGTA TGTGGCGTCA A 151

(2) INFORMATION FOR SEQ ID NO: 4744:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC 60
AGGCGATAAA ATCANAGATG GTGCATCTTG GTTAGGCGAT AAAATCGGCG ATGTGTGGGA 120
TTATGTACAA CA 132

(2) INFORMATION FOR SEQ ID NO: 4745:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCGCTCT AACCAGCTGA GCTATAGGCC CATTAATTTG AATGAACAAA CATTCAAAAC 60
TGAATACAAT ATGTCACGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT 120
AGAAAGGAGG TG 132

(2) INFORMATION FOR SEQ ID NO: 4746:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA 60
GATTCAGACA GCGATTCAGA TTCAGATAGC GATTCAGATT CCGACAGTGA CTCAGATTCC 120
GACAnTGACT CGGATTCA 138

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

CATTATTGTA AACTGAACTT TTCGTCACCT GCTGGTgntt GGGGACCCCA CCAACTTGGC 60
 ACATTATTGG TAAGCTGACT TTTCGTCACCT TACTGTGTTG GGGCCCCGCC AACTTGCATT 120
 GTCTGTAGAA ATTGGGAATC CAATTTCTCT ATGTTGGGGC CCACACCCCA ACTCGACATT 180
 GCCTG 185

(2) INFORMATION FOR SEQ ID NO: 4748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGT 60
 ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA 120
 AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG 173

(2) INFORMATION FOR SEQ ID NO: 4749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC 60
 CTAAAACAGG TACATATGCC GGCTATCTGA CCTAGTCGGT TTAGATATTG CAGTGTCTGT 120
 AATTAAAGGG CATGCAACCA AGTAnCTGAG GAAACAACCT ATTTTCATGG TGTCAAAAAT 180
 TgntAAATAC GGTGTTTGAC AATTGCGCAC CT 212

(2) INFORMATION FOR SEQ ID NO: 4750:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

10 AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAAGAGT TTTAAATAAG CTTGAATTCA 60
 TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTTAAATCTT 120
 TTTATAAAAAG AAAACGTTTA 140

15

(2) INFORMATION FOR SEQ ID NO: 4751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

25

ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT 60
 GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT 120
 30 TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA 180
 TCCG 184

(2) INFORMATION FOR SEQ ID NO: 4752:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

45

GGGATCTTCC GCAATGGGCG AAAGTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT 60
 CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTTnA 120
 CGGTACCTAA TCA 133

50

(2) INFORMATION FOR SEQ ID NO: 4753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

5 GTATGCTGTG TGGCTTGTCA TGTTCCGGTT TGGTGGCGGA CCTGATTATT CCTGCGnTAT 60
 ACGCTATGGC TGGAGCAGTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT 120
 TGGCGCAAAA TATTGGTGTG GCTGTCGGTG CTGCAATGGG CG 162

(2) INFORMATION FOR SEQ ID NO: 4754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

20 AATTCGATTC CCTTAGTAGC GGCACGAAA ACGGGAAnGA GCCCAAACCA ACAAGCTTGC 60
 TTTGGGGGTT TGTAGGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT 120
 25 CTTGGGAAAG ATGA 134

(2) INFORMATION FOR SEQ ID NO: 4755:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

35 AGAGTGCCTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC 60
 ATATTACCGC AAGCTGTGGA TTGTCCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT 120
 40 TGAAGCATGn ATCGTAAGG 139

(2) INFORMATION FOR SEQ ID NO: 4756:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:

CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCACTTT CTGGTCTGTA 120

ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA 163

(2) INFORMATION FOR SEQ ID NO: 4757:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

CATGAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 60

TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ATCACAnGAT 120

TAATACCGCG TTAAATCTTT TATAAAGGAC CGTAACTTCA 160

(2) INFORMATION FOR SEQ ID NO: 4758:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG 60

GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT 120

ACTGCTGTTC TCTATTTATA CCAAnATTACT TTCGTAATTG TTAAAATTTT AAAAGGA 177

(2) INFORMATION FOR SEQ ID NO: 4759:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG 60

ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA ACnTTATGGG 120

ATTTGCT 127

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

GGGCCCCCTCG TCGGGTTACC GAATTCAGAC AAATCCGnA ATGCCAATTA ATTTAACTTG 60
 GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA 120
 AGTCCCAAAT ATATGTTAAT GAAAG 145

(2) INFORMATION FOR SEQ ID NO: 4761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCAGTGC GGCTCTTCTG GCGGTTAACC CTAAAGAGCA 60
 CCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA 120
 CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTTCTTCA AGCTTCCGCA 180
 TTAACACACC AAAACAGCTC CCACCACCAC TanATCGAnC AACACTAG 228

(2) INFORMATION FOR SEQ ID NO: 4762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

TnGCCAAATC TTAGTAGTCG CTtGGTTCGG TtGTGGTGCG ACAGCTGTGA AATCATCACT 60
 ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCGTT GCAACAGCTT GAATTGTATC 120
 AGCAGGGTTG 130

(2) INFORMATION FOR SEQ ID NO: 4763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG 60
GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA 120
GTTACATCG ACGGGGAGGT TTGGCACCTC G 151

(2) INFORMATION FOR SEQ ID NO: 4764:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC 60
CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTTACAAG CGCATTTTCG TTCAGTCAAC 120
TACTGCCA 128

(2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC 60
TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC 120
TTTCCATGTG GnaAC 135

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

GATTCTCACC CGTCTTTCGC TACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT 60
 CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC 120
 5 CACAGC 126

(2) INFORMATION FOR SEQ ID NO: 4767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC 60
 20 ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120
 GATTTTAAAC 130

(2) INFORMATION FOR SEQ ID NO: 4768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

GTAAACCCTA AAGAGCACCC CTTATACCGA AGTTACGGGG TCATTTTGCC GAGTTCCTTA 60
 35 AnGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120
 TAGGGCACCT ATTTTCCTAT CT 142

(2) INFORMATION FOR SEQ ID NO: 4769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCCC 60
 50 CGTCGATGTG AACTCTTnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120

(2) INFORMATION FOR SEQ ID NO: 4770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60
 ACCGTTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA 120
 TAGAGCTATT AAGCGTnGCC ATGAG 145

(2) INFORMATION FOR SEQ ID NO: 4771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTCGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT 60
 GTGCCTTTGG AAATGGTGAG GnGAGCGTTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC 120
 ATGTGGGA 128

(2) INFORMATION FOR SEQ ID NO: 4772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTGGCTA 60
 ATGCCTCCAT CGTGGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAAGA TATTGGTG 120
 GTACTT 126

(2) INFORMATION FOR SEQ ID NO: 4773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCTTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT 60
10 GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAGAn ACCTTGCGGT CTCAATGCGG 120
CTCATC 126

(2) INFORMATION FOR SEQ ID NO: 4774:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

25 ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC 60
TGCATCTTnA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 120
TACG 124

30

(2) INFORMATION FOR SEQ ID NO: 4775:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

40

ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC 60
ACCAACACCA CCGACACCAG AAGTGCCGAG TGAnCCAGAA ACTCCAACAC CGCCAACACC 120
45 AGAG 124

(2) INFORMATION FOR SEQ ID NO: 4776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

CCCGCTAGTC TCCACCATTT ATTTTITACA CGATGAACAT TGAAAACThA ATACAATATG 60
 CAACGTTAAT TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT 120
 5 AATCAAACAT CATAA 135

(2) INFORMATION FOR SEQ ID NO: 4777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA 60
 20 GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG GACGCTGGAT GTGCGAAACG 120
 TTGGGGGTTC AAACAGGATT TAGA 144

(2) INFORMATION FOR SEQ ID NO: 4778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

AATTTTIGAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG 60
 TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCT GTCTTCGACT GGCATGCTC 120
 CCT 123

(2) INFORMATION FOR SEQ ID NO: 4779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAAAC TATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG 60
 AACAAATATAG CTCAGGTATT ACGTTTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC 120

(2) INFORMATION FOR SEQ ID NO: 4780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCAnTGTC CTCGACTAGT GAGCTATTAC 60
 GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA 120
 TCCTTTT 127

(2) INFORMATION FOR SEQ ID NO: 4781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT 60
 GTCTTATTTT TTAAAGTAT TTAAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG 120
 CGAGACTCC 129

(2) INFORMATION FOR SEQ ID NO: 4782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCCG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT 60
 AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTCAT GTTTGnTTTG 120
 GTCAGATTTA GGACCA 136

(2) INFORMATION FOR SEQ ID NO: 4783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 60

10 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGATT ATTGnGACGG TATTGTTGG 119

(2) INFORMATION FOR SEQ ID NO: 4784:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT 60

25 nATCCCATG CATCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120

CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG 60

40 ATGACAATTT TATCTGCAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTTCTAAAC CCGnCACAC TTTATCGTGG TGGGGAGACA GTGTTcAGGC GGGCCAGTTT 60

55

AATCATTCAT AGAGTGT

137

(2) INFORMATION FOR SEQ ID NO: 4787:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

GTTTTTAACA CTGTTACCGT TTTCATCTTT TAATGTTACC GTTACGCCAG AATACCTTT 60
 TTCATCTTGG TCTTGATAC CATTTTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

(2) INFORMATION FOR SEQ ID NO: 4788:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

CATGCTTCCA CCTCGAACCT ATTAACCTnC ATCATCTTTG AGGGATCTTA TAACCGCAGT 60
 TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCCG 120
 GCCACACATA GCTACCCAGC T 141

(2) INFORMATION FOR SEQ ID NO: 4789:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

CTGGGTTCAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG 60
 AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT 120
 GCCAACGCAT AGCTGGGTA 139

(2) INFORMATION FOR SEQ ID NO: 4790:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

CATTATTTAG TATTTATGAG CTAATCAAAC AAcATAATTT TTATGGAGAG TTGATCCTG 60
10 GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG 120
CTTGCTTCG 129

(2) INFORMATION FOR SEQ ID NO: 4791:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT 60
25 TATCAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

CAAATTCTTT CGCTACTTGA ATGACAACAC TTTGTTTAC GCCTGAAATG GCTTCTTGCC 60
40 AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120
CGn 123

45

(2) INFORMATION FOR SEQ ID NO: 4793:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

AGTTTTGAAT GTTTGTTTCAT TCAAATTAAT GGGCCTATAG CTCAGCTGGT TAGAGCGCAC 120
nCTTGATAAC 130

(2) INFORMATION FOR SEQ ID NO: 4794:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60
TAACTCATTT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT 115

(2) INFORMATION FOR SEQ ID NO: 4795:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

nTTAAAAAA ATTCCCAATT TTTTTTGGGG GGTTGGGAAT TTAAAAATTT GGTTTTTTAAC 60
CCAAAGGCCCC TTTTCCCAAA AATTTAAATT CCCTTAAAAA TTAAAAATTT GGGAATTTTT 120
TTTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCCA ATTTTTAATT TAACCCTTAA 180
AACCCCCAAA CCTTTTTTCC TTTTTTAAAA TTTTTTTAAA TGGA 224

(2) INFORMATION FOR SEQ ID NO: 4796:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCAnGAT 60
GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGAACTCTT GGGGGCAGAT 120

(2) INFORMATION FOR SEQ ID NO: 4797:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

10 AATTCGATTC CCTTAGTAGC GGCGAGCGAA ACGTGAAGAG CCCCAnACCA ACAAGCTTGG 60
 CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC 120
 ATCTG 125

(2) INFORMATION FOR SEQ ID NO: 4798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

25 CAAAATAATG ACTCCTACGG GnCTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 60
 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC 113

(2) INFORMATION FOR SEQ ID NO: 4799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

40 CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCGnAGGT GGGACAAATG ATTGGGGTGA 60
 AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

(2) INFORMATION FOR SEQ ID NO: 4800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:

55

TCAGTGGCAT GATTTCGTGAA ATTGAAACGC AAGATTTTGA TATCGAnCAC CT 112

(2) INFORMATION FOR SEQ ID NO: 4801:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA 60

ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC 110

(2) INFORMATION FOR SEQ ID NO: 4802:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

GAACCAAGTT GTTATTGAAA AnTCGTTCGT AAAGTTACGG TACGCCCACC GTGAGTGCTT 60

TTACTTCTAT ATCAGCACCT ACTGTATCTT TCATTAATTT AACGTCTTCT GCAGTCGCAC 120

CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGCACC GCGCTTTGTA ATCATnCTTA 180

CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA 237

(2) INFORMATION FOR SEQ ID NO: 4803:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC 60

AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTTCGAA CCGCCGAnCC TCTG 114

(2) INFORMATION FOR SEQ ID NO: 4804:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60

10 GTTAGGGGTT TCCGCCCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

(2) INFORMATION FOR SEQ ID NO: 4805:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC GCATCAGCGT CnGTTACAGA 60

25 CCAGGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT CTGCGCAT 108

(2) INFORMATION FOR SEQ ID NO: 4806:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAACT 60

40 GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC 115

(2) INFORMATION FOR SEQ ID NO: 4807:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA 60

55 TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT 120

(2) INFORMATION FOR SEQ ID NO: 4808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC 60
 ATCATGTGCTA GCTTTTCTTG TATTAAGTGA TANTTACTAA TTGGTTTGCC GAATTGCT 118

(2) INFORMATION FOR SEQ ID NO: 4809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCCA TTGGAATTTTC 60
 TCCTATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG 120
 TACCTGACTT CAACTGACCA GGGTAGACAC 150

(2) INFORMATION FOR SEQ ID NO: 4810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGGCCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCA 60
 AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA 107

(2) INFORMATION FOR SEQ ID NO: 4811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTGnATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTCTG AGGAAGACAC 60
 5 AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTTCCA 117

(2) INFORMATION FOR SEQ ID NO: 4812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATnACTA AATCCGTCTT 60
 20 TCGACCCTGC TCGACTTGTA AGTCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA 120
 ATG 123

(2) INFORMATION FOR SEQ ID NO: 4813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60
 35 TAGCCCTAAA GCTATTTCGG AGAGAACCAG CTATCTCCAG GTTCGA 106

(2) INFORMATION FOR SEQ ID NO: 4814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60
 50 GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

(2) INFORMATION FOR SEQ ID NO: 4815:

- (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

10 ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GCGGCGGTT GAACCCGTCA TTCTGCACCA 60
 TTTATTCTTA CATATTGCCG GnCTAGCTCA ATTGGTAGAG CAACTGACCT TGTAAATCAGT 120
 AGGTT 125

15

(2) INFORMATION FOR SEQ ID NO: 4816:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

25

GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATT AATGAAGATG 60
 CTGTTGCTTA CACTGAAGAC GTTTATGnTT TCTGGCGTCC AACT 104

30

(2) INFORMATION FOR SEQ ID NO: 4817:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

40

GTCGGGTAAG TTCCGGCCCG CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACGnGAG 60
 ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG 117

45

(2) INFORMATION FOR SEQ ID NO: 4818:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

55

TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTG 120

A 121

5 (2) INFORMATION FOR SEQ ID NO: 4819:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

TCAGTTCCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GCTGGAATCG CTAGTAATCG 60

TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA 118

20 (2) INFORMATION FOR SEQ ID NO: 4820:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

30 CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTCCGAG 60

AGAACCAGCT ATCTnCAGGT TCGATTGGAA TTTCTCCGCT ACCC 104

35 (2) INFORMATION FOR SEQ ID NO: 4821:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

45 TCGTAGTGGT TTCCAACCAA GTTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTTCA 60

TTATTTTAAA TGCTCATTTA CATAGTnAAC TCGCTTTAAA ATAATTTAAC TCATGTCGCT 120

AACGTTTTCT TTTATAAAAG TTTAACGGTT TTATCTGTGG TGTCT 165

50 (2) INFORMATION FOR SEQ ID NO: 4822:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG 60

10 AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG 113

(2) INFORMATION FOR SEQ ID NO: 4823:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC 60

25 TTTGAnTTGT GACAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC 106

(2) INFORMATION FOR SEQ ID NO: 4824:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC 60

CGACCCGCAC GAAAGGCGTA ACGATTGCGG CACTGTCTCA ACTAGAGn 108

40

(2) INFORMATION FOR SEQ ID NO: 4825:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAAGCACC CCGGAAGTAG 60

nTGTAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGGTA ATGGGT 116

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA 60
 ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA 120
 ATCCTTGTAT TGC GTGTCAT AaAGTCTTTG CTCCTTGCAC 160

(2) INFORMATION FOR SEQ ID NO: 4827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC 60
 AAAGAAAATG GTTGGCCnAG TGAAACGTT TGAATCTGAC GAAACGAGAA AGAGC 115

(2) INFORMATION FOR SEQ ID NO: 4828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTTCATAATC CAAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT 60
 TCAGAAAGCT TTTGATTAACTTTAAAGTAT nCCCAATTAT AAT 103

(2) INFORMATION FOR SEQ ID NO: 4829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GGACCGAACT GTCTCAGCAG GTTCTnAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA 60
 GCCAACCCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A 111

(2) INFORMATION FOR SEQ ID NO: 4830:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

GTTGTTGGGG CCCC GCCGGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60
 TTTCGTTTCAG TCAACHACTG CCAATATAAC TTTGTAGAGC ATTGA 105

(2) INFORMATION FOR SEQ ID NO: 4831:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

ACATTGAGTC TTCGAGTCGT TGCATTTTCAC ACTGCCGnGA AAAGCCTCTA GATAGAAAAT 60
 AGGTGCCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

(2) INFORMATION FOR SEQ ID NO: 4832:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

TTnTAGAATG AACCGGCGAG TTACGATTTG ATGCAAGGTT AAGCAGTAA TGTGGAGCCG 60
 TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC 107

(2) INFORMATION FOR SEQ ID NO: 4833:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

5 TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAACCA GTGACTGTTG ACCTTGTTGT 60
 CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA 120
 TTTTCAGCAT CAATTTGATC AATC 144

10 (2) INFORMATION FOR SEQ ID NO: 4834:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

20 GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60
 GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG 108

25 (2) INFORMATION FOR SEQ ID NO: 4835:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

35 GACAATGGTA GGnGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60
 CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGCA GT 102

(2) INFORMATION FOR SEQ ID NO: 4836:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

50 TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTnGnCTT GACCTCGCGG 60
 TTTGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCAA 109

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTTCAAA GGCTCCTACC TATCCTGGTA CAAGCTGTGC 60
 CGGAATTTCa ATTGCAngC TACAGTAAAG CTCCACGGGG GTC 103

(2) INFORMATION FOR SEQ ID NO: 4838:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTTCAT AAACAATATC ACTTTAACCA AAAAATATTT 60
 GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 4839:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT 60
 ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAn AAAG 104

(2) INFORMATION FOR SEQ ID NO: 4840:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGTA GGTAGGAGCC 60
 TTGAAACGTG AGCGCTATTA GTGnAGGCGT GGTGGGTACT ACCCTAGCTG TGTTGGCTTT 120
 CTAACCC 127

(2) INFORMATION FOR SEQ ID NO: 4841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCACCC CGGGCAAGGT TGACTIONAAT TGGAAAAAAA CTTGGTTACA ACGTTATTTT 60
 CATTCACTCA ACTACTGCCA ATATAATATT GnAACTATA GGACATTAT TAGTGTTTCA 120
 GTTCT 125

(2) INFORMATION FOR SEQ ID NO: 4842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAnGCGCTC 60
 CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC 108

(2) INFORMATION FOR SEQ ID NO: 4843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTCCGATCG TAAAACTCTG TTATTAAGnA GGAACATGTG TGTAAGTAGC 60
 TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT 108

(2) INFORMATION FOR SEQ ID NO: 4844:

(A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

10 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGACCTGG GCAACGTTCT ACTCTAGCGG 60
 AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGACTTGTGT ACAATCG 117

(2) INFORMATION FOR SEQ ID NO: 4845:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

25 GACTGTTTAT CAAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG 60
 CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA 108

(2) INFORMATION FOR SEQ ID NO: 4846:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

40 CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC 60
 AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATTnTGCC TGAAAAAGAC GCACAAGT 118

(2) INFORMATION FOR SEQ ID NO: 4847:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

55 GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCCCTAA 60

(2) INFORMATION FOR SEQ ID NO: 4848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATTG TGCTCTGTAA CGTGCTTTCC AATTGGAAC GCACGTGnCC CTGCCCATAC 60
 CTACGGGACT TGACTTATAT TGTTTGCTT TGTACGTCAT TTCAACAATA GACGCCCATG 120
 CCAGCAACGC GATTACC 137

(2) INFORMATION FOR SEQ ID NO: 4849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTA CTTACCG 60
 TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACAhGGGGGG GGGGGG 116

(2) INFORMATION FOR SEQ ID NO: 4850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGhACCG 60
 TTATAGTTAC GGTCCGCCGT TTA CTTGGGGC TTCGATTCGT ATCTTCGCAG CTATATCTCA 120
 CTCCT 125

(2) INFORMATION FOR SEQ ID NO: 4851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

5 AAGTTGTATT TTAAAAATAG TTCTTTAAAT TATATACCCA CCACATTG TGGGAGAACC 60
TAAAAAAAAG CACTTCCCC AAAAATGGGA AAGTGC 96

(2) INFORMATION FOR SEQ ID NO: 4852:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGnAT 60
20 GAACCGGCGA GTTCACGATT TAGATGCAAG GTTGAAGCAG 100

(2) INFORMATION FOR SEQ ID NO: 4853:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTTA 60
35 ATCGATGGGG GACCCATAGG ATAGCGAACC TGCGATTGGA T 101

(2) INFORMATION FOR SEQ ID NO: 4854:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGACC GTGAGGAAAG 60
50 GTGAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

(2) INFORMATION FOR SEQ ID NO: 4855:

55

(A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

10 ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60
 CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

(2) INFORMATION FOR SEQ ID NO: 4856:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60
 25 TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCCT CTnTGGTAAA TCGCTAACTC 120
 CATCTCCTTA ACCCGGTA 138

(2) INFORMATION FOR SEQ ID NO: 4857:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

40 TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60
 TGGATGGCGC TATTGCTTTA GGTCATCCAT TAGGTGCTAC 100

(2) INFORMATION FOR SEQ ID NO: 4858:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

55

CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATTCAGTG CGGCTT

106

(2) INFORMATION FOR SEQ ID NO: 4859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

GTAACCTCGCC GGTTCATTCT ACAAAGGGC ACGCCAATCA CCCATTAACG GGCTCCTGAA 60
 CTAATTGTTA AGCAACACGG TTTCCAGGGT TCTATTTCCTA CTCCCCCTTT CCGGGGTnGC 120
 TTTTTCACCC TTTTTCCTCCC TCCACGGTTA CT 152

(2) INFORMATION FOR SEQ ID NO: 4860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

GCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGAnGAA TTCTAAGGTG AGCGAGCGAA 60
 CTCTCGTTAA GGAACCTCGGC AAATGACCC CGTCACTTCG 100

(2) INFORMATION FOR SEQ ID NO: 4861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA 60
 AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT 104

(2) INFORMATION FOR SEQ ID NO: 4862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60
 CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

(2) INFORMATION FOR SEQ ID NO: 4863:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAnTTTTCA ATGTA 105

(2) INFORMATION FOR SEQ ID NO: 4864:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60
 TGCCTTGCTG GATGATGCTA TGATATTGCA CATATCGAAT CAACAGTGGT GCATGAACCT 120
 GCAnTGGCT 129

(2) INFORMATION FOR SEQ ID NO: 4865:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

AAACCGCAAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60
 TCGACTACnT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT 60
 TATTTTAAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTAACT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60
 CGGTTTAGCA GAGACCTGTG TTTTGTATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

ACGAACGAT TGTCTTTCGT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60
 CTACTGCTC ATCAGGGATT ACAAACC 87

2) INFORMATION FOR SEQ ID NO: 4869:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:

CGCTCACCTT AGAATCTATT TACACTGGTG TTGGTAGGCA CTTTTTTCAA GCTTCCGATT 120
 AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA 165

(2) INFORMATION FOR SEQ ID NO: 4870:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

AATATCATTT ATAACATTAA GTAATAACTT TTTTATCTT GTCCATTTTA TTTTAAACC 60
 AAAATTTGAT TAAAAAAGTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G 111

(2) INFORMATION FOR SEQ ID NO: 4871:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTGGGC CTATCACTG CGGCTCTTCT 60
 GGGCGTTAAC CCTAAAGAGC ACCC 84

(2) INFORMATION FOR SEQ ID NO: 4872:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGGTA ACTGCATCTT CACAGGTACT 60
 ATGATTTTAC CGATCTCTCn ATGAACAGTG CCAAATCGTA C 101

(2) INFORMATION FOR SEQ ID NO: 4873:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

5 GACAGGCGTA GGCGATGGAT AACAGGTTGT ATTCCTGTAC CACCTATGAT CGTTTTAATC 60
GATGGGGGGA AGCATAGGAT AGGCGAA 87

(2) INFORMATION FOR SEQ ID NO: 4874:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

20 GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTTG ATCCCGCTAG TCTCCACCAT 60
TATTTGTACA TTGAAACTA G 81

(2) INFORMATION FOR SEQ ID NO: 4875:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG 60
35 CGAACTGAAT AAATAAGAT T 81

(2) INFORMATION FOR SEQ ID NO: 4876:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

AACGCGTTAA ATCTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG 60
50 TGGAACATAG ATTAAGTTAT TAAGGGC 87

(2) INFORMATION FOR SEQ ID NO: 4877:

55

(A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

10 ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA 60
 CGGGGAGGTT TgncCTCAAT GTGGCTCATC GGATCTTGGG G 101

(2) INFORMATION FOR SEQ ID NO: 4878:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

25 ATTTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AAACAGCTCG CTAGGTGTCT 60
 CAACTGCATG AGGTATATT 79

(2) INFORMATION FOR SEQ ID NO: 4879:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

40 ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA 60
 AAATTGGTAT GGTAATTGTG GCA 83

(2) INFORMATION FOR SEQ ID NO: 4880:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

55 CTTTCATCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 60

(2) INFORMATION FOR SEQ ID NO: 4881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG 60
 CTTACGCTT CTTGCGATTA 80

(2) INFORMATION FOR SEQ ID NO: 4882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCACG CTCAACCGTG GAGGGTCATT GGAACTGGA AAAGTTGAGT 60
 GCAGAAGAGG AAAGTGGGTT CCATGT 86

(2) INFORMATION FOR SEQ ID NO: 4883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGAC AAACAAGCTT CCATGACAAA 60
 AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT 120
 CGGTAA 127

(2) INFORMATION FOR SEQ ID NO: 4884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTTG GAGACCTCTA TTCTACCTTG AACTATGCCC 60
CTATTAAAAA TAATAAAT 78

(2) INFORMATION FOR SEQ ID NO: 4885:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60
GTGGATTGTC CTTTGGAAT GGGT 84

(2) INFORMATION FOR SEQ ID NO: 4886:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTCCG GTGGTGCACT TGCGACCAAC AATGGGTTGG AGATTGGATT 60
TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAANTGG TACCCCATCC AAAAGGG 117

(2) INFORMATION FOR SEQ ID NO: 4887:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT 60
ACCGTGAGGA AAGGTGAAAA 80

(2) INFORMATION FOR SEQ ID NO: 4888:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60

10

GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTACGGGGT CTTTGTCCGA 60

25

GTTCCCTTAAC GAGAGT 76

(2) INFORMATION FOR SEQ ID NO: 4890:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGCCCC CAACATAGGA GCTGATTTC TGTCAGCTTA CCATnATGTG GCAAGTTGGC 60

GGGGGCCCCC AAACCAAGGA GCTGGCTTTC TGTCACCTTA CCATTAATGT GGCAAGT 117

40

(2) INFORMATION FOR SEQ ID NO: 4891:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCATT GCATACTTTC AACATGAATA 60

CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCCTCGG TCTGTCTTA 109

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60
AGACCGTGTG TTTTGTAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTTCG GCAGTTCGAA 60
TCTGCCCCC TCCATTATT ATTTTAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTC CGACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60
GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

TTAGTATTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC 120
 TTATACCGAG TnGGAATCTC A 141

(2) INFORMATION FOR SEQ ID NO: 4896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTTCGGATT AATTGATTC ATTTGTGCG TAATTCAGA AGCCATTTTA TGAAAAGAGT 60
 GATTTAATTC ATAAATTTCT 80

(2) INFORMATION FOR SEQ ID NO: 4897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60
 AAACCAATTA GTA 73

(2) INFORMATION FOR SEQ ID NO: 4898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60
 TGCGTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT 60
 TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCG TGGTTT 116

(2) INFORMATION FOR SEQ ID NO: 4900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGGCGGTnTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC 60
 CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC 113

(2) INFORMATION FOR SEQ ID NO: 4901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT 60
 AAAAATAGGG AATACATG 78

(2) INFORMATION FOR SEQ ID NO: 4902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT 60
 CAAAAC TAGA TAGTAAGTAA AAGT 84

(2) INFORMATION FOR SEQ ID NO: 4903:

(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

10 TTGTCGGGTA AGTTCCGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG 60
AGACTCGGTG 70

(2) INFORMATION FOR SEQ ID NO: 4904:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

25 TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60
TCCTCTTCTT GGCTCTGCTT CTATTTGCCT CTAATGTGGC TTTTGTGTGT AATAAGTTAT 120
GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

30 (2) INFORMATION FOR SEQ ID NO: 4905:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

40 TGACTTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC 60
TTATCGTGGT GGGGA 75

45 (2) INFORMATION FOR SEQ ID NO: 4906:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

55

ACTCAGACAG TGACTCAGAT CAGATAGTg_n CTCGGATTCA GCGATTATTC AG

112

(2) INFORMATION FOR SEQ ID NO: 4907:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGACAC GTGCTACTAA
 AGGTTTACCA

60

70

(2) INFORMATION FOR SEQ ID NO: 4908:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

AGAAGATACA AATAAAG_nTA AACCCAAATT ATTCAATTC GGTGGGACAC AATAGTGTG
 ACTTTGAAGA AGATACACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC
 C

60

120

121

(2) INFORMATION FOR SEQ ID NO: 4909:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

GGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCTGA GATGTTGGGG
 TTAAGTCCCG

60

70

(2) INFORMATION FOR SEQ ID NO: 4910:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

5 GGACACCCGG AGAACTGAAA CATTAGTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60
 TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

(2) INFORMATION FOR SEQ ID NO: 4911:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

15 nTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAATAAC 60
 20 TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT AACTTTTGAT 120
 GTAAACTTTG GCACATCAGC TTTTAGTGTG TTTTCG 155

(2) INFORMATION FOR SEQ ID NO: 4912:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

30 CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTAGGAGCT 60
 AGCCGTCGA 69

(2) INFORMATION FOR SEQ ID NO: 4913:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

45 TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA 60
 GCGGAACGT 69

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA 60
ATACTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 4915:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTTCCGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT 60
CATCCGCTCA 70

(2) INFORMATION FOR SEQ ID NO: 4916:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTCACTCC 60
CCTTCCG 67

(2) INFORMATION FOR SEQ ID NO: 4917:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

TCCACCGTTG ACTAAGGTTT CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120
GGCGCACGTA GGCGATGATA CAGGTTATAT CCTACACCT A 161

5 (2) INFORMATION FOR SEQ ID NO: 4918:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCGTTGGC TTTCTGATTA GGTACCGCA AGATGTGCAC AGTTACTTAC 60
ACATATGT 68

20 (2) INFORMATION FOR SEQ ID NO: 4919:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60
AGTGACAATA CTTCAGGG 78

35 (2) INFORMATION FOR SEQ ID NO: 4920:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTTTCGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTTCGATTTCG 60
TACTTCGC 68

50 (2) INFORMATION FOR SEQ ID NO: 4921:

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

5 AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC 60
TTTACTG 67

(2) INFORMATION FOR SEQ ID NO: 4922:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

20 GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT 60
GTCATG 66

(2) INFORMATION FOR SEQ ID NO: 4923:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

35 GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA 60
TCGTGGGTGG GAG 73

(2) INFORMATION FOR SEQ ID NO: 4924:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

50 GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTTATTT TTTACACGAT GACATGAAAC 60
TGATGACATA TGCACCGTAA TTCCAAAAA 89

(2) INFORMATION FOR SEQ ID NO: 4925:

- (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

10 AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT 60
ACCTCCAA 68

(2) INFORMATION FOR SEQ ID NO: 4926:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

25 ACGAAAGGCG TAACGATTG GGCATGATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60
CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

40 ATTTCTATTA ATTATTTGCA TAGAAATCAG CTTTTTTGAT ATGTATTTTA TAATGTACAG 60
CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

55 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC 60

(2) INFORMATION FOR SEQ ID NO: 4929:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60
 GTGGGTCCCG ACACAGAGAA ATT 83

(2) INFORMATION FOR SEQ ID NO: 4930:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGGTAGAG CACTTGGTTT GGGACCAAGG GGTGCGAGTT CGAATCCTGT CTTCCCGATT 60
 ACTCTA 66

(2) INFORMATION FOR SEQ ID NO: 4931:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60
 GACCG 65

(2) INFORMATION FOR SEQ ID NO: 4932:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA 60
CACCAGTGGG CGA 73

5 (2) INFORMATION FOR SEQ ID NO: 4933:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT 60
GTCTG 65

20 (2) INFORMATION FOR SEQ ID NO: 4934:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTCTG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnt 60
TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTCGGGGT AACAAATGTA CAGGTTGGTG 120

35 (2) INFORMATION FOR SEQ ID NO: 4935:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT 60
GGATAACGGT TG 72

50 (2) INFORMATION FOR SEQ ID NO: 4936:

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

5 CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTT CTCCATATCT 60
CTGC 64

(2) INFORMATION FOR SEQ ID NO: 4937:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT 60
20 TGGT 64

(2) INFORMATION FOR SEQ ID NO: 4938:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60
35 GAT 63

(2) INFORMATION FOR SEQ ID NO: 4939:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

TAGAAATCAG CTTTTTTGCA TATGTATTTT ATAATGTACA GCTCGTTGAG CTGCTATTTT 60
CCT 63

50 (2) INFORMATION FOR SEQ ID NO: 4940:

55

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60
 TAGCTCAG 68

(2) INFORMATION FOR SEQ ID NO: 4941:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTCG ATTCCCTTAG TAGCGGCGAG 60
 CG 62

(2) INFORMATION FOR SEQ ID NO: 4942:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG 60
 TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

(2) INFORMATION FOR SEQ ID NO: 4943:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AAACATTATT 60

55

(2) INFORMATION FOR SEQ ID NO: 4944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60
 GACGAATACG TAATTGA 77

(2) INFORMATION FOR SEQ ID NO: 4945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTGAAGTT 60
 CAGGTAACAC TGAAT 75

(2) INFORMATION FOR SEQ ID NO: 4946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT 60
 TCCCTATAGC GGCGnCGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120
 TACAGCGCTG ACACT 135

(2) INFORMATION FOR SEQ ID NO: 4947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

GATTTGGGCT CTTCCATTTT GCTCGCCGCT ACTAAGGGAA TCGAATTTCC TTTCTCTTCC 60

T 61

(2) INFORMATION FOR SEQ ID NO: 4948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

GCTTTTGAGG AATTTAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAT 60

TGTTTGAATC 70

(2) INFORMATION FOR SEQ ID NO: 4949:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60

CTATTC 66

(2) INFORMATION FOR SEQ ID NO: 4950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT 60

TCACCGTAGG CATGCTGG 78

(2) INFORMATION FOR SEQ ID NO: 4951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAAATAAT GCGCGAGGAA GAGGGATTCG AACCCCCGTG GCCCGTTAAG 60

10

G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC 60

25

TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA 59

40

(2) INFORMATION FOR SEQ ID NO: 4954:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

50

CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT 59

10

(2) INFORMATION FOR SEQ ID NO: 4956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

20

AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTTAG TTCACGCGGG TTTTGCTTGG TAAATCTAT ATTTTACTTA CTTATCTAGT 60

35

TTTCAATGTA CAATTC 77

(2) INFORMATION FOR SEQ ID NO: 4958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAA 59

50

(2) INFORMATION FOR SEQ ID NO: 4959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

5 GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 59

(2) INFORMATION FOR SEQ ID NO: 4960:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAAGTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA 59

(2) INFORMATION FOR SEQ ID NO: 4961:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

30 ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA 59

(2) INFORMATION FOR SEQ ID NO: 4962:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA 59

(2) INFORMATION FOR SEQ ID NO: 4963:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50 (D) TOPOLOGY: linear

55

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGA CTGCCGG TGACAAACCG 60

(2) INFORMATION FOR SEQ ID NO: 4964:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

15 TAGTTTTGGT ACGTAACAA ATTTATTGA AGAAACAATC TCAAATAAAG AATTGTTTG 59

(2) INFORMATION FOR SEQ ID NO: 4965:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG 59

(2) INFORMATION FOR SEQ ID NO: 4966:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

40 TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTT TCAGTTCCG 59

(2) INFORMATION FOR SEQ ID NO: 4967:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTTCGCT ATGTATATCG CATTAAACGT 60

(2) INFORMATION FOR SEQ ID NO: 4968:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTTGTAGAGG CGACGCCCAG TCAAAGTCCG CGCTGACACT GTCTCCCACC 60

(2) INFORMATION FOR SEQ ID NO: 4969:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG 59

(2) INFORMATION FOR SEQ ID NO: 4970:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTACCCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60

TTACG 65

(2) INFORMATION FOR SEQ ID NO: 4971:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGACTTGATG ACAATCGACT 60

(2) INFORMATION FOR SEQ ID NO: 4972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60

AGGTAGG 67

(2) INFORMATION FOR SEQ ID NO: 4973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAACATGTC ATAAGAAATA CTAATTC 58

(2) INFORMATION FOR SEQ ID NO: 4974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA 58

(2) INFORMATION FOR SEQ ID NO: 4975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GACGCCACAT CCTTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG 60

(2) INFORMATION FOR SEQ ID NO: 4976:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTTTCGA CCCTGACTCG ACTTG TAGGT CTCGCAGTCA AGCTCCCTT 59

(2) INFORMATION FOR SEQ ID NO: 4977:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT 58

(2) INFORMATION FOR SEQ ID NO: 4978:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG 58

(2) INFORMATION FOR SEQ ID NO: 4979:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC 60

(2) INFORMATION FOR SEQ ID NO: 4980:

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

10 AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

GTGGTGTGTT AGGGCACTCT ATACGGGTAA CAAAGTACGA CATTAGACGG ATCATCTGGA 60

AAGATGAATC AAAGT 75

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTTTTCATT TTCATTTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

50 TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

55

- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

10 GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60
GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

25 CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:

35 TGATGAAGGT CTTGGATCG TAAACTCTG TTATTAGGGA AGACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

50 AAAGAATTG CGCAAACGC TATCGATACT GAAGGCGTT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

55

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA

57

10

(2) INFORMATION FOR SEQ ID NO: 4989:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

20

TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG

57

(2) INFORMATION FOR SEQ ID NO: 4990:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT

60

35

G

61

(2) INFORMATION FOR SEQ ID NO: 4991:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTCCATCC TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTC

60

50

ACCGA

65

(2) INFORMATION FOR SEQ ID NO: 4992:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT 57

10

(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

20

CCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACG 57

(2) INFORMATION FOR SEQ ID NO: 4994:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGTTTCGG GTCTACGACA AATACTAAAC GCCTATTCAG ACTCGCTTTC GCTACGG 57

35

(2) INFORMATION FOR SEQ ID NO: 4995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

45

CAAACCTCTCG TGGTGTGACG GCGGGTGTGG TACAAGCCCC GGGAACGTAT TCACCGTAGC 60

ATGCCCGTCT ACG 73

50

(2) INFORMATION FOR SEQ ID NO: 4996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

5 ACTAATTTCT ATAGGAAAAG TATTCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG 60
TAAGC 65

(2) INFORMATION FOR SEQ ID NO: 4997:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

ATTGGATTCC CAATTTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT 58

20

(2) INFORMATION FOR SEQ ID NO: 4998:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

30

AACTTCAACA GGTTTTGCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG 56

(2) INFORMATION FOR SEQ ID NO: 4999:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTGT 56

45

(2) INFORMATION FOR SEQ ID NO: 5000:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC 56

(2) INFORMATION FOR SEQ ID NO: 5001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC 56

(2) INFORMATION FOR SEQ ID NO: 5002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTCCGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG 56

(2) INFORMATION FOR SEQ ID NO: 5003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA 56

(2) INFORMATION FOR SEQ ID NO: 5004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

(2) INFORMATION FOR SEQ ID NO: 5005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCCTAGAA GCCGATG 57

(2) INFORMATION FOR SEQ ID NO: 5006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCCAC TCCCCTG 57

(2) INFORMATION FOR SEQ ID NO: 5007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA 60
AACCAAAGA 69

(2) INFORMATION FOR SEQ ID NO: 5008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTT AGTCAACTAC TGCCAATATA ACTTCGT 57

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:

ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC

(2) INFORMATION FOR SEQ ID NO: 5010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:

GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTIAC
TTGGG

(2) INFORMATION FOR SEQ ID NO: 5011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:

TTTACTTGTA TTGGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA

(2) INFORMATION FOR SEQ ID NO: 5012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:

CCTTATACAT CACCTTTACG GTTTTAGCAG AACCTGTGT TTTTGTATAA ACAGTCGCTT

(2) INFORMATION FOR SEQ ID NO: 5013:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

10 GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAAA TTGTGCAAGT TGGCGGGTCC 60
 ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

25 TAGGGTAGTA TCCACCAAGT GGCCTCCACG TAAGCTAGCG CTTACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTGAA 60
 40 GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA 105

(2) INFORMATION FOR SEQ ID NO: 5016:

45

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTATATGC TTATTCTTT ATTTATTATT ATTACAATTA CATTTT 56

55

(2) INFORMATION FOR SEQ ID NO: 5017:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

10 TCTGTAGAAA TTGGGGAATC CAATTCTCT TGGTTTGGGT CCCATCCCCA ACTTGCACAT 60
TATTG 65

(2) INFORMATION FOR SEQ ID NO: 5018:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

25 GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCCAATTT CTACAGACAA TGCAAC 56

(2) INFORMATION FOR SEQ ID NO: 5019:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC 55

40

(2) INFORMATION FOR SEQ ID NO: 5020:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

50 TACGGCGTTT AGTATTTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

55

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCCTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCCA

55

10

(2) INFORMATION FOR SEQ ID NO: 5022:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

20

AGAGTTCACA TCGACGGGGA GGTTCGAC CTCGATGTCG GCTCATCGCA TCCTG

55

(2) INFORMATION FOR SEQ ID NO: 5023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTTCCTT TCGAACACGG ACCTTATCAC CCATGGTC

58

35

(2) INFORMATION FOR SEQ ID NO: 5024:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

45

TAAAGGCTAA ACTACCAATG TTTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT

55

(2) INFORMATION FOR SEQ ID NO: 5025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGGAATT 60
5 CCA 63

(2) INFORMATION FOR SEQ ID NO: 5026:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGCGTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60
20 AACG 64

(2) INFORMATION FOR SEQ ID NO: 5027:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

35 (2) INFORMATION FOR SEQ ID NO: 5028:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

45 GGGCCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

(2) INFORMATION FOR SEQ ID NO: 5029:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:

CGTAACTATA ACGGTCCTAA GGTAGCCGAA ATTCCTTGTC GGGTAAGTTC CGAC

54

(2) INFORMATION FOR SEQ ID NO: 5030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:

ATCCCCGGGG CCCCAACACA GAGAATTTTCG AAAAGAAATT CTACAGGCAA TGCAAGT

57

(2) INFORMATION FOR SEQ ID NO: 5031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTC

54

(2) INFORMATION FOR SEQ ID NO: 5032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:

TCCCTATCCG TCGTGGGCGT AGGAAATTG AGAGGAGCTG TCCTTAGTAC GAGA

54

(2) INFORMATION FOR SEQ ID NO: 5033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:

(2) INFORMATION FOR SEQ ID NO: 5034:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC 54

(2) INFORMATION FOR SEQ ID NO: 5035:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA 54

(2) INFORMATION FOR SEQ ID NO: 5036:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAACCTCTG TGTTCCGGCAT GGGAACAGGT GTGA 54

(2) INFORMATION FOR SEQ ID NO: 5037:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG CGGAAG 56

(2) INFORMATION FOR SEQ ID NO: 5038:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

10 GACCGGGATG GACATACCTC TGGTGTACCA GTTTGTCGTG CCAACGCATA AGCT 54

(2) INFORMATION FOR SEQ ID NO: 5039:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTCACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG 54

25 (2) INFORMATION FOR SEQ ID NO: 5040:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

35

TTATAACACG TATGCTTGGG GAGTGTAATA AGCTTGATCA GAGATTCCnA TGGAACCAG 60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG 105

40

(2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

GCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC 54

50

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs

55

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG

54

10

(2) INFORMATION FOR SEQ ID NO: 5043:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

20

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA

53

(2) INFORMATION FOR SEQ ID NO: 5044:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCAGATT CCGACGGATT TCACGTGCT

59

35

(2) INFORMATION FOR SEQ ID NO: 5045:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG

60

TT

62

50

(2) INFORMATION FOR SEQ ID NO: 5046:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

CGTCATCCCC ACCTTCCTCC GGTGTGTCAC CGGCAGTCAA CTTAGAGTGC CCA

53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG

53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA

53

(2) INFORMATION FOR SEQ ID NO: 5049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAAATTCTC AATGTGTTT

59

(2) INFORMATION FOR SEQ ID NO: 5050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAGAC GACTTCATG 60
TTACGTTGAC TTTAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G 111

5 (2) INFORMATION FOR SEQ ID NO: 5051:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA 53

30 (2) INFORMATION FOR SEQ ID NO: 5053:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

55

(2) INFORMATION FOR SEQ ID NO: 5055:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAAGCAC TGTTTGGACG AGG 53

(2) INFORMATION FOR SEQ ID NO: 5056:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCTTTT GCATAATTGA 60
CAA 63

(2) INFORMATION FOR SEQ ID NO: 5057:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCCGCCAA CTGCAATTGT CTGTAGAATT CCTTTTCGAA ATTC 54

(2) INFORMATION FOR SEQ ID NO: 5058:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG 53

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:

TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA

(2) INFORMATION FOR SEQ ID NO: 5060:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:

AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT

(2) INFORMATION FOR SEQ ID NO: 5061:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:

TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC

(2) INFORMATION FOR SEQ ID NO: 5062:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC ACATCAGCGT CA

(2) INFORMATION FOR SEQ ID NO: 5063:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTTCTTT TTATTTTGAC GTTTTAGACA TA

52

10

(2) INFORMATION FOR SEQ ID NO: 5064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

20

CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTTC CGACCGTTCT GGGGGGAAC

60

TTGGAGCGCC TCCGTT

76

25

(2) INFORMATION FOR SEQ ID NO: 5065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

35

CCACCGCTTG TGCGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT

54

(2) INFORMATION FOR SEQ ID NO: 5066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGGACAATG GTAGG

55

50

(2) INFORMATION FOR SEQ ID NO: 5067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA

52

(2) INFORMATION FOR SEQ ID NO: 5068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA

60

GCGAGCCGGAA ACAACAACAA CG

82

(2) INFORMATION FOR SEQ ID NO: 5069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTCGGTC TA

52

(2) INFORMATION FOR SEQ ID NO: 5070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCAT CACAGCTCAG CCTTAACGAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GA

52

(2) INFORMATION FOR SEQ ID NO: 5072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA

53

(2) INFORMATION FOR SEQ ID NO: 5073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTCCG CAATGGGCGA AA

52

(2) INFORMATION FOR SEQ ID NO: 5074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTTAAAG AGTGCCTAAT AGCTCACTAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AAACTTCCCT TTGG

74

(2) INFORMATION FOR SEQ ID NO: 5076:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAATC AGACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAA GAT

53

(2) INFORMATION FOR SEQ ID NO: 5077:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT CGCTAGAGTA GA

52

(2) INFORMATION FOR SEQ ID NO: 5078:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTGGG CACTGTCTCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5079:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGACC AGAAATGATG GTATTTAATA AT

52

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:

AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG

(2) INFORMATION FOR SEQ ID NO: 5081:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:

CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA

(2) INFORMATION FOR SEQ ID NO: 5082:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:

CAGACACGGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA

(2) INFORMATION FOR SEQ ID NO: 5083:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:

AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTTCCTA

CG

(2) INFORMATION FOR SEQ ID NO: 5084:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

10

GTGTACCAGT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG

52

(2) INFORMATION FOR SEQ ID NO: 5085:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATTC GAATGCGAAC

60

CCGAGGAGCG GATTAACA

78

25

(2) INFORMATION FOR SEQ ID NO: 5086:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT

52

(2) INFORMATION FOR SEQ ID NO: 5087:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

50

AAGTTGTTCT CAGTTCGGAT TGTAAGTCTGC AACTCGACTA CATGAAGCTG G

51

(2) INFORMATION FOR SEQ ID NO: 5088:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATACTTTTAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T

51

10

(2) INFORMATION FOR SEQ ID NO: 5089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

20

AGAACGTAAA TTTAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G

51

(2) INFORMATION FOR SEQ ID NO: 5090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCGGTC C

51

35

(2) INFORMATION FOR SEQ ID NO: 5091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

45

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T

51

(2) INFORMATION FOR SEQ ID NO: 5092:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCCCTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCCA

55

(2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A

51

(2) INFORMATION FOR SEQ ID NO: 5094:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A

51

(2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT

60

ATTGTGCCAC CGATTGA

77

(2) INFORMATION FOR SEQ ID NO: 5096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG

52

(2) INFORMATION FOR SEQ ID NO: 5097:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

GGGTCTGTTT TCTAATTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A

51

(2) INFORMATION FOR SEQ ID NO: 5098:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T

51

(2) INFORMATION FOR SEQ ID NO: 5099:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:

CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A

51

(2) INFORMATION FOR SEQ ID NO: 5100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A

51

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTCAT ATTCTAGTCA GGGGCCCCAA 60
CACA 64

(2) INFORMATION FOR SEQ ID NO: 5102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG 58

(2) INFORMATION FOR SEQ ID NO: 5103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 5104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTCGCCATT AATACTACGT ATTAACATGT AAT 53

(2) INFORMATION FOR SEQ ID NO: 5105:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

10 ATTTCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT 50

(2) INFORMATION FOR SEQ ID NO: 5106:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTCGA 50

25 (2) INFORMATION FOR SEQ ID NO: 5107:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

35

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT 50

(2) INFORMATION FOR SEQ ID NO: 5108:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA 50

50

(2) INFORMATION FOR SEQ ID NO: 5109:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT

50

(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTCCGT CTA

53

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCGCCTGA GGAGTACGAC CTC

53

(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT

50

(2) INFORMATION FOR SEQ ID NO: 5113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

AGAnTTTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCAATG

50

(2) INFORMATION FOR SEQ ID NO: 5114:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTGA TTCACACTG

50

(2) INFORMATION FOR SEQ ID NO: 5115:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAC TCATTATCAA GTTATGCACG TGTAATGAA TTCGGCTTTA TCGAA

55

(2) INFORMATION FOR SEQ ID NO: 5116:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTACTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA

50

(2) INFORMATION FOR SEQ ID NO: 5117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTh

50

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

(2) INFORMATION FOR SEQ ID NO: 5119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACTTTTAC TTACTATCTA

(2) INFORMATION FOR SEQ ID NO: 5120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGTTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG

(2) INFORMATION FOR SEQ ID NO: 5121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:

ATAATCCTGT AGTCGAAAAT GTTGCTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG

T

(2) INFORMATION FOR SEQ ID NO: 5122:

(A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

TAGCGACTCA GATTGAGACA GCGATTGAGA CAGCGACTCA GACTCAGATA

50

10

7

(2) INFORMATION FOR SEQ ID NO: 5123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT

50

7

(2) INFORMATION FOR SEQ ID NO: 5124:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

TACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCCAGAGAAG GTCTCTATCT

60

35

C

2) INFORMATION FOR SEQ ID NO: 5125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

.GAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT

60

A

.GAA

64

50

A

2) INFORMATION FOR SEQ ID NO: 5126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT 57

10

(2) INFORMATION FOR SEQ ID NO: 5127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

20

GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG 50

(2) INFORMATION FOR SEQ ID NO: 5128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTTTA GCAGTTGTTG CTTGTTCAA TTTTATGGGG CCATTTATGG 50

35

(2) INFORMATION FOR SEQ ID NO: 5129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

45

TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A 51

(2) INFORMATION FOR SEQ ID NO: 5130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGGTCGAATC CTCTTTT

57

(2) INFORMATION FOR SEQ ID NO: 5131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A

51

(2) INFORMATION FOR SEQ ID NO: 5132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A

51

(2) INFORMATION FOR SEQ ID NO: 5133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTCAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC

59

(2) INFORMATION FOR SEQ ID NO: 5134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

(2) INFORMATION FOR SEQ ID NO: 5135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACnAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG

50

(2) INFORMATION FOR SEQ ID NO: 5136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT

50

(2) INFORMATION FOR SEQ ID NO: 5138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC

50

(2) INFORMATION FOR SEQ ID NO: 5139:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

10 GGTTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC 52

(2) INFORMATION FOR SEQ ID NO: 5140:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT 56

25 (2) INFORMATION FOR SEQ ID NO: 5141:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

35

AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA 52

(2) INFORMATION FOR SEQ ID NO: 5142:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT 56

50

(2) INFORMATION FOR SEQ ID NO: 5143:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAAC AATTACATC CAAACCTTCA TCACTCACGC GCGTTGCTC CGTCAGCTTT 60
CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCTTTTGG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA

50

(2) INFORMATION FOR SEQ ID NO: 5148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAAATAA TGACTCCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 5149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAAAC TG AACATCTTA AGTACCCGGA GAAAGAGAAA

50

(2) INFORMATION FOR SEQ ID NO: 5150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTCGC ACTACCATCG ACGCTAAGGG AGCTTAACTT CTGTGGTTCG GCATGG

56

(2) INFORMATION FOR SEQ ID NO: 5151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

(2) INFORMATION FOR SEQ ID NO: 5152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAAC TT GCACACTATT GTAAGCTGAC TTTCCTCCA 59

(2) INFORMATION FOR SEQ ID NO: 5153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTCGGATAC TGTTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA 60

ATACA 65

(2) INFORMATION FOR SEQ ID NO: 5154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60

TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

(2) INFORMATION FOR SEQ ID NO: 5155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

(2) INFORMATION FOR SEQ ID NO: 5156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC 58

(2) INFORMATION FOR SEQ ID NO: 5157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAACTCC GGTATAGGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT G 51

(2) INFORMATION FOR SEQ ID NO: 5158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC 50

(2) INFORMATION FOR SEQ ID NO: 5159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T 51

(2) INFORMATION FOR SEQ ID NO: 5160:

(A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

10 AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTCGCTG CCCTTTGTAT 60
 T 61

2) INFORMATION FOR SEQ ID NO: 5161:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

3ACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51

25 A

2) INFORMATION FOR SEQ ID NO: 5162:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

CGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55

C

2) INFORMATION FOR SEQ ID NO: 5163:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

TTGATCTGT ATTAAAAATG ATATTTTCTA TCTTTTCTTT ATTATTAACG TCTATGACGT 60

50 C

STAGTATAA GATTCCGTGT A 81

C

2) INFORMATION FOR SEQ ID NO: 5164:

55

- (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

10 GTTCGAATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60
 AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

25 CAGGGGTCTT TCGTCCTGTG TGGGTAAGT CATCTTCACA GGTACTATGA TTCA 55

(2) INFORMATION FOR SEQ ID NO: 5166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

35 AAGCTGAGGC CGACAGCGTA GGCGATGGAT GACAGGTTGA TATTGCCGGT ACCACCCGAT 60

40 AA 62

(2) INFORMATION FOR SEQ ID NO: 5167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

50 CTTGCGTCTC CAGTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CG 52

(2) INFORMATION FOR SEQ ID NO: 5168:

55

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

10 TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAACTAG ATAAGTAGTA AATATA 56

(2) INFORMATION FOR SEQ ID NO: 5169:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA 55

(2) INFORMATION FOR SEQ ID NO: 5170:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

35 CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA 52

(2) INFORMATION FOR SEQ ID NO: 5171:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAAGTTC TnAGGCAATG TAAAAAAGCT GATTCTATT 50

(2) INFORMATION FOR SEQ ID NO: 5172:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:

5 AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTCTGAAG 60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn 50

(2) INFORMATION FOR SEQ ID NO: 5174:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

30 CAACTCTCGT TAAGGAACTC GGCAAATAC CCCGTAACCT CGGAGTAGGT CTCTTTA 57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA 60

(2) INFORMATION FOR SEQ ID NO: 5176:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

GTAACGGACG CGCTCAAAGG TTCCTCACA ATGGTTGGAA ATCATTGATA

50

(2) INFORMATION FOR SEQ ID NO: 5177:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

AGTTACGTTT TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG

50

(2) INFORMATION FOR SEQ ID NO: 5178:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCCGT CGGCAATCTG GGG

53

(2) INFORMATION FOR SEQ ID NO: 5179:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

CGGTAACTTC ATACCTTTTA ACATATTTTG CATTGATTG CGTTTACCTT TTTTACCTTT

60

ACCGCCACCA GTGAACTGTT TCA

83

(2) INFORMATION FOR SEQ ID NO: 5180:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

TTTAAA

66

(2) INFORMATION FOR SEQ ID NO: 5181:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

GTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC
GCAATAT

60

67

(2) INFORMATION FOR SEQ ID NO: 5182:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCACTAG CGAAGGCAAC TTTCT

55

(2) INFORMATION FOR SEQ ID NO: 5183:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT

50

(2) INFORMATION FOR SEQ ID NO: 5184:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

CC

62

(2) INFORMATION FOR SEQ ID NO: 5185:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGT

(2) INFORMATION FOR SEQ ID NO: 5186:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTAA GTTGGGCACT CTAAGTTGAC TGCCGnGnC ACCnAAGAAG

(2) INFORMATION FOR SEQ ID NO: 5187:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:

TTAATACGTT GCAATCCAAT CGCACGCTTC GCCTATCCTA CTGCCnTCCC

(2) INFORMATION FOR SEQ ID NO: 5188:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCCC TTACCGCAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

(2) INFORMATION FOR SEQ ID NO: 5190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGnAC CCTTGACCG ACTACAGCCC AGATCGATGA

(2) INFORMATION FOR SEQ ID NO: 5191:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT

(2) INFORMATION FOR SEQ ID NO: 5192:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 320 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
 1 5 10 15

EP 0 786 519 A2

	20	25	30
5	Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys 35 40 45		
	Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu 50 55 60		
10	Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys 65 70 75 80		
	Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp 85 90 95		
15	Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr 100 105 110		
	Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp 115 120 125		
20	Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala 130 135 140		
	Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Xaa Glu Gly 145 150 155 160		
25	Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu 165 170 175		
	Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser 180 185 190		
30	Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu 195 200 205		
	Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys 210 215 220		
35	Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Ile 225 230 235 240		
	Ile Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu 245 250 255		
40	Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu 260 265 270		
	Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys 275 280 285		
45	Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu 290 295 300		
50	Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln 305 310 315 320		

55 (2) INFORMATION FOR SEQ ID NO:5193:

(A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

Met	Asn	Lys	Val	Ile	Lys	Met	Leu	Val	Val	Thr	Leu	Ala	Phe	Leu	Leu	1	5	10	15
Val	Leu	Ala	Gly	Cys	Ser	Gly	Asn	Ser	Asn	Lys	Gln	Ser	Ser	Asp	Asn	20	25	30	
Lys	Asp	Lys	Glu	Thr	Thr	Ser	Ile	Lys	His	Ala	Met	Gly	Thr	Thr	Glu	35	40	45	
Ile	Lys	Gly	Lys	Pro	Lys	Arg	Val	Val	Thr	Leu	Tyr	Gln	Gly	Ala	Thr	50	55	60	
Asp	Val	Ala	Val	Ser	Leu	Gly	Val	Lys	Pro	Val	Gly	Ala	Val	Glu	Ser	65	70	75	80
Trp	Thr	Gln	Lys	Pro	Lys	Phe	Glu	Tyr	Ile	Lys	Asn	Asp	Leu	Lys	Asp	85	90	95	
Thr	Lys	Ile	Val	Gly	Gln	Glu	Pro	Ala	Pro	Asn	Leu	Glu	Glu	Ile	Ser	100	105	110	
Lys	Leu	Lys	Pro	Asp	Leu	Ile	Val	Ala	Ser	Lys	Val	Arg	Asn	Glu	Lys	115	120	125	
Val	Tyr	Asp	Gln	Leu	Ser	Lys	Ile	Ala	Pro	Thr	Val	Ser	Thr	Asp	Thr	130	135	140	
Val	Phe	Lys	Phe	Lys	Asp	Thr	Thr	Lys	Leu	Met	Gly	Lys	Ala	Leu	Gly	145	150	155	160
Lys	Glu	Lys	Glu	Ala	Glu	Asp	Leu	Leu	Lys	Lys	Tyr	Asp	Asp	Lys	Val	165	170	175	
Ala	Ala	Phe	Gln	Lys	Asp	Ala	Lys	Ala	Lys	Tyr	Lys	Asp	Ala	Trp	Pro	180	185	190	
Leu	Lys	Ala	Ser	Val	Val	Asn	Phe	Arg	Ala	Asp	His	Thr	Arg	Ile	Tyr	195	200	205	
Ala	Gly	Gly	Tyr	Ala	Gly	Glu	Ile	Leu	Asn	Asp	Leu	Gly	Phe	Lys	Arg	210	215	220	
Asn	Lys	Asp	Leu	Gln	Lys	Gln	Val	Asp	Asn	Gly	Lys	Asp	Ile	Ile	Gln	225	230	235	240
Leu	Thr	Ser	Lys	Glu	Ser	Ile	Pro	Leu	Met	Asn	Ala	Asp	His	Ile	Phe	245	250	255	

Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys
260 265 270

5 Thr Glu Ser Glu Trp Thr Ser Ser Lys Glu Trp Lys Asn Leu Asp Ala
275 280 285

Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ile Thr Trp Asn
290 295 300

10 Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr
305 310 315 320

Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys
325 330

15

(2) INFORMATION FOR SEQ ID NO:5194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

20

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

30 Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile
1 5 10 15

Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly
20 25 30

35 Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr
35 40 45

Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe
50 55 60

40 Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val
65 70 75 80

Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val
85 90 95

45

Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala
100 105 110

50 Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly
115 120 125

Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile
130 135 140

55 Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn
145 150 155 160

EP 0 786 519 A2

Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn
165 170 175

5 Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala
180 185 190

Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr
195 200 205

10 Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu
210 215 220

Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp
225 230 235 240

15 Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu
245 250 255

Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val
260 265 270

20 Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly
275 280 285

25 Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn
290 295 300

Lys Asn Leu Arg Leu Xaa Ser His Lys Gln
305 310

(2) INFORMATION FOR SEQ ID NO:5195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 280 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala
1 5 10 15

Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser
20 25 30

Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp
35 40 45

Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn
50 55 60

55 Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe
65 70 75 80

EP 0 786 519 A2

Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser
85 95

5 Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys
100 105 110

Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro
115 120 125

10 Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala
130 135 140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys
145 150 155 160

15 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala
165 170 175

Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn
180 185 190

20 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile
195 200 205

25 Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile
210 215 220

Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile
225 230 235 240

30 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp
245 250 255

Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys
260 265 270

35 Ala Ile Glu Thr Ser Leu Ala Lys
275 280

(2) INFORMATION FOR SEQ ID NO:5196:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val
1 5 10 15

55 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys
20 25 30

Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys
 35 40 45
 5 Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Glu Leu Asp Ile Lys Thr
 50 55 60
 Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile
 65 70 75 80
 10 Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys
 85 90 95
 Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro
 100 105 110
 15 Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys
 115 120 125
 Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe
 130 135 140
 20 Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val
 145 150 155 160
 Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp
 165 170 175
 25 Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr
 180 185 190
 Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile
 195 200 205
 30 Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala
 210 215 220
 Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln
 225 230 235 240
 Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp
 245 250 255
 40 Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala
 260 265 270
 Lys

(2) INFORMATION FOR SEQ ID NO:5197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

5	Met	Lys	Lys	Ile	Lys	Tyr	Ile	Leu	Val	Val	Phe	Val	Leu	Ser	Leu	Thr	1	5	10	15
	Val	Leu	Ser	Gly	Cys	Ser	Leu	Pro	Gly	Leu	Gly	Ser	Lys	Ser	Thr	Lys	20	25	30	
10	Asn	Asp	Val	Lys	Ile	Thr	Ala	Leu	Ser	Thr	Ser	Glu	Ser	Gln	Ile	Ile	35	40	45	
	Ser	His	Met	Leu	Arg	Leu	Leu	Ile	Glu	His	Asp	Thr	His	Gly	Lys	Ile	50	55	60	
15	Lys	Pro	Thr	Leu	Val	Asn	Asn	Leu	Gly	Ser	Ser	Thr	Ile	Gln	His	Asn	65	70	75	80
	Ala	Leu	Ile	Asn	Gly	Asp	Ala	Asn	Ile	Ser	Gly	Val	Arg	Tyr	Asn	Gly	85	90	95	
20	Thr	Asp	Leu	Thr	Gly	Ala	Leu	Lys	Glu	Ala	Pro	Ile	Lys	Asn	Pro	Lys	100	105	110	
	Lys	Ala	Met	Ile	Ala	Thr	Gln	Gln	Gly	Phe	Lys	Lys	Lys	Phe	Asp	Gln	115	120	125	
25	Thr	Phe	Phe	Asp	Ser	Tyr	Gly	Phe	Ala	Asn	Thr	Tyr	Ala	Phe	Met	Val	130	135	140	
	Thr	Lys	Glu	Thr	Ala	Lys	Lys	Tyr	His	Leu	Glu	Thr	Val	Ser	Asp	Leu	145	150	155	160
30	Ala	Lys	His	Ser	Lys	Asp	Leu	Arg	Leu	Gly	Met	Asp	Ser	Ser	Trp	Met	165	170	175	
	Asn	Arg	Lys	Gly	Asp	Gly	Tyr	Glu	Gly	Phe	Lys	Lys	Glu	Tyr	Gly	Phe	180	185	190	
35	Asp	Phe	Gly	Thr	Val	Arg	Pro	Met	Gln	Ile	Gly	Leu	Val	Tyr	Asp	Ala	195	200	205	
40	Leu	Asn	Ser	Glu	Lys	Leu	Asp	Val	Ala	Leu	Gly	Tyr	Ser	Thr	Asp	Gly	210	215	220	
	Arg	Ile	Ala	Ala	Tyr	Asp	Leu	Lys	Val	Leu	Lys	Asp	Asp	Lys	Gln	Phe	225	230	235	240
45	Phe	Pro	Pro	Tyr	Ala	Ala	Ser	Ala	Val	Ala	Thr	Asn	Glu	Leu	Leu	Arg	245	250	255	
	Gln	His	Pro	Glu	Leu	Lys	Thr	Thr	Ile	Asn	Lys	Leu	Thr	Gly	Lys	Ile	260	265	270	
50	Ser	Thr	Ser	Glu	Met	Gln	Arg	Leu	Asn	Tyr	Glu	Ala	Asp	Gly	Lys	Gly	275	280	285	
55	Lys	Glu	Pro	Ala	Val	Val	Ala	Glu	Glu	Phe	Leu	Lys	Lys	His	His	Tyr	290	295	300	

Phe Asp Lys Gln Lys Gly Gly His Lys
305 310

(2) INFORMATION FOR SEQ ID NO:5198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1 5 10 15
Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
20 20 25 30
Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
25 35 40 45
Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
50 55 60
Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
30 65 70 75 80
Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
85 90 95
Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
35 100 105 110
Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
115 120 125
Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
40 130 135 140
Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
45 145 150 155 160
Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
165 170 175
Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile
50 180 185 190
Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
195 200 205
Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
55 210 215 220

EP 0 786 519 A2

Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
225 230 235 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
245 250 255

Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
260 265 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1 5 10 15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
20 25 30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
35 40 45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
50 55 60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
65 70 75 80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
85 90 95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
100 105 110

Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
115 120 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
130 135 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
145 150 155 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
165 170 175

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile
 180 185 190
 Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
 5 195 200 205
 Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
 210 215 220
 Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
 10 225 230 235 240
 Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
 245 250 255
 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
 15 260 265 270
 Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
 275 280

(2) INFORMATION FOR SEQ ID NO:5200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu
 1 5 10 15
 Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn
 20 25 30
 Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn
 35 40 45
 Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn
 50 55 60
 Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys
 65 70 75 80
 Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu
 85 90 95
 Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn
 100 105 110
 Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys
 115 120 125

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn
 130 135 140
 Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile
 145 150 155 160
 Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro
 165 170 175
 Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu
 180 185 190
 Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys
 195 200 205

(2) INFORMATION FOR SEQ ID NO:5201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile
 1 5 10 15
 Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser
 20 25 30
 Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn
 35 40 45
 Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu
 50 55 60
 Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn
 65 70 75 80
 Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp
 85 90 95
 Asp Ile Asn Thr Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu
 100 105 110
 Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser
 115 120 125
 Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser
 130 135 140
 Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr

Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys
 165 170 175

Arg Ala Cys Glu Pro Asp Lys Tyr
 180

(2) INFORMATION FOR SEQ ID NO:5202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile
 1 5 10 15

Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
 20 25 30

Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
 35 40 45

Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
 50 55 60

Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
 65 70 75 80

Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
 85 90 95

Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
 100 105 110

Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
 115 120 125

Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn
 130 135 140

Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
 145 150 155 160

Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val
 165 170 175

Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
 180 185 190

Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys

(2) INFORMATION FOR SEQ ID NO:5203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

```

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser
1           5           10           15

Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
20           25           30

Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
35           40           45

Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
50           55           60

Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
65           70           75           80

Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
85           90           95

Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
100          105          110

Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
115          120          125

Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
130          135          140

Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
145          150          155          160

Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
165          170          175

Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
180          185          190

Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
195          200          205

Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
210          215          220

```

225 230 235 240
 Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro
 245 250 255
 Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln
 260 265 270
 Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile
 275 280

(2) INFORMATION FOR SEQ ID NO:5204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:

Met Lys Lys Phe Ile Gly Ser Val Leu Ala Thr Thr Leu Ile Leu Gly
 1 5 10 15
 Gly Cys Ser Thr Met Glu Asn Glu Ser Lys Lys Asp Thr Lys Thr Glu
 20 25 30
 Thr Lys Ser Val Pro Glu Glu Met Glu Ala Ser Lys Tyr Val Gly Gln
 35 40 45
 Gly Phe Gln Pro Pro Ala Glu Lys Asn Ala Ile Glu Phe Ala Lys Lys
 50 55 60
 His Arg Lys Glu Phe Glu Lys Val Gly Glu Gln Phe Phe Lys Asp Asn
 65 70 75 80
 Phe Gly Leu Lys Val Lys Ala Thr Asn Val Val Gly Lys Asp Asp Gly
 85 90 95
 Val Glu Val Tyr Val His Cys Glu Asp His Gly Ile Val Phe Asn Ala
 100 105 110
 Ser Leu Pro Leu Tyr Lys Asp Ala Ile His Gln Lys Gly Ser Met Arg
 115 120 125
 Ser Asn Asp Asn Gly Asp Asp Met Ser Met Met Val Gly Thr Val Leu
 130 135 140
 Ser Gly Phe Glu Tyr Arg Ala Gln Lys Glu Lys Tyr Asp Asn Leu Tyr
 145 150 155 160
 Lys Phe Phe Lys Glu Asn Glu Lys Lys Tyr Gln Tyr Thr Gly Phe Thr
 165 170 175

180 185 190
 Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr
 195 200 205
 5 Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met
 210 215 220
 Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val
 10 225 230 235 240
 Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val
 245 250 255
 Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys
 15 260 265 270
 Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn
 275 280 285
 20 Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val
 290 295 300
 His Ser Lys Asp Glu
 305

(2) INFORMATION FOR SEQ ID NO:5205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

40 Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly
 1 5 10 15
 Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu
 20 25 30
 45 Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln
 35 40 45
 Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys
 50 55 60
 50 Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met
 65 70 75 80
 Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser
 85 90 95

EP 0 786 519 A2

	100		105		110
	Val Gln Ser Lys Leu Asn Gln Ile Ser Asn Asp Ile Gln Ser Ala His				
	115		120		125
5	Thr Ser Tyr Lys Asp Ala Ile Asp Gly Leu Ser Leu Ser Asp Asp Asp				
	130		135		140
	Lys Lys Thr Ser Lys Asn Ile Asp Lys Leu Asn Ser Asp Leu Asn His				
10	145		150		155
	Ala Phe Asp Asp Ile Lys Asn Gly Tyr Gln Asn Lys Asp Lys Lys Gln				
	165		170		175
	Leu Thr Lys Gly Gln Gln Ala Leu Ser Lys Leu Asn Leu Asn Ala Lys				
15	180		185		190
	Ser				

20 (2) INFORMATION FOR SEQ ID NO:5206:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

35	Met Lys Arg Leu Leu Phe Val Met Ile Ala Phe Val Phe Ile Leu Ala
	1 5 10 15
	Ala Cys Gly Asn Asn Ser Ser Lys Asp Lys Glu Ala Ser Lys Asp Ser
	20 25 30
40	Lys Thr Ile Asn Val Gly Thr Glu Gly Thr Tyr Ala Pro Phe Ser Phe
	35 40 45
	His Asp Lys Asp Gly Lys Leu Thr Gly Tyr Asp Ile Asp Val Ile Lys
	50 55 60
45	Ala Val Ala Lys Glu Glu Gly Leu Lys Leu Lys Phe Asn Glu Thr Ser
	65 70 75 80
	Trp Asp Ser Met Phe Ala Gly Leu Asp Ala Gly Arg Phe Asp Val Ile
	85 90 95
50	Ala Asn Gln Val Gly Ile Asn Pro Asp Arg Glu Lys Lys Tyr Lys Phe
	100 105 110
	Ser Lys Pro Tyr Thr Phe Ser Ser Ala Val Leu Val Ile Arg Glu Asn
55	115 120 125

EP 0 786 519 A2

130 135 140

Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala
 145 150 155 160

5 Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu Leu
 165 170 175

Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp
 180 185 190

10 Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn
 195 200 205

Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp
 210 215 220

15 Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn
 225 230 235 240

Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser
 245 250 255

20 Lys Ser Lys

(2) INFORMATION FOR SEQ ID NO:5207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

Met Gly Val His Ser Met Lys Leu Lys Arg Leu Phe Ala Val Val Ile
 1 5 10 15

Ala Met Leu Leu Val Leu Ala Gly Cys Ser Asn Ser Asn Asp Asn Asn
 20 25 30

Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln
 35 40 45

Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Leu Ala Ser
 50 55 60

Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly
 65 70 75 80

Gly Ser Gly Ala Leu Arg Lys Gln Ile Glu Ser Gly Ala Pro Val Asp
 85 90 95

100 105 110
 Asn Lys Ala His Asp Thr Tyr Lys Tyr Ala Lys Asn Ser Leu Val Leu
 115 120 125
 5
 Ile Gly Asp Lys Asp Ser Asn Tyr Thr Ser Val Lys Asp Leu Lys Asp
 130 135 140
 Asn Asp Lys Leu Ala Leu Gly Glu Val Lys Thr Val Pro Ala Gly Lys
 145 150 155 160
 10
 Tyr Ala Lys Gln Tyr Leu Asp Asn Asn Asn Leu Phe Lys Glu Val Glu
 165 170 175
 Ser Xaa Ile Val Tyr Ala Lys Asp Val Lys Gln Val Leu Asn Tyr Val
 180 185 190
 15
 Xaa Lys Gly Asn Ala Lys Gln Gly Phe Val Tyr
 195 200

20 (2) INFORMATION FOR SEQ ID NO:5208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu
 1 5 10 15
 35
 Leu Leu Gly Ala Cys Gly Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp
 20 25 30
 Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile
 35 40 45
 40
 Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys
 50 55 60
 45
 Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile
 65 70 75 80
 Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu
 85 90 95
 50
 Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys
 100 105 110
 Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe
 115 120 125
 55

EP 0 786 519 A2

[illegible]

(2) INFORMATION FOR SEQ ID NO:5209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

50 Met Lys Arg Leu Ser Ile Ile Val Ile Ile Gly Ile Phe Ile Ile Thr
1 5 10 15
Gly Cys Asp Trp Gln Arg Thr Ser Lys Glu Arg Ser Lys Asn Ala Gln
20 25 30

EP 0 786 519 A2

	35	40	45
5	Asn Leu Met Met Thr Lys Lys Leu Leu Ser Gln Tyr Asn His Pro Lys 50 55 60		
	Tyr Lys Leu Glu Leu Val Lys Phe Asn Asn Trp Pro Asp Leu Met Asp 65 70 75 80		
10	Ala Leu Asn Ser Gly Arg Ile Asp Gly Ala Ser Thr Leu Ile Glu Leu 85 90 95		
	Ala Met Lys Ser Lys Gln Lys Gly Ser Asn Ile Lys Ala Val Ala Leu 100 105 110		
15	Gly His His Glu Gly Asn Val Ile Met Gly Gln Lys Gly Met His Leu 115 120 125		
	Asn Glu Phe Asn Asn Asn Gly Asp Asp Tyr His Phe Gly Ile Pro His 130 135 140		
20	Arg Tyr Ser Thr His Tyr Leu Leu Leu Glu Glu Leu Arg Lys Gln Leu 145 150 155 160		
	Lys Ile Lys Pro Gly His Phe Ser Tyr His Glu Met Ser Pro Ala Glu 165 170 175		
25	Met Pro Ala Ala Leu Ser Glu His Arg Ile Thr Gly Tyr Ser Val Ala 180 185 190		
	Glu Pro Phe Gly Ala Leu Gly Glu Lys Leu Gly Lys Gly Lys Thr Leu 195 200 205		
30	Lys His Gly Asp Asp Val Ile Pro Asp Ala Tyr Cys Cys Val Leu Val 210 215 220		
	Leu Arg Gly Glu Leu Leu Asp Gln His Lys Asp Val Ala Gln Ala Phe 225 230 235 240		
35	Val Gln Asp Tyr Lys Lys Ser Gly Phe Lys Met Asn Asp Arg Lys Gln 245 250 255		
	Ser Val Asp Ile Met Thr His His Phe Lys Gln Ser Arg Asp Val Leu 260 265 270		
40	Thr Gln Ser Ala Ala Trp Thr Ser Tyr Gly Asp Leu Thr Ile Lys Pro 275 280 285		
	Ser Gly Tyr Gln Glu Ile Thr Thr Leu Val Lys Gln His His Leu Phe 290 295 300		
45	Asn Pro Pro Ala Tyr Asp Asp Phe Val Glu Pro Ser Leu Tyr Lys Glu 305 310 315 320		
50	Ala Ser Arg Ser		

(2) INFORMATION FOR SEQ ID NO:5210:

55 (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val
 1 5 10 15

Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser
 15 20 25 30

Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys
 35 40 45

Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly
 20 50 55 60

Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu
 65 70 75 80

Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys
 25 85 90 95

Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp
 100 105 110

Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys
 30 115 120 125

Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln
 35 130 135 140

Val Asp Tyr Trp
 145

(2) INFORMATION FOR SEQ ID NO:5211:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

Trp Pro Cys Ala Thr Xaa Gln Glx Glu Trp Trp Ser Arg His Xaa Trp
 1 5 10 15

55

20

25

30

His

5

(2) INFORMATION FOR SEQ ID NO:5212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

20 Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys
 1 5 10 15
 Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn
 20 25 30
 25 Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
 35 40 45
 Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
 50 55 60
 30 Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
 65 70 75 80
 Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
 85 90 95
 35 Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
 100 105 110
 Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
 115 120 125
 40 Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
 130 135 140
 45 Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
 145 150 155 160
 Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro
 165 170 175
 50 Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
 180 185 190
 Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn
 195 200 205
 55

EP 0 786 519 A2

	210		215		220
	Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg Leu				
	225		230		235 240
5	Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp Gln				
		245		250	255
	Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly				
10		260		265	270
	Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp				
		275		280	285
	Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala				
15		290		295	300
	Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg				
	305		310		315 320
20	Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val				
		325		330	335
	Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp				
		340		345	350
25	Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr				
		355		360	365
	Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala				
		370		375	380
30	Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala Trp Lys Arg Asn Lys				
	385		390		395 400
	Tyr Gly Thr Tyr Tyr Met Glu Glu Ser Ala Arg Phe Thr Asn Gly Asn				
		405		410	415
35	Gln Pro Ile Thr Val Arg Lys Val Gly Pro Phe Leu Ser Cys Pro Val				
		420		425	430
	Gly Tyr Gln Phe Gln Pro Gly Gly Tyr Cys Asp Tyr Thr Glu Val Met				
40		435		440	445
	Leu Gln Asp Gly His Val Trp Val Gly Tyr Thr Trp Glu Gly Gln Arg				
		450		455	460
45	Tyr Tyr Leu Pro Ile Arg Thr Trp Asn Gly Ser Ala Pro Pro Asn Gln				
	465		470		475 480
	Ile Leu Gly Asp Leu Trp Gly Glu Ile Ser				
		485		490	

(2) INFORMATION FOR SEQ ID NO:5213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

5
 10 Gly Asp Lys Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu
 1 5 10 15
 Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala
 20 25 30
 15 Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile
 35 40 45
 Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val
 50 55 60
 20 Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly
 65 70 75 80
 Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys
 85 90 95
 25 Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu
 100 105 110
 Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe
 115 120 125
 30 Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val
 130 135 140
 35 Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp
 145 150 155 160
 Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr
 165 170 175
 40 Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His
 180 185 190
 Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln
 195 200 205
 45 Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu
 210 215 220
 50 Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala
 225 230 235 240
 Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe
 245 250 255
 55 Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn
 260 265 270

275

280

285

Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys
290 295

(2) INFORMATION FOR SEQ ID NO:5214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn
1 5 10 15
Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr
20 25 30
Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro
35 40 45
Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn
50 55 60
Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro
65 70 75 80
Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp
85 90 95
Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala
100 105 110
Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln
115 120 125
Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg
130 135 140
Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys
145 150 155 160
Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu
165 170 175
Val Lys

(2) INFORMATION FOR SEQ ID NO:5215:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys	Glu	Arg	Val	Leu	Met	Lys	Lys	Leu	Leu	Thr	Ala	Ser	Ile	Ile	Ala	1	5	10	15
Cys	Ser	Val	Val	Met	Gly	Val	Gly	Leu	Val	Asn	Thr	Ser	Ala	Glu	Ala	20	25	30	
Ala	Ser	Gly	Asn	Ser	Ile	Asp	Thr	Val	Lys	Gln	Leu	Ile	Lys	Gly	Asp	35	40	45	
Gln	Ser	Leu	Glu	Asn	Val	Lys	Ile	Gly	Glu	Ser	Ile	Lys	Asp	Val	Leu	50	55	60	
Thr	Lys	Tyr	Lys	Asn	Pro	Met	Tyr	Ser	Tyr	Asn	Glu	Asp	Gly	Thr	Glu	65	70	75	80
His	Tyr	Tyr	Glu	Phe	His	Thr	Lys	Lys	Gly	Met	Leu	Leu	Val	Thr	Thr	85	90	95	
Asp	Gly	Lys	Lys	Asn	Asn	Gly	Lys	Val	Thr	His	Ile	Ser	Met	Met	Tyr	100	105	110	
Asn	Asp	Ala	Asn	Gly	Pro	Thr	Tyr	Gln	Ala	Val	Lys	Asn	Tyr	Val	Gly	115	120	125	
Lys	Ala	Val	Thr	His	Thr	Glu	Tyr	Ser	Lys	Val	Ala	Gly	Asn	Phe	Gly	130	135	140	
Tyr	Ile	Glu	Lys	Gly	Lys	Thr	Thr	Tyr	Gln	Phe	Ala	Ser	Ala	Pro	Lys	145	150	155	160
Asp	Lys	Asn	Ile	Lys	Leu	Tyr	Arg	Ile	Asp	Leu	Glu	Lys	165	170					

(2) INFORMATION FOR SEQ ID NO:5216:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

[illegible]

(2) INFORMATION FOR SEQ ID NO:5217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

Met	Lys	Arg	Asn	Phe	Pro	Lys	Leu	Ile	Ala	Leu	Ser	Leu	Ile	Phe	Ser
1				5					10					15	
Leu	Ser	Val	Thr	Pro	Ile	Ala	Asn	Ala	Glu	Ser	Asn	Ser	Asn	Ile	Lys
			20					25					30		
Ala	Lys	Asp	Lys	Lys	His	Val	Gln	Val	Asn	Val	Glu	Asp	Lys	Ser	Val
		35					40					45			
Pro	Thr	Asp	Val	Arg	Asn	Leu	Ala	Gln	Lys	Asp	Tyr	Leu	Ser	Tyr	Val
	50					55					60				

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:5218:

3215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr
 1 5 10 15
 Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp
 20 25 30
 Glu Gln His Tyr Thr Tyr Thr His Glu Leu Gly Glu Met Asp Asn His
 35 40 45
 Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu
 50 55 60
 Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala
 65 70 75 80
 Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr
 85 90 95
 Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val
 100 105 110
 Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln
 115 120 125
 Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys
 130 135

(2) INFORMATION FOR SEQ ID NO:5220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile Lys Asn Glu Asp Val
 1 5 10 15

[illegible]

(2) INFORMATION FOR SEQ ID NO:5221:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

	Ile	Met	Ala	Tyr	Asp	Gly	Leu	Phe	Thr	Lys	Lys	Met	Val	Glu	Ser	Leu
	1				5					10					15	
45	Gln	Phe	Leu	Thr	Thr	Gly	Arg	Val	His	Lys	Ile	Asn	Gln	Pro	Asp	Asn
				20					25					30		
	Asp	Thr	Ile	Leu	Met	Val	Val	Arg	Gln	Asn	Arg	Gln	Asn	His	Gln	Leu
50			35					40					45			
	Leu	Leu	Ser	Ile	His	Pro	Asn	Phe	Ser	Arg	Leu	Gln	Leu	Thr	Thr	Lys
		50					55					60				
	Lys	Tyr	Asp	Asn	Pro	Phe	Asn	Pro	Pro	Met	Phe	Ala	Arg	Val	Phe	Arg
55	65					70					75					80

	85	90	95
5	Asp Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp 100 105 110		
	Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn 115 120 125		
10	Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His 130 135 140		
	Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn 145 150 155 160		
15	Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr 165 170 175		
	Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala 180 185 190		
20	Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn 195 200 205		
	Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu 210 215 220		
25	Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile 225 230 235 240		
	Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys 245 250 255		
30	Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp 260 265 270		
	Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys 275 280 285		
35	Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys 290 295 300		
40	Tyr Gln Asn Lys Leu Ala Ser 305 310		

(2) INFORMATION FOR SEQ ID NO:5222:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: protein
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

1	5	10	15
Glu Gln Leu Tyr Gly Glu Leu Ile Thr Ala Asn Ile Tyr Arg Ile Lys	20	25	30
Gln Gly Asp Lys Glu Val Thr Ala Leu Asn Tyr Tyr Thr Asn Glu Glu	35	40	45
Val Val Ile Pro Leu Asn Pro Thr Lys Ser Pro Ser Ala Asn Ala Gln	50	55	60
Tyr Tyr Tyr Lys Gln Tyr Xaa Arg Met Lys Thr Arg Xaa Arg Glu Leu	65	70	80
Gln His Gln Ile Gln Leu Thr Lys Asp Asn Ile Asp Tyr Phe Ser Thr	85	90	95
Ile Glu Gln Gln Leu His His Ile Ser Val His Asp Ile Asp Glu Ile	100	105	110
Arg Asp Glu Leu Ala Glu Gln Gly Phe Met Lys Gln Arg Lys Asn Gln	115	120	125
Thr Lys Lys Lys Lys Ala Gln Ile Gln Leu Gln His Tyr Val Ser Thr	130	135	140
Asp Gly Asp Asp Ile Tyr Val Gly Lys Asn Asn Lys Gln Asn Asp Tyr	145	150	155
Leu Thr Asn Lys Lys Ala Lys Lys Thr His Thr Trp Leu His Thr Lys	165	170	175
Asp Ile Pro Gly Ser His Val Val Ile Phe Asn Asp Ala Pro Ser Asp	180	185	190
Thr Thr Ile Lys Glu Ala Ala Met Leu Ala Gly Tyr Phe Ser Lys Ala	195	200	205
Gly Asn Ser Gly Gln Ile Pro Val Asp Tyr Thr Leu Ile Lys Asn Val	210	215	220
His Lys Pro Ser Gly Ala Lys Pro Gly Phe Val Thr Tyr Asp Asn Gln	225	230	235
Lys Thr Leu Tyr Ala	245		

(2) INFORMATION FOR SEQ ID NO:5223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser
 1 5 10 15
 Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg
 20 25 30
 Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu
 10 35 40 45
 Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn
 50 55 60
 Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe
 15 65 70 75 80
 Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr
 85 90 95
 20
 Asp Leu Lys

(2) INFORMATION FOR SEQ ID NO:5224:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu
 1 5 10 15
 40 Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn
 20 25 30
 Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn
 35 40 45
 45 Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu
 50 55 60
 Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu
 50 65 70 75 80
 Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr
 85 90 95
 55 Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly
 100 105 110

115

120

125

His Ser Ile

130

5

(2) INFORMATION FOR SEQ ID NO:5225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

20

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
1 5 10 15

25

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
20 25 30

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
35 40 45

30

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
50 55 60

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
65 70 75 80

35

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
85 90 95

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
100 105 110

40

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
115 120 125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
130 135 140

45

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
145 150 155 160

50

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
165 170 175

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
180 185 190

55

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
195 200 205

EP 0 786 519 A2

	210	215	220
	Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly		
	225	230	235 240
5	Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn		
		245	250 255
	Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val		
10		260	265 270
	Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys		
		275	280 285
	Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr		
15		290	295 300
	Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp		
		305	310 315 320
	Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly		
20		325	330 335
	Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu		
		340	345 350
25	Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr		
		355	360 365
	Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly		
30		370	375 380
	Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro		
		385	390 395 400
	Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn		
35		405	410 415
	Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu		
		420	425 430
40	Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr		
		435	440 445
	Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr		
		450	455 460
45	Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly		
		465	470 475 480
	Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp		
50		485	490 495
	Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr		
		500	505 510
55	Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser		
		515	520 525

530

535

540

(2) INFORMATION FOR SEQ ID NO:5226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His
 1 5 10 15
 Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val
 20 25 30
 Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile
 35 40 45
 Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His
 50 55 60
 Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe
 65 70 75 80
 Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe
 85 90 95
 Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu
 100 105 110
 Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly
 115 120 125
 Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro
 130 135 140
 Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile
 145 150 155 160
 Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val
 165 170 175
 Lys

(2) INFORMATION FOR SEQ ID NO:5227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala
 1 5 10 15
 Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln
 20 25 30
 His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro
 35 40 45
 Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly
 50 55 60
 Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu
 65 70 75 80
 Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu
 85 90 95
 Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met
 100 105 110
 Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp
 115 120 125
 Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu Lys Gln
 130 135 140
 Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys
 145 150 155 160
 Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe
 165 170 175
 Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe
 180 185 190
 Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr
 195 200 205
 Cys

(2) INFORMATION FOR SEQ ID NO:5228:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

5 Thr Phe Arg Ile Ile Phe Leu Leu Ser Ile Arg Lys Arg Ser Asn Arg
 1 5 10 15
 Thr His Val Ser Ile His Trp Ser Thr Val Asn Lys Glu Glu Ile Cys
 20 25 30
 10 Leu Arg Val Lys Asp Asn Leu Gln Gln Ile Ser Thr Gln Ile Asn Asp
 35 40 45
 Lys Ser Glu Lys Asn Asn Phe Ser Thr Lys Pro Asn Val Ile Ala Val
 50 55 60
 15 Thr Lys Tyr Val Thr Ile Glu Arg Ala Lys Glu Ala Tyr Glu Ala Gly
 65 70 75 80
 Ile Arg His Phe Gly Glu Asn Arg Leu Glu Gly Phe Phe Gln Lys Lys
 85 90 95
 20 Glu Ala Leu Pro Ser Asp Ala Val Ile His Phe Ile Gly Ser Leu Gln
 100 105 110
 25 Ser Arg Lys Val Lys Asp Val Ile Asn Asp Val Asp Tyr Phe His Ala
 115 120 125
 Leu Asp Arg Leu Ser Leu Ala Lys Glu Ile Asn Lys Arg Ala Glu His
 130 135 140
 30 Lys Ile Lys Cys Phe Leu Gln Val Asn Val Ser Gly Glu Ala Ser Lys
 145 150 155 160
 His Gly Ile Ala Leu Glu Asp Val Asp Gln Phe Ile Asp Asp Leu Lys
 165 170 175
 35 Lys Tyr Asp Lys Ile Glu Ile Val Gly Leu Met Thr Met Ala Pro Leu
 180 185 190
 Thr Asp Asp Glu Ala Tyr Ile Arg Ser Leu Phe Lys Gln Leu Arg Leu
 195 200 205
 40 Lys Lys Glu Glu Ile Gln Arg Leu Asn Leu Glu Tyr Ala Pro Cys Asp
 210 215 220
 45 Glu Leu Ser Met Gly Met Ser Asn Asp Tyr Leu Ile Ala Val Glu Glu
 225 230 235 240
 Gly Ala Thr Phe Val Arg Ile Gly Thr Lys Leu Val Gly Glu Glu Glu
 245 250 255

50

(2) INFORMATION FOR SEQ ID NO:5229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

55

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

10 Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys
 1 5 10 15
 Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr
 20 25 30
 15 Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp
 35 40 45
 Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn
 50 55 60
 20 Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp
 65 70 75 80
 Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser
 85 90 95
 25 Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly
 100 105 110
 Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val
 115 120 125
 Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala
 130 135 140
 35 Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg
 145 150 155 160
 Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln
 165 170 175
 40 Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile
 180 185 190
 Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly
 195 200 205
 45 Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr
 210 215 220
 Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly
 225 230 235 240
 Leu Gly Ala Trp Gly Phe
 245

55

(2) INFORMATION FOR SEQ ID NO:5230:

(A) LENGTH: 519 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

Lys	Glu	Pro	His	Lys	Met	Lys	Lys	Ile	Tyr	Lys	Ser	Leu	Thr	Val	Ser	1	5	10	15
Ala	Ile	Val	Ala	Thr	Val	Ser	Leu	Ser	Ala	Leu	Pro	Gln	Ser	Leu	Ala	20	25	30	
Ile	Thr	His	Glu	Ser	Gln	Pro	Thr	Lys	Gln	Gln	Arg	Thr	Val	Leu	Phe	35	40	45	
Asp	Arg	Ser	His	Gly	Gln	Thr	Ala	Gly	Ala	Ala	Asp	Trp	Val	Ser	Asp	50	55	60	
Gly	Ala	Phe	Ser	Asp	Tyr	Ala	Asp	Ser	Ile	Gln	Lys	Gln	Gly	Tyr	Asp	65	70	75	80
Val	Lys	Ala	Ile	Asp	Gly	His	Ser	Asn	Ile	Thr	Glu	Ala	Ser	Leu	Lys	85	90	95	
Ser	Ser	Lys	Ile	Phe	Val	Ile	Pro	Glu	Ala	Asn	Ile	Pro	Phe	Lys	Glu	100	105	110	
Ser	Glu	Gln	Ala	Ala	Ile	Val	Lys	Tyr	Val	Lys	Gln	Gly	Gly	Asn	Val	115	120	125	
Val	Phe	Ile	Ser	Asp	His	Tyr	Asn	Ala	Asp	Arg	Asn	Leu	Asn	Arg	Ile	130	135	140	
Asp	Ser	Ser	Glu	Ala	Met	Asn	Gly	Tyr	Arg	Arg	Gly	Ala	Tyr	Glu	Asp	145	150	155	160
Met	Ser	Lys	Gly	Met	Asn	Ala	Glu	Glu	Lys	Ser	Ser	Thr	Ala	Met	Gln	165	170	175	
Gly	Val	Lys	Ser	Ser	Asp	Trp	Leu	Ser	Thr	Asn	Phe	Gly	Val	Arg	Phe	180	185	190	
Arg	Tyr	Asn	Ala	Leu	Gly	Asp	Leu	Asn	Thr	Ser	Asn	Ile	Val	Ser	Ser	195	200	205	
Lys	Glu	Ser	Phe	Gly	Ile	Thr	Glu	Gly	Val	Lys	Ser	Val	Ser	Met	His	210	215	220	
Ala	Gly	Ser	Thr	Leu	Ala	Ile	Thr	Asn	Pro	Glu	Lys	Ala	Lys	Gly	Ile	225	230	235	240
Val	Tyr	Thr	Pro	Glu	Gln	Leu	Pro	Ala	Lys	Ser	Lys	Trp	Ser	His	Ala	245	250	255	

Val Asp Gln Gly Ile Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr
 260 265 270
 5 Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp
 275 280 285
 Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn
 290 295 300
 10 Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly
 305 310 315 320
 Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly
 325 330 335
 15 Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu
 340 345 350
 Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro
 355 360 365
 20 Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe
 370 375 380
 Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn
 385 390 395 400
 25 Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe
 405 410 415
 30 Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile
 420 425 430
 His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val
 435 440 445
 35 Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys
 450 455 460
 Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys
 465 470 475 480
 40 Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu
 485 490 495
 45 Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr
 500 505 510
 Leu Ile Thr Thr Asp Phe Lys
 515

(2) INFORMATION FOR SEQ ID NO:5231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

5	Arg	Asp	Glu	Arg	Ile	Lys	Thr	Met	Thr	Asn	Ser	Ser	Lys	Ser	Phe	Thr	1	-5-	10	15
	Lys	Phe	Met	Ala	Ala	Ser	Ala	Val	Phe	Thr	Met	Gly	Phe	Leu	Ser	Val	20	25	30	
10	Pro	Thr	Ala	Gly	Ala	Glu	Gln	Thr	Asn	Gln	Ile	Ala	Asn	Lys	Pro	Gln	35	40	45	
	Ala	Ile	Gln	Trp	His	Thr	Asn	Leu	Thr	Asn	Glu	Arg	Phe	Thr	Thr	Ile	50	55	60	
15	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Ala	Pro	Glu	His	Thr	Phe	Gln	Ala	65	70	75	80
	Tyr	Asp	Lys	Ser	His	Asn	Glu	Leu	Lys	Ala	Ser	Tyr	Ile	Glu	Ile	Asp	85	90	95	
20	Leu	Gln	Arg	Thr	Lys	Asp	Gly	His	Leu	Val	Ala	Met	His	Asp	Glu	Thr	100	105	110	
	Val	Asn	Arg	Thr	Thr	Asn	Gly	His	Gly	Lys	Val	Glu	Asp	Tyr	Thr	Leu	115	120	125	
25	Asp	Glu	Leu	Lys	Gln	Leu	Asp	Ala	Gly	Ser	Trp	Phe	Asn	Lys	Lys	Tyr	130	135	140	
	Pro	Lys	Tyr	Ala	Arg	Ala	Ser	Tyr	Lys	Asn	Ala	Lys	Val	Pro	Thr	Leu	145	150	155	160
30	Asp	Glu	Ile	Leu	Glu	Arg	Tyr	Gly	Pro	Asn	Ala	Asn	Tyr	Tyr	Ile	Glu	165	170	175	
35	Thr	Lys	Ser	Pro	Asp	Val	Tyr	Pro	Gly	Met	Glu	Glu	Gln	Leu	Leu	Ala	180	185	190	
	Ser	Leu	Lys	Lys	His	His	Leu	Leu	Asn	Asn	Asn	Lys	Leu	Lys	Asn	Gly	195	200	205	
40	His	Val	Met	Ile	Gln	Ser	Phe	Ser	Asp	Glu	Ser	Leu	Lys	Lys	Ile	His	210	215	220	
	Arg	Gln	Asn	Lys	His	Val	Pro	Leu	Val	Lys	Leu	Val	Asp	Lys	Gly	Glu	225	230	235	240
45	Leu	Gln	Gln	Phe	Asn	Asp	Gln	Arg	Leu	Lys	Glu	Ile	Arg	Ser	Tyr	Ala	245	250	255	
50	Ile	Gly	Leu	Gly	Pro	Asp	Tyr	Thr	Asp	Leu	Thr	Glu	Gln	Asn	Thr	His	260	265	270	
	His	Leu	Lys	Asp	Leu	Gly	Phe	Ile	Val	His	Pro	Tyr	Thr	Val	Asn	Glu	275	280	285	

Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe
 290 295 300

Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys
 305 310 315

(2) INFORMATION FOR SEQ ID NO:5232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Ile Leu Cys Leu Thr
 1 5 10 15
 Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr
 20 25 30
 Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala
 35 40 45
 Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu
 50 55 60
 Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys
 65 70 75 80
 Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu
 85 90 95
 Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser
 100 105 110
 Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp
 115 120 125
 Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala
 130 135 140
 Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe
 145 150 155 160
 Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr
 165 170 175
 His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe
 180 185 190
 Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Thr Ala Arg
 195 200 205

Asp Tyr Ala Ile Leu Asp Leu His Val Ile Lys Glu Thr Pro Lys Ile
 210 215 220
 5 Leu Asp Phe Thr Lys Gln Leu Ala Pro Thr Thr His Ala Val Thr Tyr
 225 230 235 240
 Tyr Thr Phe Asn Phe Ser Leu Glu Gly Ala Lys Met Ser Leu Pro Gly
 245 250 255
 10 Thr Asp Gly Leu Lys Thr Gly Ser Ser Asp Thr Ala Asn Tyr Asn His
 260 265 270
 Thr Ile Thr Thr Lys Arg Gly Lys Phe Arg Ile Asn Gln Val Ile Met
 275 280 285
 15 Gly Ala Gly Asp Tyr Lys Asn Leu Gly Gly Glu Lys Gln Arg Asn Met
 290 295 300
 Met Gly Asn Ala Leu Met Glu Arg Ser Phe Asp Gln Tyr Lys Tyr Val
 305 310 315 320
 20 Lys Ile Leu Ser Lys Gly Glu Gln Arg Ile Asn Gly Lys Lys Tyr Tyr
 325 330 335
 Val Glu Asn Asp Leu Tyr Asp Val Leu Pro Ser Asp Phe Ser Lys Lys
 340 345 350
 25 Asp Tyr Lys Leu Val Val Glu Asp Gly Lys Val His Ala Asp Tyr Pro
 355 360 365
 Arg Glu Phe Ile Asn Lys Asp Tyr Gly Pro Pro Thr Val Glu Val His
 370 375 380
 30 Gln Pro Ile Ile Gln Lys Ala Asn Thr Val Ala Lys Ser Met Trp Glu
 385 390 395 400
 35 Glu His Pro Leu Phe Thr Ile Ile Gly Gly Thr Cys Leu Val Ala Gly
 405 410 415
 Leu Ala Leu Ile Val His Met Ile Ile Asn Arg Leu Phe Arg Lys Arg
 420 425 430
 40 Lys

(2) INFORMATION FOR SEQ ID NO:5233:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

[illegible]

(2) INFORMATION FOR SEQ ID NO:5234:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 497 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

45	Asn	His	Cys	Asn	Arg	Ile	Glu	Arg	Lys	Met	Ala	Met	Ser	Asn	Asn	Phe
	1				5					10					15	
	Lys	Asp	Asp	Phe	Glu	Lys	Asn	Arg	Gln	Ser	Ile	Asp	Thr	Asn	Ser	His
				20					25					30		
50	Gln	Asp	His	Thr	Glu	Asp	Val	Glu	Lys	Asp	Gln	Ser	Glu	Leu	Glu	His
			35					40					45			
	Gln	Asp	Thr	Ile	Glu	Asn	Thr	Glu	Gln	Gln	Phe	Pro	Pro	Arg	Asn	Ala
		50					55					60				
55	Gln	Arg	Arg	Lys	Arg	Arg	Arg	Asp	Leu	Ala	Thr	Asn	His	Asn	Lys	Gln
	65					70					75					80

EP 0 786 519 A2

	Val	His	Asn	Glu	Ser	Gln	Thr	Ser	Glu	Asp	Asn	Val	Gln	Asn	Glu	Ala	
					85					90					95		
5	Gly	Thr	Ile	Asp	Asp	Arg	Gln	Val	Glu	Ser	Ser	His	Ser	Thr	Glu	Ser	
				100					105					110			
	Gln	Glu	Pro	Ser	His	Gln	Asp	Ser	Thr	Pro	Gln	His	Glu	Glu	Glu	Tyr	
			115					120					125				
10	Tyr	Asn	Lys	Asn	Ala	Phe	Ala	Met	Asp	Lys	Ser	His	Pro	Glu	Pro	Ile	
		130					135					140					
	Glu	Asp	Asn	Asp	Lys	His	Asp	Thr	Ile	Lys	Asn	Ala	Glu	Asn	Asn	Thr	
	145					150					155					160	
15	Glu	His	Ser	Thr	Val	Ser	Asp	Lys	Ser	Glu	Ala	Glu	Gln	Ser	Gln	Gln	
					165					170					175		
	Pro	Lys	Pro	Tyr	Phe	Thr	Thr	Gly	Ala	Asn	Gln	Ser	Glu	Thr	Ser	Lys	
				180					185						190		
20	Asn	Glu	His	Asp	Asn	Asp	Ser	Val	Lys	Gln	Asp	Gln	Asp	Glu	Pro	Lys	
			195					200					205				
	Glu	His	His	Asn	Gly	Lys	Lys	Ala	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	
25		210					215					220					
	Gly	Val	Ala	Gly	Ala	Ala	Gly	Ala	Met	Ala	Ala	Ser	Lys	Ala	Lys	Lys	
	225					230					235					240	
	His	Ser	Asn	Asp	Ala	Gln	Asn	Lys	Ser	Asn	Ser	Gly	Lys	Ala	Asn	Asn	
30					245					250					255		
	Ser	Thr	Glu	Asp	Lys	Ala	Ser	Gln	Asp	Lys	Ser	Lys	Asp	His	His	Asn	
				260					265					270			
35	Gly	Lys	Lys	Gly	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	Gly	Leu	Ala	Gly	
			275					280					285				
	Gly	Ala	Ala	Ser	Lys	Ser	Ala	Ser	Ala	Ala	Ser	Lys	Pro	His	Ala	Ser	
		290					295					300					
40	Asn	Asn	Ala	Ser	Gln	Asn	His	Asp	Glu	His	Asp	Asn	His	Asp	Arg	Asp	
	305					310					315					320	
	Lys	Glu	Arg	Lys	Lys	Gly	Gly	Met	Ala	Lys	Val	Leu	Leu	Pro	Leu	Ile	
45					325					330					335		
	Ala	Ala	Val	Leu	Ile	Ile	Gly	Ala	Leu	Ala	Ile	Phe	Gly	Gly	Met	Ala	
				340					345					350			
	Leu	Asn	Asn	His	Asn	Asn	Gly	Thr	Lys	Glu	Asn	Lys	Ile	Ala	Asn	Thr	
50			355					360					365				
	Asn	Lys	Asn	Asn	Ala	Asp	Glu	Ser	Lys	Asp	Lys	Asp	Thr	Ser	Lys	Asp	
		370					375					380					
55	Ala	Ser	Lys	Asp	Lys	Ser	Lys	Ser	Thr	Asp	Ser	Asp	Lys	Ser	Lys	Glu	
	385					390					395					400	

Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn
 405 410 415
 Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln Gln
 5 420 425 430
 Ala Asn Gln Asn Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln
 435 440 445
 Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln
 10 450 455 460
 Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala
 465 470 475 480
 Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile
 15 485 490 495
 Pro

(2) INFORMATION FOR SEQ ID NO:5235:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 886 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn
 1 5 10 15
 Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr
 20 25 30
 Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser
 35 40 45
 Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp Lys Ile
 50 55 60
 Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp
 65 70 75 80
 Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn
 85 90 95
 Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala
 100 105 110
 Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe
 115 120 125

EP 0 786 519 A2

	Gln	Leu	Leu	Asp	Lys	Asn	Asn	Glu	Thr	Gln	Tyr	Tyr	His	Phe	Phe	Ser	
	130						135						140				
5	Ile	Lys	Asp	Pro	Ala	Asp	Val	Tyr	Tyr	Thr	Lys	Lys	Lys	Ala	Glu	Val	
	145					150					155					160	
	Glu	Leu	Asp	Ile	Asn	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr	
					165					170					175		
10	Glu	Asn	Asn	Gln	Lys	Leu	Pro	Val	Arg	Leu	Val	Ser	Tyr	Ser	Pro	Val	
				180					185					190			
	Pro	Glu	Asp	His	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asp	Gly	Thr	Gln	
			195					200					205				
15	Glu	Leu	Lys	Ile	Val	Ser	Ser	Thr	Gln	Ile	Asp	Asp	Gly	Glu	Glu	Thr	
	210						215					220					
	Asn	Tyr	Asp	Tyr	Thr	Lys	Leu	Val	Phe	Ala	Lys	Pro	Ile	Tyr	Asn	Asp	
	225					230					235					240	
20	Pro	Ser	Leu	Val	Lys	Ser	Asp	Thr	Asn	Asp	Ala	Val	Val	Thr	Asn	Asp	
					245					250					255		
	Gln	Ser	Ser	Ser	Val	Ala	Ser	Asn	Gln	Thr	Asn	Thr	Asn	Thr	Ser	Asn	
25					260				265					270			
	Gln	Asn	Ile	Ser	Thr	Ile	Asn	Asn	Ala	Asn	Asn	Gln	Pro	Gln	Ala	Thr	
			275					280					285				
30	Thr	Asn	Met	Ser	Gln	Pro	Ala	Gln	Pro	Lys	Ser	Ser	Thr	Asn	Ala	Asp	
	290						295					300					
	Gln	Ala	Ser	Ser	Gln	Pro	Ala	His	Glu	Thr	Asn	Ser	Asn	Gly	Asn	Thr	
	305					310					315					320	
35	Asn	Asp	Lys	Thr	Asn	Glu	Ser	Ser	Asn	Gln	Ser	Asp	Val	Asn	Gln	Gln	
					325					330					335		
	Tyr	Pro	Pro	Ala	Asp	Glu	Ser	Leu	Gln	Asp	Ala	Ile	Lys	Asn	Pro	Ala	
				340					345					350			
40	Ile	Ile	Asp	Lys	Glu	His	Thr	Ala	Asp	Asn	Trp	Arg	Pro	Ile	Asp	Phe	
			355					360					365				
	Gln	Met	Lys	Asn	Asp	Lys	Gly	Glu	Arg	Gln	Phe	Tyr	His	Tyr	Ala	Ser	
45		370					375					380					
	Thr	Val	Glu	Pro	Ala	Thr	Val	Ile	Phe	Thr	Lys	Thr	Gly	Pro	Ile	Ile	
	385					390					395					400	
	Glu	Leu	Gly	Leu	Lys	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr	
50					405					410					415		
	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Val	Glu	Leu	Val	Ser	Tyr	Asp	Ser	Asp	
				420					425					430			
55	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asn	Gly	Thr	Arg	Glu	
		435						440					445				

EP 0 786 519 A2

	Val	Lys	Ile	Val	Ser	Ser	Ile	Glu	Tyr	Gly	Glu	Asn	Ile	His	Glu	Asp	
	450						455					460					
5	Tyr	Asp	Tyr	Thr	Leu	Met	Val	Phe	Ala	Gln	Pro	Ile	Thr	Asn	Asn	Pro	
	465					470					475					480	
	Asp	Asp	Tyr	Val	Asp	Glu	Glu	Thr	Tyr	Asn	Leu	Gln	Lys	Leu	Leu	Ala	
					485					490						495	
10	Pro	Tyr	His	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Glu	
				500					505					510			
	Lys	Leu	Gln	Glu	Lys	Leu	Pro	Glu	Lys	Tyr	Lys	Ala	Glu	Tyr	Lys	Lys	
			515					520					525				
15	Lys	Leu	Asp	Gln	Thr	Arg	Val	Glu	Leu	Ala	Asp	Gln	Val	Lys	Ser	Ala	
			530				535					540					
	Val	Thr	Glu	Phe	Glu	Asn	Val	Thr	Pro	Thr	Asn	Asp	Gln	Leu	Thr	Asp	
	545					550					555					560	
20	Leu	Gln	Glu	Ala	His	Phe	Val	Val	Phe	Glu	Ser	Glu	Glu	Asn	Ser	Glu	
					565					570					575		
	Ser	Val	Met	Asp	Gly	Phe	Val	Glu	His	Pro	Phe	Tyr	Thr	Ala	Thr	Leu	
25				580					585					590			
	Asn	Gly	Gln	Lys	Tyr	Val	Val	Met	Lys	Thr	Lys	Asp	Asp	Ser	Tyr	Trp	
			595					600					605				
30	Lys	Asp	Leu	Ile	Val	Glu	Gly	Lys	Arg	Val	Thr	Thr	Val	Ser	Lys	Asp	
		610					615						620				
	Pro	Lys	Asn	Asn	Ser	Arg	Thr	Leu	Ile	Phe	Pro	Tyr	Ile	Pro	Asp	Lys	
		625				630					635					640	
35	Ala	Val	Tyr	Asn	Ala	Ile	Val	Lys	Val	Val	Val	Ala	Asn	Ile	Gly	Tyr	
					645					650					655		
	Glu	Gly	Gln	Tyr	His	Val	Arg	Ile	Ile	Asn	Gln	Asp	Ile	Asn	Thr	Lys	
				660					665					670			
40	Asp	Asp	Asp	Thr	Ser	Gln	Asn	Asn	Thr	Ser	Glu	Pro	Leu	Asn	Val	Gln	
			675					680						685			
	Thr	Gly	Gln	Glu	Gly	Lys	Val	Ala	Asp	Thr	Asp	Val	Ala	Glu	Asn	Ser	
45		690					695					700					
	Ser	Thr	Ala	Thr	Asn	Pro	Lys	Asp	Ala	Ser	Asp	Lys	Ala	Asp	Val	Ile	
		705				710					715					720	
	Glu	Pro	Glu	Ser	Asp	Val	Val	Lys	Asp	Ala	Asp	Asn	Asn	Ile	Asp	Lys	
50					725					730					735		
	Asp	Val	Gln	His	Asp	Val	Asp	His	Leu	Ser	Asp	Met	Ser	Asp	Asn	Asn	
				740					745					750			
55	His	Phe	Asp	Lys	Tyr	Asp	Leu	Lys	Glu	Met	Asp	Thr	Gln	Ile	Ala	Lys	
			755					760					765				

EP 0 786 519 A2

Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val Gly Met
770 775 780

5 Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys
785 790 795 800

Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr Gly Lys
805 810 815

10 Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys
820 825 830

Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile His Lys
835 840 845

15 Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser
850 855 860

Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Thr Lys Asn Trp Arg
865 870 875 880

20 Asn Asn Xaa Gln Ala Asn
885

(2) INFORMATION FOR SEQ ID NO:5236:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:

Asn Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile
1 5 10 15

40 Leu Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Xaa His Ser
20 25 30

Ile Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys
35 40 45

45 Glu Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val
50 55 60

50 Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn
65 70 75 80

Asp Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys
85 90 95

55 Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys
100 105 110

Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu
 115 120 125
 Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys
 130 135 140
 Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr
 145 150 155 160
 Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly
 165 170 175
 Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser
 180 185 190
 Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly
 195 200 205
 Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro
 210 215 220
 Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys
 225 230 235

(2) INFORMATION FOR SEQ ID NO:5237:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr
 1 5 10 15
 Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr
 20 25 30
 Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val
 35 40 45
 Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly
 50 55 60
 Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr
 65 70 75 80
 Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala
 85 90 95
 Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr
 100 105 110

Leu Asn Ile Ser Ala Thr Pro Ala Pro Lys Gln Glu Gln Ser Gln Thr
 115 120 125
 5 Thr Thr Glu Ser Thr Thr Pro Lys Thr Lys Val Thr Thr Pro Pro Ser
 130 135 140
 Thr Asn Thr Pro Gln Pro Met Gln Ser Thr Lys Ser Asp Thr Pro Gln
 145 150 155 160
 10 Ser Pro Thr Ile Lys Gln Ala Gln Thr Asp Met Thr Pro Lys Tyr Glu
 165 170 175
 Asp Leu Arg Ala Tyr Tyr Thr Lys Pro Ser Phe Glu Phe Glu Lys Gln
 180 185 190
 15 Phe Gly Phe Met Leu Lys Pro Trp Thr Thr Val Arg Phe Met Asn Val
 195 200 205
 Ile Pro Asn Arg Phe Ile Tyr Lys Ile Ala Leu Val Gly Lys Asp Glu
 210 215 220
 20 Lys Lys Tyr Lys Asp Gly Pro Tyr Asp Asn Ile Asp Val Phe Ile Val
 225 230 235 240
 25 Leu Glu Asp Asn Lys Tyr Gln Leu Lys Lys Tyr Ser Val Gly Gly Ile
 245 250 255
 Thr Lys Thr Asn Ser Lys Lys Val Asn His Lys Val Glu Leu Ser Ile
 260 265 270
 30 Thr Lys Lys Asp Asn Gln Gly Met Ile Ser Arg Asp Val Ser Glu Tyr
 275 280 285
 Met Ile Thr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu
 290 295 300
 35 Arg Lys Gln Leu Ile Glu Lys His Asn Leu Tyr Gly Asn Met Gly Ser
 305 310 315 320
 40 Gly Thr Ile Val Ile Lys Met Lys Asn Gly Gly Lys Tyr Thr Phe Glu
 325 330 335
 Leu His Lys Lys Leu Gln Glu His Arg Met Ala Asp Val Ile Asp Gly
 340 345 350
 45 Thr Asn Ile Asp Asn Ile Glu Val Asn Ile Lys
 355 360

(2) INFORMATION FOR SEQ ID NO:5238:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

5 Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val
 1 5 10 15
 Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala
 20 25 30
 10 Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser
 35 40 45
 Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn
 50 55 60
 15 Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys
 65 70 75 80
 Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile
 85 90 95
 20 Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr
 100 105 110
 Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr
 115 120 125
 25 Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn
 130 135 140
 Val Asp Thr Lys Lys Gln
 145 150
 30

(2) INFORMATION FOR SEQ ID NO:5239:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

45 Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp
 1 5 10 15
 Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly
 20 25 30
 50 Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile
 35 40 45
 Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gly
 50 55 60

EP 0 786 519 A2

5 Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu Met
 65 70 75 80
 Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu
 85 90 95
 Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr
 100 105 110
 10 Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser
 115 120 125
 Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys
 130 135 140
 15 Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu
 145 150 155 160
 Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser
 165 170 175
 20 Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val
 180 185 190
 Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile
 195 200 205
 25 Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr
 210 215 220
 Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu
 225 230 235

(2) INFORMATION FOR SEQ ID NO:5240:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

45 Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val
 1 5 10 15
 Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser
 20 25 30
 50 Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys
 35 40 45
 55 Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val
 50 55 60

EP 0 786 519 A2

Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu
65 70 75 80

Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys
85 90 95

Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe
100 105 110

Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu
115 120 125

Phe Asp Val Lys Ala
130

(2) INFORMATION FOR SEQ ID NO:5241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val
1 5 10 15

Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly
20 25 30

Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro
35 40 45

Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp
50 55 60

Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser
65 70 75 80

Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp
85 90 95

Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn
100 105 110

Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala
115 120 125

Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly
130 135 140

Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu
145 150 155 160

EP 0 786 519 A2

	Pro	Ile	Gly	Val	Val	Gly	Ala	Val	Val	Ala	Trp	Asn	Phe	Pro	Met	Leu	
					165						170				175		
5	Leu	Ala	Ala	Trp	Lys	Ile	Ala	Pro	Ala	Ile	Ala	Ala	Gly	Asn	Thr	Ile	
					180				185					190			
	Val	Ile	Gln	Pro	Ser	Ser	Ser	Thr	Pro	Leu	Ser	Leu	Leu	Glu	Val	Ala	
					195			200					205				
10	Lys	Ile	Phe	Gln	Glu	Val	Leu	Pro	Lys	Gly	Val	Val	Asn	Ile	Leu	Thr	
		210					215					220					
	Gly	Lys	Gly	Ser	Glu	Ser	Gly	Asn	Ala	Ile	Phe	Asn	His	Asp	Gly	Val	
		225				230					235					240	
15	Asp	Lys	Leu	Ser	Phe	Thr	Gly	Ser	Thr	Asp	Val	Gly	Tyr	Gln	Val	Ala	
					245					250					255		
	Glu	Ala	Ala	Ala	Lys	His	Leu	Val	Pro	Ala	Thr	Leu	Glu	Leu	Gly	Gly	
					260				265					270			
20	Lys	Ser	Ala	Asn	Ile	Ile	Leu	Asp	Asp	Ala	Asn	Leu	Asp	Leu	Ala	Val	
			275					280					285				
	Glu	Gly	Ile	Gln	Leu	Gly	Ile	Leu	Phe	Asn	Gln	Gly	Glu	Val	Cys	Ser	
25			290				295					300					
	Ala	Gly	Ser	Arg	Leu	Leu	Val	His	Glu	Lys	Ile	Tyr	Asp	Gln	Leu	Val	
						310					315					320	
30	Pro	Arg	Leu	Gln	Glu	Ala	Phe	Ser	Asn	Ile	Lys	Val	Gly	Asn	Pro	Gln	
					325					330					335		
	Asp	Glu	Ala	Thr	Gln	Met	Gly	Ser	Gln	Thr	Gly	Lys	Asp	Gln	Leu	Asp	
					340				345					350			
35	Lys	Ile	Gln	Ser	Tyr	Ile	Asp	Ala	Ala	Lys	Glu	Ser	Asp	Ala	Gln	Ile	
			355				360						365				
	Leu	Ala	Gly	Gly	His	Arg	Leu	Thr	Glu	Asn	Gly	Leu	Asp	Lys	Gly	Phe	
			370				375					380					
40	Phe	Phe	Glu	Pro	Thr	Leu	Ile	Ala	Val	Pro	Asp	Asn	His	His	Lys	Leu	
						390					395					400	
	Ala	Gln	Glu	Glu	Ile	Phe	Gly	Pro	Val	Leu	Thr	Val	Ile	Lys	Val	Lys	
					405					410					415		
45	Asp	Asp	Gln	Glu	Ala	Ile	Asp	Ile	Ala	Asn	Asp	Ser	Glu	Tyr	Gly	Leu	
					420				425					430			
	Ala	Gly	Gly	Val	Phe	Ser	Gln	Asn	Ile	Thr	Arg	Ala	Leu	Asn	Ile	Ala	
			435					440					445				
50	Lys	Ala	Val	Arg	Thr	Gly	Arg	Ile	Trp	Ile	Asn	Thr	Tyr	Asn	Gln	Val	
			450				455					460					
55	Pro	Glu	Gly	Ala	Pro	Phe	Gly	Gly	Tyr	Lys	Lys	Ser	Gly	Ile	Gly	Arg	
						470					475					480	

Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile
 485 490 495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr
 500 505

(2) INFORMATION FOR SEQ ID NO:5242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
 1 5 10 15

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
 20 25 30

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
 35 40 45

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
 50 55 60

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
 65 70 75 80

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
 85 90 95

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
 100 105 110

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
 115 120 125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
 130 135 140

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
 145 150 155 160

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
 165 170 175

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
 180 185 190

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
 195 200 205

EP 0 786 519 A2

Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val Thr Val
 210 215 220
 5 Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly
 225 230 235 240
 Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn
 245 250 255
 10 Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val
 260 265 270
 Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys
 275 280 285
 15 Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr
 290 295 300
 Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp
 305 310 315 320
 20 Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly
 325 330 335
 Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu
 340 345 350
 25 Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr
 355 360 365
 Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly
 370 375 380
 30 Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro
 385 390 395 400
 35 Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn
 405 410 415
 Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu
 420 425 430
 40 Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr
 435 440 445
 Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr
 450 455 460
 45 Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly
 465 470 475 480
 Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp
 485 490 495
 50 Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr
 500 505 510
 55 Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser
 515 520 525

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His
530 535 540

(2) INFORMATION FOR SEQ ID NO:5243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln
1 5 10 15
Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln
20 20 25 30
Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly
25 35 40 45
Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp
50 55 60
Met Ile His His Gly Arg Ala Val Arg Arg Gly Ala Pro Asn Thr Phe
30 65 70 75 80
Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln
85 90 95
Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala
35 100 105 110
Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr
115 120 125
Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser
40 130 135 140
Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala
145 150 155 160
Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val
45 165 170 175
Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser
180 185 190
Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr
50 195 200 205
Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu
55 210 215 220

His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val
225 230 235 240

Asp Gly Leu Lys Gln Tyr Asp Gln Glu Val Lys Ser Gly Ala Phe Pro
245 250 255

Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn
260 265 270

Asn Asp

(2) INFORMATION FOR SEQ ID NO:5244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val
1 5 10 15

Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile
20 25 30

Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly
35 40 45

Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr
50 55 60

Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe
65 70 75 80

Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys
85 90 95

Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys
100 105 110

Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val
115 120 125

Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr
130 135 140

Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr
145 150 155 160

Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu
165 170 175

EP 0 786 519 A2

	Ala	Ile	Leu	Thr	Thr	Asp	Thr	Cys	Thr	Lys	His	Ile	Ala	Val	Ser	Leu	
				180					185					190			
5	Lys	Ile	Asp	Gly	Lys	Thr	Val	Thr	Ile	Gly	Gly	Ser	Thr	Lys	Gly	Ser	
			195					200					205				
	Gly	Met	Ile	His	Pro	Asn	Met	Ala	Thr	Met	Leu	Ala	Phe	Ile	Thr	Thr	
		210					215					220					
10	Asp	Ala	Ser	Ile	Glu	Ser	Asn	Thr	Leu	His	Gln	Leu	Leu	Lys	Ser	Ser	
	225					230					235					240	
	Thr	Asp	His	Thr	Phe	Asn	Met	Ile	Thr	Val	Asp	Gly	Asp	Thr	Ser	Thr	
					245					250					255		
15	Asn	Asp	Met	Val	Leu	Val	Met	Ala	Asn	His	Gln	Val	Glu	His	Gln	Ile	
			260						265					270			
	Leu	Ser	Gln	Asp	His	Pro	Gln	Trp	Glu	Thr	Phe	Val	Asp	Ala	Phe	Asn	
20			275					280					285				
	Phe	Val	Cys	Thr	Phe	Leu	Ala	Lys	Ala	Ile	Ala	Arg	Asp	Gly	Glu	Gly	
		290					295					300					
25	Ala	Thr	Lys	Leu	Ile	Ser	Val	Asn	Val	Ser	Gly	Ala	Lys	Ser	Ile	Ser	
	305					310					315					320	
	Asp	Ala	Arg	Lys	Ile	Gly	Lys	Thr	Ile	Val	Ser	Ser	Asn	Leu	Val	Lys	
				325						330					335		
30	Ser	Ala	Ile	Phe	Gly	Glu	Asp	Ala	Asn	Phe	Gly	Arg	Ile	Ile	Thr	Ala	
			340						345					350			
	Ile	Gly	Tyr	Ser	Gly	Cys	Glu	Ile	Asp	Pro	Asn	Cys	Thr	Tyr	Val	Gln	
35			355					360					365				
	Leu	Asn	Gln	Ile	Pro	Val	Val	Asp	Lys	Gly	Met	Ala	Val	Leu	Phe	Asp	
		370					375					380					
	Glu	Gln	Ala	Met	Ser	Asn	Thr	Leu	Thr	His	Glu	Asn	Val	Thr	Ile	Asp	
40	385					390					395					400	
	Val	Gln	Leu	Gly	Leu	Gly	Asn	Ala	Ala	Ala	Thr	Ala	Tyr	Gly	Cys	Asp	
				405					410						415		
45	Leu	Ser	Tyr	Asp	Tyr	Val	Arg	Ile	Asn	Ala	Ser	Tyr	Arg	Thr			
				420					425					430			

(2) INFORMATION FOR SEQ ID NO:5245:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 469 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

5	Asn	Pro	Ala	Leu	Thr	Val	Phe	Ala	Phe	Ile	Met	Ile	Ile	Ser	Ile	Leu	1	5	10	15
	Leu	Ala	Tyr	Val	Phe	Lys	Trp	Leu	Gly	Leu	Val	Asp	Asp	Val	Leu	Leu	20	25	30	
10	Met	Val	Ile	Ile	Ile	Ser	Thr	Ile	Ser	Leu	Gly	Val	Val	Val	Pro	Thr	35	40	45	
	Leu	Lys	Glu	Met	Asn	Ile	Met	Arg	Thr	Thr	Ile	Gly	Gln	Phe	Ile	Leu	50	55	60	
15	Leu	Val	Ala	Val	Leu	Ala	Asp	Leu	Val	Thr	Met	Ile	Leu	Leu	Thr	Val	65	70	75	80
	Tyr	Gly	Ala	Ile	Asn	Gly	Gln	Gly	Gly	Ser	Thr	Ile	Trp	Leu	Ile	Gly	85	90	95	
20	Ile	Leu	Val	Val	Phe	Thr	Ala	Ile	Ser	Tyr	Ile	Leu	Gly	Val	Gln	Phe	100	105	110	
25	Lys	Arg	Met	Ser	Phe	Leu	Gln	Lys	Leu	Met	Asp	Gly	Thr	Thr	Gln	Ile	115	120	125	
	Gly	Ile	Arg	Ala	Val	Phe	Ala	Leu	Ile	Ile	Leu	Leu	Val	Ala	Leu	Ala	130	135	140	
30	Glu	Gly	Val	Gly	Ala	Glu	Asn	Ile	Leu	Gly	Ala	Phe	Leu	Ala	Gly	Val	145	150	155	160
	Val	Val	Ser	Leu	Leu	Asn	Pro	Asp	Glu	Glu	Met	Val	Glu	Lys	Leu	Asp	165	170	175	
35	Ser	Phe	Gly	Tyr	Gly	Phe	Phe	Ile	Pro	Ile	Phe	Phe	Ile	Met	Xaa	Gly	180	185	190	
	Val	Asp	Leu	Asn	Ile	Pro	Ser	Leu	Ile	Lys	Glu	Pro	Lys	Leu	Leu	Ile	195	200	205	
40	Ile	Ile	Pro	Ile	Leu	Ile	Val	Ala	Phe	Ile	Ile	Ser	Lys	Leu	Ile	Pro	210	215	220	
45	Val	Met	Phe	Ile	Arg	Arg	Trp	Phe	Asp	Met	Lys	Thr	Thr	Ile	Ala	Ser	225	230	235	240
	Ala	Phe	Leu	Leu	Thr	Ser	Thr	Leu	Ser	Leu	Val	Ile	Ala	Ala	Ala	Lys	245	250	255	
50	Ile	Ser	Glu	Arg	Leu	Asn	Ala	Ile	Ser	Ala	Glu	Thr	Ser	Gly	Ile	Leu	260	265	270	
	Ile	Leu	Ser	Ala	Val	Ile	Thr	Cys	Val	Phe	Val	Pro	Ile	Ile	Phe	Lys	275	280	285	
55	Lys	Leu	Phe	Pro	Val	Pro	Asp	Glu	Phe	Asn	Arg	Lys	Ile	Glu	Val	Ser	290	295	300	

Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr
 305 310 315 320
 Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp
 5 325 330 335
 Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr
 340 345 350
 Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val
 10 355 360 365
 Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu
 370 375 380
 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr
 15 385 390 395 400
 Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser
 20 405 410 415
 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn
 420 425 430
 Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln
 25 435 440 445
 Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe
 450 455 460
 Gly Gly Asp Ile Ile
 30 465

(2) INFORMATION FOR SEQ ID NO:5246:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 414 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala
 1 5 10 15
 Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala
 50 20 25 30
 Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu
 35 40 45
 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu
 55 50 55 60

EP 0 786 519 A2

	Asn	Ile	Tyr	Arg	Arg	Leu	Thr	Asp	Ser	Glu	Glu	Gln	Leu	Lys	Gly	Glu	
	65					70					75					80	
5	Asn	Leu	Ile	Ile	Ser	Ala	Thr	Thr	Glu	Val	Phe	Lys	Pro	Ile	Met	Ser	
					85					90					95		
	Ser	Thr	Leu	Val	Thr	Ile	Ile	Val	Phe	Leu	Pro	Leu	Val	Phe	Val	Ser	
				100					105					110			
10	Gly	Ser	Val	Gly	Glu	Met	Phe	Arg	Pro	Phe	Ala	Leu	Ala	Ile	Ala	Phe	
			115					120					125				
	Ser	Leu	Leu	Ala	Ser	Leu	Leu	Val	Ser	Ile	Thr	Leu	Val	Pro	Ala	Leu	
		130					135					140					
15	Ala	Ala	Thr	Leu	Phe	Lys	Lys	Gly	Val	Lys	Arg	Arg	Asn	Lys	Gln	His	
	145					150					155					160	
	Gln	Glu	Gly	Leu	Gly	Val	Val	Ser	Thr	Thr	Tyr	Lys	Lys	Val	Leu	His	
				165						170					175		
20	Trp	Ser	Leu	Asn	His	Lys	Trp	Ile	Val	Ile	Ile	Leu	Ser	Thr	Leu	Ile	
				180					185					190			
	Leu	Val	Ala	Thr	Ile	Val	Phe	Gly	Gly	Pro	Arg	Leu	Gly	Thr	Ser	Phe	
25			195					200					205				
	Ile	Ser	Ala	Gly	Asp	Asp	Lys	Phe	Leu	Ala	Ile	Thr	Tyr	Thr	Pro	Lys	
		210				215						220					
30	Pro	Gly	Glu	Thr	Glu	Gln	Ala	Val	Leu	Asn	His	Ala	Lys	Asp	Val	Glu	
	225				230						235				240		
	Lys	Tyr	Leu	Lys	Gln	Lys	Lys	His	Val	Lys	Thr	Ile	Gln	Tyr	Ser	Val	
				245					250					255			
35	Gly	Gly	Ser	Ser	Pro	Val	Asp	Pro	Thr	Gly	Ser	Thr	Asn	Ser	Met	Ala	
				260				265					270				
	Ile	Met	Val	Glu	Tyr	Asp	Asn	Asp	Thr	Pro	Asn	Phe	Asp	Val	Glu	Ala	
		275				280						285					
40	Asp	Lys	Val	Ile	Lys	His	Ala	Asp	Gly	Phe	Lys	His	Pro	Gly	Glu	Trp	
	290					295						300					
	Lys	Asn	Gln	Asp	Leu	Gly	Thr	Gly	Ala	Gly	Asn	Lys	Ser	Val	Glu	Val	
45	305				310					315					320		
	Thr	Val	Lys	Gly	Pro	Ser	Met	Asp	Ala	Ile	Lys	Ser	Thr	Val	Lys	Asp	
				325					330					335			
	Ile	Glu	Gln	Lys	Met	Lys	Gln	Val	Lys	Gly	Leu	Ala	Asn	Val	Lys	Ser	
50			340					345					350				
	Asp	Leu	Ser	Gln	Thr	Tyr	Asp	Gln	Tyr	Glu	Ile	Lys	Val	Asp	Gln	Asn	
		355				360						365					
55	Lys	Ala	Ala	Glu	Asn	Gly	Ile	Ser	Ala	Ser	Gln	Leu	Ala	Met	His	Leu	
	370				375						380						

Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly
 385 390 395 400

Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala
 405 410

(2) INFORMATION FOR SEQ ID NO:5247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu
 1 5 10 15
 Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu
 20 25 30
 Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile
 35 40 45
 Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp
 50 55 60
 Ile Val Leu Phe Ile Leu Leu Gly Val Leu Leu Arg Ala Thr Val
 65 70 75 80
 Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys
 85 90 95
 His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile
 100 105 110
 Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro
 115 120 125
 Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro
 130 135 140
 Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu
 145 150 155 160
 Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe
 165 170 175
 Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn
 180 185 190
 Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu
 195 200 205

EP 0 786 519 A2

	Lys	Leu	Phe	Asn	Arg	Thr	Glu	Gln	Thr	Glu	Lys	His	Ile	Tyr	Asp	Asp	
	210						215					220					
5	Ser	Thr	Gln	Phe	Arg	Thr	Leu	Thr	Met	Arg	Ile	Leu	Arg	Ser	Ala	Phe	
	225					230					235					240	
	Leu	Ser	Gly	Leu	Met	Leu	Glu	Phe	Ile	Ser	Met	Leu	Gly	Ile	Gly	Leu	
					245					250					255		
10	Val	Ala	Leu	Glu	Ala	Thr	Leu	Ser	Leu	Val	Val	Phe	His	Asn	Ile	Asp	
				260					265					270			
	Phe	Lys	Thr	Ala	Ala	Ile	Ala	Ile	Ile	Leu	Ala	Pro	Glu	Phe	Tyr	Asn	
			275					280					285				
15	Ala	Ile	Lys	Asp	Leu	Gly	Gln	Ala	Phe	His	Thr	Gly	Lys	Gln	Ser	Glu	
	290					295						300					
	Gly	Ala	Ser	Asp	Val	Val	Phe	Glu	Phe	Leu	Glu	Gln	Pro	Asn	Tyr	Asn	
	305				310						315					320	
20	Asn	Glu	Phe	Leu	Leu	Lys	Tyr	Glu	Glu	Asn	Gln	Lys	Pro	Phe	Ile	Gln	
					325					330						335	
	Leu	Thr	Asp	Ile	Ser	Phe	Arg	Tyr	Asp	Asp	Ser	Asp	Arg	Leu	Val	Leu	
25				340					345					350			
	Asn	Asp	Leu	Asn	Leu	Glu	Ile	Phe	Lys	Gly	Asp	Gln	Ile	Ala	Leu	Val	
			355					360					365				
	Gly	Pro	Ser	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Thr	His	Leu	Ile	Ala	Gly	
30			370				375					380					
	Val	Tyr	Gln	Pro	Thr	Ile	Gly	Thr	Ile	Ser	Thr	Asn	Gln	Arg	Asp	Leu	
	385					390					395					400	
	Asn	Ile	Gly	Ile	Leu	Ser	Gln	Gln	Pro	Tyr	Ile	Phe	Ser	Ala	Ser	Ile	
35					405					410					415		
	Lys	Glu	Asn	Ile	Thr	Met	Phe	Lys	Asp	Ile	Glu	Asn	Asn	Thr	Ile	Glu	
			420						425					430			
40	Glu	Val	Leu	Asp	Glu	Val	Gly	Leu	Leu	Asp	Lys	Val	Gln	Ser	Phe	Thr	
			435				440						445				
	Lys	Gly	Ile	Asn	Thr	Ile	Ile	Gly	Glu	Gly	Gly	Glu	Met	Leu	Ser	Gly	
		450					455					460					
45	Gly	Gln	Met	Arg	Arg	Ile	Glu	Leu	Cys	Arg	Leu	Leu	Val	Met	Lys	Pro	
	465					470					475					480	
	Asp	Leu	Val	Ile	Phe	Asp	Glu	Pro	Ala	Thr	Gly	Leu	Asp	Ile	Gln	Thr	
				485						490					495		
50	Glu	His	Met	Ile	Gln	Asn	Val	Leu	Phe	Gln	His	Phe	Lys	Asp	Thr	Thr	
				500					505					510			
	Met	Ile	Val	Ile	Ala	His	Arg	Asp	Asn	Thr	Ile	Arg	His	Leu	Gln	Arg	
55			515					520					525				

Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile
530 535 540

Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu
545 550 555

(2) INFORMATION FOR SEQ ID NO:5248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe
1 5 10 15

Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu
20 25 30

Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met
35 40 45

Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly Met Ala Gly Ser Thr
50 55 60

Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr
65 70 75 80

Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp
85 90 95

Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val
100 105 110

Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala
115 120 125

Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val
130 135 140

Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile
145 150 155 160

Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu
165 170 175

Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr
180 185 190

Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly Met Asp
195 200 205

Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe
 210 215 220
 Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val
 225 230 235 240
 Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly
 245 250 255
 Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu
 260 265 270
 Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala
 275 280 285
 Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr
 290 295 300
 Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn
 305 310 315 320
 Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr
 325 330 335
 Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn
 340 345 350
 Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg
 355 360 365
 Leu Ala Thr Thr His Pro Ala Asn Thr Ile Met Ser Asn Ile Ile Asn
 370 375 380
 Gln Ile Asn Gln Ile Met Gln Tyr Lys
 385 390

(2) INFORMATION FOR SEQ ID NO:5249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu
 1 5 10 15
 Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val
 20 25 30
 Gly Thr Leu Ile Gly Phe Gly Leu Leu Ser Ser Lys Glu Ala Asp Ala
 35 40 45

EP 0 786 519 A2

	Ser	Glu	Asn	Ser	Val	Thr	Gln	Ser	Asp	Ser	Ala	Ser	Asn	Glu	Ser	Lys	
	50						55					60					
5	Ser	Asn	Asp	Ser	Ser	Ser	Val	Ser	Ala	Ala	Pro	Lys	Thr	Asp	Asp	Thr	
	65					70					75					80	
	Asn	Val	Ser	Asp	Thr	Lys	Thr	Ser	Ser	Asn	Thr	Asn	Asn	Gly	Glu	Thr	
					85					90					95		
10	Ser	Val	Ala	Gln	Asn	Pro	Ala	Gln	Gln	Glu	Thr	Thr	Gln	Ser	Ser	Ser	
				100					105					110			
	Thr	Asn	Ala	Thr	Thr	Glu	Glu	Thr	Pro	Val	Thr	Gly	Glu	Ala	Thr	Thr	
			115					120					125				
15	Thr	Thr	Thr	Asn	Gln	Ala	Asn	Thr	Pro	Ala	Thr	Thr	Gln	Ser	Ser	Asn	
		130					135					140					
	Thr	Asn	Ala	Glu	Glu	Leu	Val	Asn	Gln	Thr	Ser	Asn	Glu	Thr	Thr	Ser	
	145					150					155					160	
20	Asn	Asp	Thr	Asn	Thr	Val	Ser	Ser	Val	Asn	Ser	Pro	Gln	Asn	Ser	Thr	
					165					170					175		
	Asn	Ala	Glu	Asn	Val	Ser	Thr	Thr	Gln	Asp	Thr	Ser	Thr	Glu	Ala	Thr	
25				180					185					190			
	Pro	Ser	Asn	Asn	Glu	Ser	Ala	Pro	Gln	Ser	Thr	Asp	Ala	Ser	Asn	Lys	
			195					200					205				
30	Asp	Val	Val	Asn	Gln	Ala	Val	Asn	Thr	Ser	Ala	Pro	Arg	Met	Arg	Ala	
		210					215					220					
	Phe	Ser	Leu	Ala	Ala	Val	Ala	Ala	Asp	Ala	Pro	Val	Ala	Gly	Thr	Asp	
	225					230				235						240	
35	Ile	Thr	Asn	Gln	Leu	Thr	Asn	Val	Thr	Val	Gly	Ile	Asp	Ser	Gly	Thr	
				245						250					255		
	Thr	Val	Tyr	Pro	His	Gln	Ala	Gly	Tyr	Val	Lys	Leu	Asn	Tyr	Gly	Phe	
				260					265					270			
40	Ser	Val	Pro	Asn	Ser	Ala	Val	Lys	Gly	Asp	Thr	Phe	Lys	Ile	Thr	Val	
			275					280					285				
	Pro	Lys	Glu	Leu	Asn	Leu	Asn	Gly	Val	Thr	Ser	Thr	Ala	Lys	Val	Pro	
		290					295					300					
45	Pro	Ile	Met	Ala	Gly	Asp	Gln	Val	Leu	Ala	Asn	Gly	Val	Ile	Asp	Ser	
	305					310					315					320	
	Asp	Gly	Asn	Val	Ile	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asn	Thr	Lys	Asp	
					325					330					335		
50	Asp	Val	Lys	Ala	Thr	Leu	Thr	Met	Pro	Ala	Tyr	Ile	Asp	Pro	Glu	Asn	
				340					345					350			
55	Val	Lys	Lys	Thr	Gly	Asn	Val	Thr	Leu	Ala	Thr	Gly	Ile	Gly	Ser	Thr	
			355					360					365				

EP 0 786 519 A2

	Thr	Ala	Asn	Lys	Thr	Val	Leu	Val	Asp	Tyr	Glu	Lys	Tyr	Gly	Lys	Phe	
	370						375					380					
5	Tyr	Asn	Leu	Ser	Ile	Lys	Gly	Thr	Ile	Asp	Gln	Ile	Asp	Lys	Thr	Asn	
	385					390					395					400	
	Asn	Thr	Tyr	Arg	Gln	Thr	Ile	Tyr	Val	Asn	Pro	Ser	Gly	Asp	Asn	Val	
					405					410					415		
10	Ile	Ala	Pro	Val	Leu	Thr	Gly	Asn	Leu	Lys	Pro	Asn	Thr	Asp	Ser	Asn	
				420					425					430			
	Ala	Leu	Ile	Asp	Gln	Gln	Asn	Thr	Ser	Ile	Lys	Val	Tyr	Lys	Val	Asp	
			435					440						445			
15	Asn	Ala	Ala	Asp	Leu	Ser	Glu	Ser	Tyr	Phe	Val	Asn	Pro	Glu	Asn	Phe	
			450				455					460					
	Glu	Asp	Val	Thr	Asn	Ser	Val	Asn	Ile	Thr	Phe	Pro	Asn	Pro	Asn	Gln	
	465					470					475					480	
20	Tyr	Lys	Val	Glu	Phe	Asn	Thr	Pro	Asp	Asp	Gln	Ile	Thr	Thr	Pro	Tyr	
					485					490					495		
	Ile	Val	Val	Val	Asn	Gly	His	Ile	Asp	Pro	Asn	Ser	Lys	Gly	Asp	Leu	
25					500				505					510			
	Ala	Leu	Arg	Ser	Thr	Leu	Tyr	Gly	Tyr	Asn	Ser	Asn	Ile	Ile	Trp	Arg	
			515					520						525			
30	Ser	Met	Ser	Trp	Asp	Asn	Glu	Val	Ala	Phe	Asn	Asn	Gly	Ser	Gly	Ser	
		530					535					540					
	Gly	Asp	Gly	Ile	Asp	Lys	Pro	Val	Val	Pro	Glu	Gln	Pro	Asp	Glu	Pro	
	545					550					555					560	
35	Gly	Glu	Ile	Glu	Pro	Ile	Pro	Glu	Asp	Ser	Asp	Ser	Asp	Pro	Gly	Ser	
					565					570					575		
	Asp	Ser	Gly	Ser	Asp	Ser	Asn	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Gly	Ser	
				580					585					590			
40	Asp	Ser	Thr	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	
			595					600					605				
	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	
			610				615					620					
45	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Ser	Asp	Ser	
	625					630					635					640	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
					645				650						655		
50	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
					660				665					670			
55	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
			675				680						685				

EP 0 786 519 A2

	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
	690						695						700			
5	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
	705					710					715					720
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					725					730					735	
10	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					740					745					750	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					755					760					765	
15	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					770				775						780	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
20					785				790						795	800
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					805					810					815	
25	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					820					825					830	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Gly	Ser
					835					840					845	
30	Asp	Ser	Asp	Ser	Ser	Ser	Asp	Ser	Asp	Ser	Glu	Ser	Asp	Ser	Asn	Ser
							855						860			
	Asp	Ser	Glu	Ser	Val	Ser	Asn	Asn	Asn	Val	Val	Pro	Pro	Asn	Ser	Pro
35							870					875				880
	Lys	Asn	Gly	Thr	Asn	Ala	Ser	Asn	Lys	Asn	Glu	Ala	Lys	Asp	Ser	Lys
					885						890					895
40	Glu	Pro	Leu	Pro	Asp	Thr	Gly	Ser	Glu	Asp	Glu	Ala	Asn	Thr	Ser	Leu
					900					905					910	
	Ile	Trp	Gly	Leu	Leu	Ala	Ser	Ile	Gly	Ser	Leu	Leu	Leu	Phe	Arg	Arg
					915				920						925	
45	Lys	Lys	Glu	Asn	Lys	Asp	Lys	Lys								
					930			935								

(2) INFORMATION FOR SEQ ID NO:5250:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 194 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

5 Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala
 1 5 10 15
 Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro
 20 25 30
 10 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu
 35 40 45
 Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys
 50 55 60
 15 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys
 65 70 75 80
 Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr
 85 90 95
 20 Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn
 100 105 110
 Leu Lys His Lys Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys
 115 120 125
 25 Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys
 130 135 140
 Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala
 145 150 155 160
 Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln
 165 170 175
 35 Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys
 180 185 190
 Ile Leu

(2) INFORMATION FOR SEQ ID NO:5251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

55 Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp
 1 5 10 15

Val Thr Asp Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser
 20 25 30
 5 Leu Asn Phe Asn Asn Leu Asp Gln Ser Lys Asn Tyr Val Ile Lys Tyr
 35 40 45
 Glu Gly Tyr Tyr Asp Ser Asn Ala Ser Asn Leu Glu Phe Gln Thr His
 50 55 60
 10 Leu Phe Gly Tyr Tyr Asn Tyr Tyr Thr Ser Asn Leu Thr Trp Lys
 65 70 75 80
 Asn Gly Val Ala Phe Tyr Ser Asn Asn Ala Gln Gly Asp Gly Lys Asp
 85 90 95
 15 Lys Leu Lys Glu Pro Ile Ile Glu His Ser Thr Pro Ile Glu Leu Glu
 100 105 110
 Phe Lys Ser Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile
 115 120 125
 20 Glu Glu Ser Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala
 130 135 140
 Val Glu Gly Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu
 145 150 155 160
 25 Asp Ser Ile His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys
 165 170 175
 30 His His Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly
 180 185 190
 Gly Gln Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Asp Ser
 195 200 205
 35 Thr Lys Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu
 210 215 220
 Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu Val Asp
 225 230 235 240
 40 Glu Leu Pro Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile
 245 250 255
 Thr Glu Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn
 260 265 270
 45 Gly His Gly Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His
 275 280 285
 Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn Ser Gly
 290 295 300
 50 Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu
 305 310 315 320
 55 Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile
 325 330 335

His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys
 340 345 350
 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe
 5 355 360 365
 Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu Ile Ile
 370 375 380
 Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His
 10 385 390 395 400
 Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His
 405 410 415
 Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val
 15 420 425 430
 Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro
 435 440 445
 Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro
 20 450 455 460
 Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala
 25 465 470 475 480
 Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val
 485 490 495
 Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro
 30 500 505 510
 Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly
 515 520 525
 Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile
 35 530 535 540
 Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn His Lys Ala
 545 550 555

(2) INFORMATION FOR SEQ ID NO:5252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu
 1 5 10 15

EP 0 786 519 A2

Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val
20 25 30

5 Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn
35 40 45

Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp
50 55 60

10 Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu
65 70 75 80

Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro
85 90 95

15 Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile
100 105 110

Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys
115 120 125

20 Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr
130 135 140

25 Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu
145 150 155 160

Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg
165 170 175

30 Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys
180 185 190

Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln
195 200 205

35 Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys
210 215 220

Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser
225 230 235 240

40 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala
245 250

(2) INFORMATION FOR SEQ ID NO:5253:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr
 1 5 10 15
 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
 5 20 25 30
 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu
 35 40 45
 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser
 10 50 55 60
 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp
 65 70 75 80
 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser
 15 85 90 95
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys
 100 105 110
 Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys
 115 120 125
 Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser
 130 135 140
 Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln
 145 150 155 160
 Arg Lys Lys

(2) INFORMATION FOR SEQ ID NO:5254:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1027 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr
 1 5 10 15
 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
 20 25 30
 Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu
 35 40 45
 Gln Lys Thr Thr Thr Val Glu Glu Asn Gly Asn Ser Ala Thr Asp Asn
 50 55 60

EP 0 786 519 A2

	Lys Thr Ser Glu Thr Gln Thr Thr Ala Thr Asn Val Asn His Ile Glu	65	70	75	80
5	Glu Thr Gln Ser Tyr Asn Ala Thr Val Thr Glu Gln Pro Ser Asn Ala	85	90	95	
	Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Ala Val Gln Ala Pro Gln	100	105	110	
10	Thr Ala Gln Pro Ala Asn Ile Glu Thr Val Lys Glu Glu Val Val Lys	115	120	125	
	Glu Glu Ala Lys Pro Gln Val Lys Glu Thr Thr Gln Ser Gln Asp Asn	130	135	140	
15	Ser Gly Asp Gln Arg Gln Val Asp Leu Thr Pro Lys Lys Ala Thr Gln	145	150	155	160
	Asn Gln Val Ala Glu Thr Gln Val Glu Val Ala Gln Pro Arg Thr Ala	165	170	175	
20	Ser Glu Ser Lys Pro Arg Val Thr Arg Ser Ala Asp Val Ala Glu Ala	180	185	190	
	Lys Glu Ala Ser Asn Ala Lys Val Glu Thr Gly Thr Asp Val Thr Ser	195	200	205	
25	Lys Val Thr Val Glu Ile Gly Ser Ile Glu Gly His Asn Asn Thr Asn	210	215	220	
	Lys Val Glu Pro His Ala Gly Gln Arg Ala Val Leu Lys Tyr Lys Leu	225	230	235	240
30	Lys Phe Glu Asn Gly Leu His Gln Gly Asp Tyr Phe Asp Phe Thr Leu	245	250	255	
	Ser Asn Asn Val Asn Thr His Gly Val Ser Thr Ala Arg Lys Val Pro	260	265	270	
35	Glu Ile Lys Asn Gly Ser Val Val Met Ala Thr Gly Glu Val Leu Glu	275	280	285	
40	Gly Gly Lys Ile Arg Tyr Thr Phe Thr Asn Asp Ile Glu Asp Lys Val	290	295	300	
	Asp Val Thr Ala Glu Leu Glu Ile Asn Leu Phe Ile Asp Pro Lys Thr	305	310	315	320
45	Val Gln Thr Asn Gly Asn Gln Thr Ile Thr Ser Thr Leu Asn Glu Glu	325	330	335	
	Gln Thr Ser Lys Glu Leu Asp Val Lys Tyr Lys Asp Gly Ile Gly Asn	340	345	350	
50	Tyr Tyr Ala Asn Leu Asn Gly Ser Ile Glu Thr Phe Asn Lys Ala Asn	355	360	365	
	Asn Arg Phe Ser His Val Ala Phe Ile Lys Pro Asn Asn Gly Lys Thr	370	375	380	

EP 0 786 519 A2

	Thr	Ser	Val	Thr	Val	Thr	Gly	Thr	Leu	Met	Lys	Gly	Ser	Asn	Gln	Asn	385	390	395	400
5	Gly	Asn	Gln	Pro	Lys	Val	Arg	Ile	Phe	Glu	Tyr	Leu	Gly	Asn	Asn	Glu	405	410	415	
	Asp	Ile	Ala	Lys	Ser	Val	Tyr	Ala	Asn	Thr	Thr	Asp	Thr	Ser	Lys	Phe	420	425	430	
10	Lys	Glu	Val	Thr	Ser	Asn	Met	Ser	Gly	Asn	Leu	Asn	Leu	Gln	Asn	Asn	435	440	445	
	Gly	Ser	Tyr	Ser	Leu	Asn	Ile	Glu	Asn	Leu	Asp	Lys	Thr	Tyr	Val	Val	450	455	460	
15	His	Tyr	Asp	Gly	Glu	Tyr	Leu	Asn	Gly	Thr	Asp	Glu	Val	Asp	Phe	Arg	465	470	475	480
	Thr	Gln	Met	Val	Gly	His	Pro	Glu	Gln	Leu	Tyr	Lys	Tyr	Tyr	Tyr	Asp	485	490	495	
20	Arg	Gly	Tyr	Thr	Leu	Thr	Trp	Asp	Asn	Gly	Leu	Val	Leu	Tyr	Ser	Asn	500	505	510	
	Lys	Ala	Asn	Gly	Asn	Glu	Lys	Asn	Gly	Pro	Ile	Ile	Gln	Asn	Asn	Lys	515	520	525	
25	Phe	Glu	Tyr	Lys	Glu	Asp	Thr	Ile	Lys	Glu	Thr	Leu	Thr	Gly	Gln	Tyr	530	535	540	
	Asp	Lys	Asn	Leu	Val	Thr	Thr	Val	Glu	Glu	Glu	Tyr	Asp	Ser	Ser	Thr	545	550	555	560
30	Leu	Asp	Ile	Asp	Tyr	His	Thr	Ala	Ile	Asp	Gly	Gly	Gly	Gly	Tyr	Val	565	570	575	
	Asp	Gly	Tyr	Ile	Glu	Thr	Ile	Glu	Glu	Thr	Asp	Ser	Ser	Ala	Ile	Asp	580	585	590	
35	Ile	Asp	Tyr	His	Thr	Ala	Val	Asp	Ser	Glu	Ala	Gly	His	Val	Gly	Gly	595	600	605	
	Tyr	Thr	Glu	Ser	Ser	Glu	Glu	Ser	Asn	Pro	Ile	Asp	Phe	Glu	Glu	Ser	610	615	620	
40	Thr	His	Glu	Asn	Ser	Lys	His	His	Ala	Asp	Val	Val	Glu	Tyr	Glu	Glu	625	630	635	640
45	Asp	Thr	Asn	Pro	Gly	Gly	Gly	Gln	Val	Thr	Thr	Glu	Ser	Asn	Leu	Val	645	650	655	
	Glu	Phe	Asp	Glu	Glu	Ser	Thr	Lys	Gly	Ile	Val	Thr	Gly	Ala	Val	Ser	660	665	670	
50	Asp	His	Thr	Thr	Val	Glu	Asp	Thr	Lys	Glu	Tyr	Thr	Thr	Glu	Ser	Asn	675	680	685	
	Leu	Ile	Glu	Leu	Val	Asp	Glu	Leu	Pro	Glu	Glu	His	Gly	Gln	Ala	Gln	690	695	700	
55																				

EP 0 786 519 A2

	Gly	Pro	Val	Glu	Glu	Ile	Thr	Lys	Asn	Asn	His	His	Ile	Ser	His	Ser	705	710	715	720
5	Gly	Leu	Gly	Thr	Glu	Asn	Gly	His	Gly	Asn	Tyr	Asp	Val	Ile	Glu	Glu	725	730	735	
	Ile	Glu	Glu	Asn	Ser	His	Val	Asp	Ile	Lys	Ser	Glu	Leu	Gly	Tyr	Glu	740	745	750	
10	Gly	Gly	Gln	Asn	Ser	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Thr	Glu	Glu	755	760	765	
	Asp	Lys	Pro	Lys	Tyr	Glu	Gln	Gly	Gly	Asn	Ile	Val	Asp	Ile	Asp	Phe	770	775	780	
15	Asp	Ser	Val	Pro	Gln	Ile	His	Gly	Gln	Asn	Lys	Gly	Asn	Gln	Ser	Phe	785	790	795	800
	Glu	Glu	Asp	Thr	Glu	Lys	Asp	Lys	Pro	Lys	Tyr	Glu	His	Gly	Gly	Asn	805	810	815	
20	Ile	Ile	Asp	Ile	Asp	Phe	Asp	Ser	Val	Pro	His	Ile	His	Gly	Phe	Asn	820	825	830	
	Lys	His	Thr	Glu	Ile	Ile	Glu	Glu	Asp	Thr	Asn	Lys	Asp	Lys	Pro	Ser	835	840	845	
25	Tyr	Gln	Phe	Gly	Gly	His	Asn	Ser	Val	Asp	Phe	Glu	Glu	Asp	Thr	Leu	850	855	860	
30	Pro	Lys	Val	Ser	Gly	Gln	Asn	Glu	Gly	Gln	Gln	Thr	Ile	Glu	Glu	Asp	865	870	875	880
	Thr	Thr	Pro	Pro	Ile	Val	Pro	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	885	890	895	
35	Ser	Glu	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	900	905	910	
	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	Pro	Glu	915	920	925	
40	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ala	Glu	Pro	Gly	Lys	Pro	930	935	940	
	Val	Pro	Pro	Ala	Lys	Glu	Glu	Pro	Lys	Lys	Pro	Ser	Lys	Pro	Val	Glu	945	950	955	960
45	Gln	Gly	Lys	Val	Val	Thr	Pro	Val	Ile	Glu	Ile	Asn	Glu	Lys	Val	Lys	965	970	975	
	Ala	Val	Ala	Pro	Thr	Lys	Lys	Pro	Gln	Ser	Lys	Lys	Ser	Glu	Leu	Pro	980	985	990	
50	Glu	Thr	Gly	Gly	Glu	Glu	Ser	Thr	Asn	Lys	Gly	Met	Leu	Phe	Gly	Gly	995	1000	1005	
55	Leu	Phe	Ser	Ile	Leu	Gly	Leu	Ala	Leu	Leu	Arg	Arg	Asn	Lys	Lys	Asn	1010	1015	1020	

His Lys Ala
1025

(2) INFORMATION FOR SEQ ID NO:5255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

Gly	Glu	Lys	Cys	Met	Phe	Leu	Ala	Trp	Asn	Glu	Ile	Arg	Arg	Asn	Lys	1	5	10	15
Leu	Lys	Phe	Gly	Leu	Ile	Ile	Gly	Val	Leu	Thr	Met	Ile	Ser	Tyr	Leu	20	25	30	
Leu	Phe	Leu	Leu	Ser	Gly	Leu	Ala	Asn	Gly	Leu	Ile	Asn	Met	Asn	Lys	35	40	45	
Glu	Gly	Ile	Asp	Lys	Trp	Gln	Ala	Asp	Ala	Ile	Val	Leu	Asn	Lys	Asp	50	55	60	
Ala	Asn	Gln	Thr	Val	Gln	Gln	Ser	Val	Phe	Asn	Lys	Lys	Asp	Ile	Glu	65	70	75	80
Asn	Lys	Tyr	Lys	Lys	Gln	Ala	Thr	Leu	Lys	Gln	Thr	Gly	Glu	Ile	Val	85	90	95	
Ser	Asn	Gly	His	Gln	Lys	Asp	Asn	Val	Leu	Val	Phe	Gly	Val	Glu	Lys	100	105	110	
Ser	Ser	Phe	Leu	Val	Pro	Ser	Leu	Ile	Glu	Gly	His	Lys	Ala	Thr	Lys	115	120	125	
Asp	Asn	Glu	Val	Leu	Ala	Asp	Glu	Thr	Leu	Lys	Asn	Lys	Gly	Leu	Lys	130	135	140	
Leu	Gly	Asp	Thr	Leu	Ser	Leu	Ser	Xaa	Xaa	Arg						145	150	155	

Claims

- Computer readable medium having recorded thereon a nucleotide sequence of the Staphylococcus aureus genome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least 95 % identical to a nucleotide sequence depicted in SEQ ID NOS:1-5,191.
- Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements:

(a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191;

(b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and

(c) retrieval means for obtaining said homologous sequence(s) of step (b).

6. A method for identifying commercially important nucleic acid fragments of the *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

7. A method for identifying an expression modulating fragment of *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.

8. A protein-encoding nucleic acid fragment of the *Staphylococcus aureus* genome, wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.

9. The nucleic acid fragment of claim 8 which is DNA.

10. The nucleic acid fragment of claim 8 which is RNA.

11. A vector comprising a fragment of claim 8.

12. A fragment of the *Staphylococcus aureus* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.

13. A vector comprising a fragment of claim 12.

14. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome of claim 8.

15. A method for producing a polypeptide in a host cell comprising the steps of:

(a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and

(b) isolating said protein.

16. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome

of claim 12.

17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 30 to 300 bases 5' to any one of the fragments of the *Staphylococcus aureus* genome depicted in Seq ID Nos:1-5,191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.

18. A nucleic acid molecule being a homolog of any of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:

(a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-5,191 and Tables 2 and 3, including fragments thereof;

(b) identifying members of said library which contain sequences that hybridize to said target sequence;

(c) isolating the nucleic acid molecules from said members identified in step (b).

19. A DNA molecule being a homolog of any one of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:

(a) isolating mRNA, DNA, or cDNA produced from an organism;

(b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification;

(c) isolating said amplified sequences produced in step (b).

20. A polypeptide encoded by a fragment of claim 8.

21. An antibody which selectively binds to any one of the polypeptides of claim 20.

22. A kit for analyzing samples for the presence of polynucleotides derived from *Staphylococcus aureus*, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences, that will hybridize to a *staphylococcus aureus* polynucleotide under stringent hybridization conditions, and a suitable container.

23. A *Staphylococcus aureus* polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.

24. A *Staphylococcus aureus* polypeptide antigen comprising at least one epitope derived from a *Staphylococcus aureus* polypeptide selected from the group consisting of SEQ ID NOS:5,192 to 5,255.

25. A polypeptide comprising at least one epitope encoded by a *Staphylococcus aureus* amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4.

26. The polypeptide of claim 24 or 25, wherein said polypeptide is fixed to a solid phase.

27. A diagnostic kit for detecting *Staphylococcus aureus* infection comprising

(a) an isolated polypeptide antigen of claim 24, and

(b) means for detecting the binding of an antibody contained in a biological fluid to said antigen.

28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier.

29. A method of vaccinating an individual against *Staphylococcus aureus* infection comprising, administering to an individual the vaccine composition of claim 28.

Figure 1

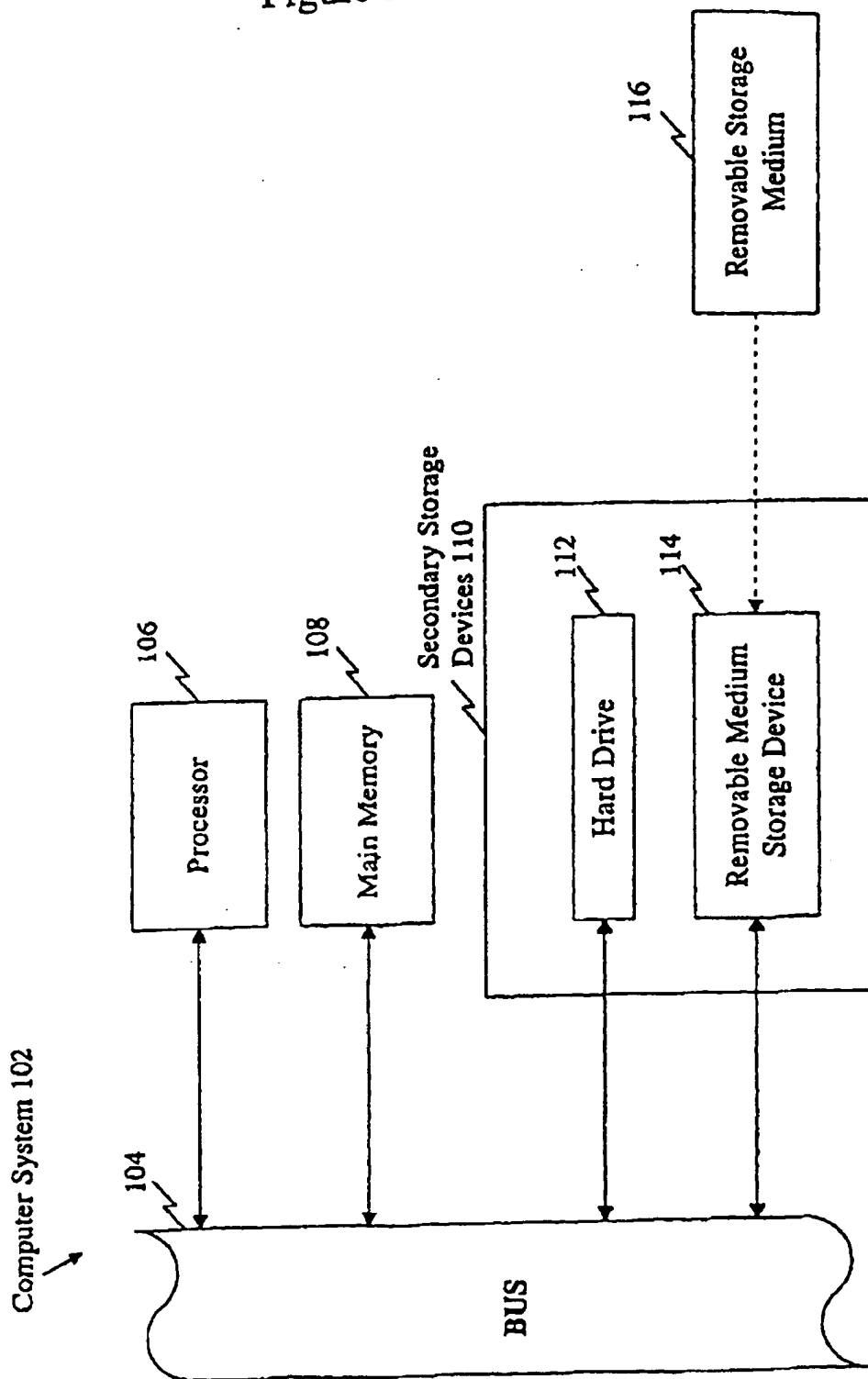
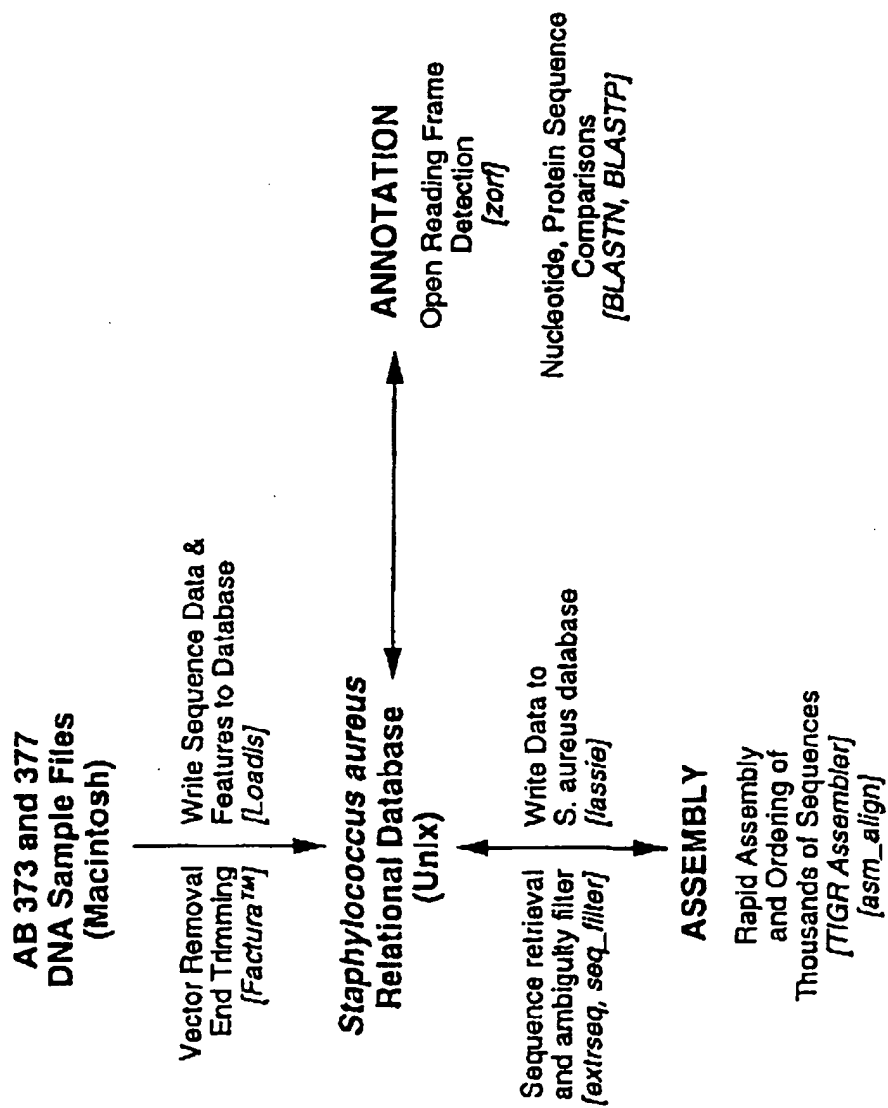


Figure 2





(12) **EUROPEAN PATENT APPLICATION**

(88) Date of publication A3:
14.10.1998 Bulletin 1998/42

(43) Date of publication A2:
30.07.1997 Bulletin 1997/31

(21) Application number: 97100117.7

(22) Date of filing: 07.01.1997

(51) Int Cl.⁶: **C12N 15/31**, G06F 17/30,
C12N 1/21, C12P 21/02,
C12Q 1/68, C07K 16/12,
C07K 14/31, A61K 39/085
// (C12N1/21, C12R1:445)

(84) Designated Contracting States:
AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC
NL PT SE
Designated Extension States:
AL LT LV RO SI

(30) Priority: 05.01.1996 US 9861

(71) Applicant: **HUMAN GENOME SCIENCES, INC.**
Rockville, MD 20850-3338 (US)

(72) Inventors:
• **Kunsch, Charles A.**
Gaithersburg, Maryland 20882 (US)

- **Choi, Gil H.**
Rockville, Maryland 20850 (US)
- **Barash, Steven C.**
Rockville, Maryland 20850 (US)
- **Dillon, Patrick J.**
Gaithersburg, Maryland 20879 (US)
- **Fannon, Michael R.**
Silver Spring, Maryland 20906 (US)
- **Rosen, Craig A.**
Laytonsville, Maryland 20882 (US)

(74) Representative: **VOSSIUS & PARTNER**
Postfach 86 07 67
81634 München (DE)

(54) **Staphylococcus aureus polynucleotides and sequences**

(57) The present invention provides polynucleotide sequences of the genome of *Staphylococcus aureus*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynu-

cleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number

which under Rule 45 of the European Patent Convention EP 97 10 0117 shall be considered, for the purposes of subsequent proceedings, as the European search report

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
X	"EMBL Database entry SA55RR, accession no. L36472, 17th November 1994, C.J. GREEN AND B.S. VOLD: "An unusual rRNA-tRNA gene organization in Staphylococcus aureus" EMBL NUCLEOTIDE SEQUENCE, XP002036821 ---	1-29	C12N15/31 G06F17/30 C12N1/21 C12P21/02 C12Q1/68 C07K16/12 C07K14/31 A61K39/085 //(C12N1/21, C12R1:445)
Y	BURKS C. ET AL.: "GenBank" NUCLEIC ACIDS RESEARCH., vol. 20, 1992, OXFORD GB, pages 2065-2069, XP002036820 * the whole document * ---	1-29	
Y	US 5 292 874 A (GEN-PROBE INC.) 8 March 1994 *whole document* ---	1-29	
Y	US 5 187 775 A (DNASTAR, INC.) 16 February 1993 *whole document* ---	1-29	
-/--			TECHNICAL FIELDS SEARCHED (Int.Cl.6)
			C12N G06F C12P C12Q C07K A61K
INCOMPLETE SEARCH			
<p>The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.</p> <p>Claims searched completely :</p> <p>Claims searched incompletely :</p> <p>Claims not searched :</p> <p>Reason for the limitation of the search:</p> <p>Article 52 (2)(d) EPC - Presentation of information - Claims 1-4 concerns computer readable media characterised solely by the information stored thereon. However, search has been carried out as far as possible.</p>			
Place of search		Date of completion of the search	Examiner
MUNICH		31 July 1998	Chakravarty, A
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document			

EPO FORM 1500 01.92 (P04C07)



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 97 10 0117

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (InCL.6)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
Y	FLEISCHMANN R D ET AL: "WHOLE-GENOME RANDOM SEQUENCING AND ASSEMBLY OF HAEMOPHILUS INFLUENZAE RD" SCIENCE, vol. 269, no. 5223, 28 July 1995, pages 496-498, 507 - 512, XP000517090 * the whole document *	1-29	
X	DATABASE EMBL European Bioinformatics Institute Accession No. U21636, 21 November 1995 ZHANG Q. ET AL.: XP002073245 * abstract *	1-29	
X	DATABASE PIR Accession No. S15269, 13 January 1995 KONTINEN V.P. ET AL.: XP002073246 * abstract *	1-29	TECHNICAL FIELDS SEARCHED (Incl. Cl. 6)
X	DATABASE GENESEQ DERWENT Accession No. Q24523, 10 November 1992 YAMAZAKI H. ET AL.: XP002073247 * abstract *	1-29	
X	DATABASE PIR Accession No. S54820, 8 July 1995 MAHE B. ET AL.: XP002073248 * abstract *	1-29	

	-/--		



**European Patent
Office**

PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 97 10 0117

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.CI.8)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
X	DATABASE EMBL European Bioinformatics Institute Accession No. X56347, 6 March 1991 HOCH J.A.: XP002073249 * abstract *	1-29	
X	DATABASE PIR Accession number: A53310, 8 September 1995 TANIMOTO K. ET AL.: XP002073250 * abstract *	1-29	
X	DATABASE EMBL European Bioinformatics Institute Accession number: U38418, 9 December 1995 CHUNG Y.J. ET AL.: XP002073251 * abstract *	1-29	TECHNICAL FIELDS SEARCHED (Int.CI.6)
A	DATABASE SWISSPROT Accession number: P33362, 1 February 1994 RICHTERICH P. ET AL.: XP002073252 * abstract *	1-29	
A	DATABASE PIR Accession number: S29683, 7 October 1994 GLASER P. ET AL.: XP002073253 * abstract *	1-29	
A	DATABASE PIR Accession number: S14508, 31 December 1991 SCHREIBER L. ET AL.: XP002073254 * abstract *	1-29	
	-/--		



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 97 10 0117

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
A	DATABASE PIR Accession number: Pc1253, 30 September 1993 STUCKA R. ET AL.: XP002073255 * abstract *	1-29	
A	--- DATABASE EMBL European Bioinformatics Institute Accession number: Z54398, 4 October 1995 ODELL. C ET AL.: XP002073256 * abstract *	1-29	
A	--- DATABASE EMBL European Bioinformatics Institute Accession number: U32788, 9 August 1995 FLEISCHMANN R.D. ET AL.: XP002073258 * abstract *	1-29	TECHNICAL FIELDS SEARCHED (Int.Cl.6)
A	--- DATABASE PIR Accession number: I64181, 18 August 1995 FLEISCHMANN ET AL.: XP002073259 * abstract *	1-29	
A	--- DATABASE EMBL European Bioinformatics Institute Accession number: U32744, 9 August 1995 FLEISCHMANN R.D. ET AL.: XP002073260 * abstract *	1-29	
	--- -/--		



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 97 10 0117

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.8)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
A	DATABASE PIR Accession number: P31728, 1 July 1993 CHANYANGAM M. ET AL.: XP002073261 * abstract * -----	1-29	
			TECHNICAL FIELDS SEARCHED (Int.Cl.8)

EPO FORM 1503 03.92 (P04C10)